



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C07K 14/00	A1	(11) International Publication Number: WO 98/42738 (43) International Publication Date: 1 October 1998 (01.10.98)
<div style="display: flex; justify-content: space-between;"> <div style="width: 45%;"> (21) International Application Number: PCT/US98/05311 (22) International Filing Date: 19 March 1998 (19.03.98) </div> <div style="width: 50%;"> <div style="display: flex; justify-content: space-between;"> <div style="width: 45%;"> (30) Priority Data: 60/041,281 21 March 1997 (21.03.97) US 60/041,276 21 March 1997 (21.03.97) US 60/042,344 21 March 1997 (21.03.97) US 60/041,277 21 March 1997 (21.03.97) US 60/048,355 30 May 1997 (30.05.97) US 60/048,096 30 May 1997 (30.05.97) US 60/048,351 30 May 1997 (30.05.97) US 60/048,154 30 May 1997 (30.05.97) US 60/048,160 30 May 1997 (30.05.97) US 60/048,069 30 May 1997 (30.05.97) US 60/048,131 30 May 1997 (30.05.97) US 60/048,186 30 May 1997 (30.05.97) US 60/048,095 30 May 1997 (30.05.97) US 60/048,187 30 May 1997 (30.05.97) US 60/048,099 30 May 1997 (30.05.97) US 60/050,937 30 May 1997 (30.05.97) US 60/048,352 30 May 1997 (30.05.97) US 60/048,135 30 May 1997 (30.05.97) US 60/048,188 30 May 1997 (30.05.97) US 60/048,094 30 May 1997 (30.05.97) US 60/048,350 30 May 1997 (30.05.97) US 60/054,804 5 August 1997 (05.08.97) US </div> <div style="width: 50%;"> (71) Applicant (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): YOUNG, Paul [US/US]; 122 Beckwith Street, Gaithersburg, MD 20878 (US). GREENE, John, M. [US/US]; 872 Diamond Avenue, Gaithersburg, MD 20878 (US). FERRIE, Ann, M. [US/US]; 13203 L Astoria Hill Court, Germantown, MD 20874 (US). RUBEN, Steven, M. [US/US]; 18528 Heritage Hills Drive, Olney, MD 20832 (US). ROSEN, Craig, A. [US/US]; 22400 Rolling Hill Road, Laytonsville, MD 20882 (US). DUAN, Roxanne [US/US]; 4541 Fairfield Drive, Bethesda, MD 20814 (US). HU, Jing-Shan [CN/US]; 1247 Lakeside Drive #3034, Sunnyvale, CA 94086 (US). FLORENCE, Kimberly, A. [US/US]; 12805 Atlantic Avenue, Rockville, MD 20851 (US). OLSEN, Henrik, S. [DK/US]; 182 Kendrick Place #24, Gaithersburg, MD 20878 (US). EBNER, Reinhard [DE/US]; 9906 Shelburne Terrace #316, Gaithersburg, MD 20878 (US). BREWER, Laurie, A. [US/US]; 14920 M. Nebo Road, Poolesville, MD 20837 (US). MOORE, Paul, A. [GB/US]; Apartment 104, 1908 Holly Ridge Drive, McLean, VA 22102 (US). SHI, Yanggu [CN/US]; 437 West Side Drive, Gaithersburg, MD 20878 (US). LAFLEUR, David, W. [US/US]; 1615 Q Street, N.W. #807, Washington, DC 20009 (US). NI, Jian [CN/US]; 5502 Manorfield Road, Rockville, MD 20853 (US). (74) Agents: BROOKES, Anders, A. et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 10850 (US). (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). </div> </div> </div> <div style="text-align: center; margin-top: 10px;"> Published <i>With international search report.</i> </div> </div>		
(54) Title: 87 HUMAN SECRETED PROTEINS (57) Abstract <p>The present invention relates to 87 novel human secreted proteins and isolated nucleic acids containing the coding regions of the genes encoding such proteins. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human secreted proteins.</p>		

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87 Human Secreted Proteins

Field of the Invention

This invention relates to newly identified polynucleotides and the polypeptides encoded by these polynucleotides, uses of such polynucleotides and polypeptides, and
5 their production.

Background of the Invention

Unlike bacterium, which exist as a single compartment surrounded by a membrane, human cells and other eucaryotes are subdivided by membranes into many functionally distinct compartments. Each membrane-bounded compartment, or
10 organelle, contains different proteins essential for the function of the organelle. The cell uses "sorting signals," which are amino acid motifs located within the protein, to target proteins to particular cellular organelles.

One type of sorting signal, called a signal sequence, a signal peptide, or a leader sequence, directs a class of proteins to an organelle called the endoplasmic reticulum
15 (ER). The ER separates the membrane-bounded proteins from all other types of proteins. Once localized to the ER, both groups of proteins can be further directed to another organelle called the Golgi apparatus. Here, the Golgi distributes the proteins to vesicles, including secretory vesicles, the cell membrane, lysosomes, and the other organelles.

20 Proteins targeted to the ER by a signal sequence can be released into the extracellular space as a secreted protein. For example, vesicles containing secreted proteins can fuse with the cell membrane and release their contents into the extracellular space - a process called exocytosis. Exocytosis can occur constitutively or after receipt of a triggering signal. In the latter case, the proteins are stored in secretory vesicles (or
25 secretory granules) until exocytosis is triggered. Similarly, proteins residing on the cell membrane can also be secreted into the extracellular space by proteolytic cleavage of a "linker" holding the protein to the membrane.

Despite the great progress made in recent years, only a small number of genes encoding human secreted proteins have been identified. These secreted proteins include
30 the commercially valuable human insulin, interferon, Factor VIII, human growth hormone, tissue plasminogen activator, and erythropoietin. Thus, in light of the pervasive role of secreted proteins in human physiology, a need exists for identifying and characterizing novel human secreted proteins and the genes that encode them. This knowledge will allow one to detect, to treat, and to prevent medical disorders by using
35 secreted proteins or the genes that encode them.

Summary of the Invention

The present invention relates to novel polynucleotides and the encoded polypeptides. Moreover, the present invention relates to vectors, host cells, antibodies, and recombinant methods for producing the polypeptides and polynucleotides. Also provided are diagnostic methods for detecting disorders related to the polypeptides, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying binding partners of the polypeptides.

Detailed Description

Definitions

The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide.

In the present invention, a "secreted" protein refers to those proteins capable of being directed to the ER, secretory vesicles, or the extracellular space as a result of a signal sequence, as well as those proteins released into the extracellular space without necessarily containing a signal sequence. If the secreted protein is released into the extracellular space, the secreted protein can undergo extracellular processing to produce a "mature" protein. Release into the extracellular space can occur by many mechanisms, including exocytosis and proteolytic cleavage.

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X or the cDNA contained within the clone deposited with the ATCC. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, with or without the signal sequence, the secreted protein coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having the translated amino acid sequence generated from the polynucleotide as broadly defined.

In the present invention, the full length sequence identified as SEQ ID NO:X was often generated by overlapping sequences contained in multiple clones (contig

analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X was deposited with the American Type Culture Collection ("ATCC"). As shown in Table 1, each clone is identified by a cDNA Clone ID (Identifier) and the ATCC Deposit Number. The ATCC is located at 10801 University Boulevard,
5 Manassas, Virginia 20110-2209, USA. The ATCC deposit was made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for purposes of patent procedure.

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained
10 in SEQ ID NO:X, the complement thereof, or the cDNA within the clone deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42° C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM sodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the
15 filters in 0.1x SSC at about 65°C.

Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages
20 of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 µg/ml salmon sperm blocking DNA; followed by washes at 50°C with 1XSSPE, 0.1% SDS. In addition, to achieve even
25 lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include
30 Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

Of course, a polynucleotide which hybridizes only to polyA+ sequences (such
35 as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a

complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone).

5 The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be
10 single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability
15 or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

 The polypeptide of the present invention can be composed of amino acids joined
20 to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs,
25 as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be
30 branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a
35 nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine,

formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990); Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

"SEQ ID NO:X" refers to a polynucleotide sequence while "SEQ ID NO:Y" refers to a polypeptide sequence, both sequences identified by an integer specified in Table 1.

"A polypeptide having biological activity" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention.)

Polynucleotides and Polypeptides of the Invention

FEATURES OF PROTEIN ENCODED BY GENE NO: 1

The translation product of this gene shares sequence homology with nucleolin, which is thought to be important in macromolecule binding, as well as some membrane proteins. Preferred polypeptide fragments comprise the amino acid sequence:
DPEAADSGEPQNKRTPLPEEEYVKEEIQENEEAVKKMLVEATREFEEVVVDES
(SEQ ID NO:239); QKLKRKAEEDPEAADSGEPQNKRTPLPEEEYVKEEIQENEE
AVKKMLVEATREFEEVVVDES (SEQ ID NO:240); KAMEKSSLTQHSWQSLKDR
YLKHLRGQEHKYL LGDAPVSPSSQKLKRKAEEDPEAADSGEPQNKRTPLPEE
EYVKEEIQENEEAVKKMLVEATREFEEVVVDESPPDFEIH (SEQ ID NO:241).
Also preferred are the polynucleotide fragments encoding these polypeptide fragments.

This gene maps to chromosome 16, and therefore can be used as a marker in linkage analysis for chromosome 16.

This gene is expressed primarily in brain and kidney and to a lesser extent in wide range of tissues.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cell-cell interaction or cell-matrix interaction. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes
10 for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and kidney, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., brain and other tissue of the nervous system, and kidney, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
15 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:125 as residues: Met-1 to Trp-10.

20 The tissue distribution and homology to nucleolin indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of diseases involving cell-cell interaction or cell-extracellular matrix interaction.

FEATURES OF PROTEIN ENCODED BY GENE NO: 2

25 The translation product of this gene shares sequence homology with a porcine zona pellucida protein ZPDS.1711. (See Accession No. R39356.) These two proteins have weak homology with *Drosophila* commissureless and metal homeostasis proteins which are thought to be important in controlling growth cone guidance across the CNS midline and protecting cells against reactive oxygen toxicity. thus, based on homology, it is likely that this gene also be involved in development. Preferred polypeptide
30 fragments comprise the amino acid sequence: LPSYDEAERTKAEATIPLVGRDEDF VGRDDFDADQLRIGNDGIFMLTFFMAFLFNWIGFFLSFCLTTSAAGRYGAISG FGLSLIKWILIVRFSTYFPGYFDGQYWLWWVFLVLGFLFLRGFINYAKVRKM PETFSNLPRTRVLFI (SEQ ID NO:242); and/or AGRYGAISGFGLSLIKWILIVRFS (SEQ ID NO:243). Also preferred are polynucleotide fragments encoding these
35 polypeptide fragments. This gene maps to chromosome 5, and therefore can be used in linkage analysis as a marker for chromosome 5.

This gene is expressed primarily in kidney, adrenal gland, brain and to a lesser extent in wide range of tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, fertilization control or tissue damages by metabolites or other toxic agents. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive and urosecretion system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., kidney, adrenal gland, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to zona pellucida protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for fertility control such as contraceptive development. The homology with metal homeostasis and commissureless genes indicates the gene's function in spermatozoa guidance and protection. It would also be useful for the treatment/diagnosis of tissue damages caused by toxic metabolites and other agents since the gene product is also expressed in urosecretive tissues.

25 **FEATURES OF PROTEIN ENCODED BY GENE NO: 3**

This gene is expressed primarily in liver and to a lesser extent in placenta. Preferred polypeptide fragments comprise the amino acid sequence: MKHLSAWNFT KLTLFLQLWEI FEGSVENCQTLTSYSKLQIKYTFSRGSTFYI (SEQ ID NO:244). Also preferred are polynucleotide fragments encoding these polypeptide fragments.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, digestive and nutrient transport/utilization disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive and

circulatory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., liver, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in liver and placenta indicates that the protein product is either an extracellular enzyme or a molecule carrier. Therefore, polynucleotides and polypeptides corresponding to this gene are useful for diagnosis/treatment of digestive and nutrient transport/utilization disorders, including malabsorption and malnutrition.

FEATURES OF PROTEIN ENCODED BY GENE NO: 4

This gene shares homology with the sap47 gene of *Drosophila melanogaster*, a gene which codes for a conserved neuronal protein associated with synaptic terminals. (See Mol. Brain Res. 32:45-54 (1995); see also, Accession No. 929571.) Thus, based on homology, the gene of the present invention also should be associated with synaptic terminals. Preferred polypeptide fragments comprise the amino acid sequence:

FSSDFRTSPWESRRVESKATSARCGLWGSGPRRRPASGMFRGLSSWLGLQQP
VAGGGQPNGDAPPEQPSETVAESAEEELQQAGDQELLHQA KDFGNYLFNFASA
ATKKITESVAETAQTIKKSVEEGKIDGIIDKTIIGDFQKEQKKFVEEQHTKKSEA
AVPPWVDTNDEETIQQILALSADKRNFLRDPPAGVQFNFDQMYPV ALV ML
(SEQ ID NO:245); MRFALVPKLVKEEVFWRNYFYRVSLIKQSAQLTALAAQQQA
AGKGGEEQ (SEQ ID NO:246); STSPGVSEFVSDAFDACNLNQEDLRKEMEQL
VLDKKQEETA VLEEDSADWEKELQQELQEYEVVTESEKR DENW DK (SEQ ID
NO:247); SPWESRRVESKATSARCGLWGSGPRRRPASGMFRGLSSWLGLQQ
PVAGGGQPNGDAPPEQPS (SEQ ID NO:248); PVAGGGQPNGDAPPEQPSETV
ESAEEELQQAGDQELLHQA KDFGNYLFNFASAATKKITESVAE (SEQ ID NO:
249); and/or FQKEQKKFVEEQHTKKSEAAVPPWVDTNDEETIQQILALSADKR
NFLRDPPAGVQFNFDQMYPV ALV ML (SEQ ID NO:250). Also preferred are
polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in kidney pyramids and to a lesser extent in lung and other tissues of various types. This gene fluxes calcium in human aortic smooth muscle cells, and therefore is involved in signal transduction.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, renal and nervous disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the kidney and/or nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., kidney, lung, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in kidney and lung and homology with sap47 indicates that the protein product has regulatory or direct functions in molecular exchange with body fluids and nervous system signaling. Polynucleotides and polypeptides corresponding to this gene are useful for treatment of disorders in kidney and nervous system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 5

The translation product of this gene shares sequence homology with the mouse Ly-9.2 antigen which is thought to be an important cell surface marker in lymphoids, myeloids and hematopoietic progenitors. (See Accession No. gil198932.) Preferred polypeptide fragments comprise the amino acid sequence: PFICVARNPVSRNFSPI LARKLCEGAA (SEQ ID NO:251); and/or KEDPANTVYSTVEIPKKMENPHSLT MPDTPRL (SEQ ID NO:252). Also preferred are polynucleotide fragments encoding these polypeptide fragments. Based on homology, it is likely that this gene is also a cell surface marker, involved in hematopoiesis.

This gene is expressed primarily in activated macrophages, monocytes and T-cells and to a lesser extent in spleen and bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune and hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., blood cells, and bone marrow, and cancerous and wounded

tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those
5 comprising a sequence shown in SEQ ID NO:129 as residues: Lys-26 to Tyr-33, Arg-44 to Ile-49, Ser-53 to Lys-71, Lys-86 to Pro-91.

The tissue distribution and homology to Ly-9.2 surface immunoglobulin family indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis of immune and hematopoietic disorders. Polypeptides and polynucleotides
10 corresponding to this gene are also be used as a marker for leukemia or a modulator of the functions of the cells of macrophage/monocyte or T-cell types.

FEATURES OF PROTEIN ENCODED BY GENE NO: 6

The translation product of this gene shares sequence homology with the
15 *Drosophila* glutactin gene which is thought to be important in cell-cell interaction or cell-extracellular matrix contact.

This gene is expressed primarily in colon tissue, aorta endothelial cells and to a lesser extent in skin, breast tissue and T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as
20 reagents for differential identification of these tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the gastrointestinal tract, vascular system or T-cell development. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these
25 tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive system, cardiovascular system, and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., colon, cardiovascular tissue, skin, mammary tissue, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine,
30 synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to glutactin indicates that polynucleotides
35 and polypeptides corresponding to this gene are useful for the development and maintenance of the integrity of the basal membrane in the gastrointestinal tract and

cardiovascular system. The expression in T-cells also indicate the protein may be involved in T-cell adhesion, cell-cell interaction and development.

FEATURES OF PROTEIN ENCODED BY GENE NO: 7

The translation product of this gene shares sequence homology with MURF4 protein, an ATPase homolog, which is thought to be important in ATP hydrolysis.

This gene is expressed primarily in breast tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, breast cancer and non-neoplastic breast diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the breast tissue, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., mammary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to MURF4 gene indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neoplastic or non-neoplastic breast diseases because ATPase like protein may be involved in changed metabolic states of the breast.

FEATURES OF PROTEIN ENCODED BY GENE NO: 8

This gene shares homology to the alcohol dehydrogenase gene. Preferred polypeptide fragments comprise the amino acid sequence: ASAVLLDLPNSG GEAQAKKLGNNCVFAPADVTSEKDVQ TALALAKGKFGRVDVAVNCAGIAVAS KTYNLKKGQTHLTLEDFQRVLDVNLMGTFNVIRLVAGEMGQNEPDQGGQRGVI INTASVAAFEGQVGQAAYSASKGGIVGMTLPIARDLAPIGIRVMTIAPGLFGTPL LTSLPEKVCNFLASQVPFPSRLGDP AEY AHLVQAIENPFLNGEVIRLDGAIRMQ P (SEQ ID NO:253); and/or SVAAFEGQVGQAAYSASKGGIVGMTLPIA (SEQ ID NO:254). Polynucleotides encoding these fragments are also encompassed by the invention. Other groups have also recently cloned this gene, recognizing its homology to alcohol dehydrogenase. (See Accession No. 1778355.) Moreover, a second group

recently cloned the mouse homologue of this gene. (See Accession No. 2078284.) They found that the mouse homologue binds to amyloid beta-peptide and mediates neurotoxicity in Alzheimer's disease, calling the protein ERAB. This gene maps to chromosome X, and therefore can be used in linkage analysis as a marker for chromosome X. Therefore, mutations in the translated product of this gene may be involved in Alzheimer's disease in humans, as well as other sex linked diseases. This gene can be used as a diagnostic marker for these diseases.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:132 as residues: Arg-45 to Ser-53.

FEATURES OF PROTEIN ENCODED BY GENE NO: 9

The translation product of this gene shares weak sequence homology with rat N-methyl-D-aspartate receptor subunit and other proline-rich proteins which are thought to be important in neurotransmission or protein-protein interaction.

This gene is expressed primarily in synovial hypoxia and to a lesser extent in ovary, senescent cells and brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, synovial hypoxia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the synovia and brain, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., synovial tissue, ovary and other reproductive tissue, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in synovial hypoxia and nerve tissues, and homology to N-methyl-D-aspartate receptor subunit and other proline-rich proteins indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of synovial hypoxia and other synovial disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 10

This gene is expressed primarily in prostate and to a lesser extent in placenta and ovary.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, male and female infertility, cancer, and other hyperproliferative disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system and neoplasia, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., prostate, placenta, ovary and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:134 as residues: Pro-17 to Met-23, Ala-30 to Trp-38, Ile-49 to Trp-54, Lys-68 to Gly-74, Thr-93 to Gly-99, Met-126 to Glu-132, Gly-173 to Ser-178, Lys-205 to Tyr-214.

The tissue distribution of this gene in the prostate, placenta and ovary indicates that this gene product is useful for treatment/diagnosis of male or female infertility, endocrine disorders, fetal deficiencies, ovarian failure, amenorrhea, ovarian cancer, benign prostate hyperplasia, prostate cancer, and other forms of cancer of the reproductive system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 11

This gene is expressed primarily in the thyroid and to a lesser extent in the pineal gland. This gene maps to chromosome 10, and therefore can be used as a marker in linkage analysis for chromosome 10. Preferred polypeptide fragments comprise the amino acid sequence: HPIEWAINAATLSQFY (SEQ ID NO:256); CWIKYCLTLMQN AQLSMQDNIG (SEQ ID NO:257); KVSYLRLDFEEARELFLLGQHYVF (SEQ ID NO:258); MERRCKMHKRXIAMLEPLTVDLNPQ (SEQ ID NO:259); and/or SHIV KKINNLNKSALKY YQLFLD (SEQ ID NO:260). Also preferred are polynucleotides encoding these polypeptide fragments.

Therefore, polynucleotides and polypeptides of the invention are useful as

reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune, thyroid and pineal gland disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes

5 for differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., thyroid and pineal gland, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another

10 tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:135 as residues: Ser-2 to Ser-8, Thr-38 to Arg-44.

15 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating/detecting immune disorders such as arthritis, asthma, immune deficiency diseases (e.g., AIDS), and leukemia, as well as treating/detecting thymus disorders (e.g., Graves Disease, lymphocytic thyroiditis, hyperthyroidism, and hypothyroidism), and treating/detecting pineal gland disorders

20 (e.g., circadian rhythm disturbances associated with shift work, jet lag, blindness, insomnia and old age).

FEATURES OF PROTEIN ENCODED BY GENE NO: 12

This gene is expressed primarily in lung and tonsils.

25 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, pulmonary or immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for

30 differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the pulmonary and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., pulmonary tissue, and tonsils, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or

35 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily

fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:136 as residues: Glu-28 to Gly-49.

The tissue distribution of this gene only in lung indicates that it could play a role in the treatment/detection of lung lymphoma or sarcoma formation, pulmonary edema and embolism, bronchitis and cystic fibrosis. Its expression in tonsils indicates a potential role in the treatment/detection of immune disorders such as arthritis, asthma, immune deficiency diseases (e.g., AIDS), and leukemia, in addition to the treatment/detection of tonsillitis.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 13**

This gene is expressed primarily in lymphoid, myeloid and erythroid cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hematopoietic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, myeloid cells, and bone marrow, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The predominant tissue distribution of this gene in hematopoietic cell types indicates that the gene could be important for the treatment or detection of immune or hematopoietic disorders including arthritis, asthma, immunodeficiency diseases and leukemia. Preferred embodiments of the present invention are polypeptide fragments comprising the amino acid sequence: FTHLSTCLLSLLLVRMSGFLLLARASPSI CALDSSCFVEYCSSYSSSCFLHQHFPSLLDHLCQ (SEQ ID NO:261); or FLLL ARASPSICALDSSCFVQEY (SEQ ID NO:262). Also preferred are polynucleotide fragments encoding these polypeptide fragments.

35 **FEATURES OF PROTEIN ENCODED BY GENE NO: 14**

This gene is homologous to the *Drosophila Regena* (*Rga*) gene. (See Accession No. 1658504.) This *Drosophila* gene is thought to be a homolog of the global negative

transcriptional regulator NOT2 (CDC36) from yeast, which modifies gene expression and suppresses position effect variegation. Preferred polypeptide fragments comprise the amino acid sequence: PDGRVTNIPQGMVTDQFGMIGLLTFIRAAETDPGMVHL
 5 ALGSDLTTLGLNLNS (SEQ ID NO:263); VHLALGSDLTTLGLNLNSPENLYP (SEQ ID NO:265); EDLLFYLYYMNGGDVLQLLAVELFNRDWRYHKEERVWI TR (SEQ ID NO:264); and/or HNEDFPALPGS (SEQ ID NO:266).

This gene is expressed primarily in placenta and to a lesser extent in infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as
 10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurodegenerative and developmental disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of
 15 disorders of the above tissues or cells, particularly of the neurological system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., placenta, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having
 20 such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:138 as residues: Leu-9 to Tyr-15, Asp-34 to Gln-46, Pro-51 to Asp-57, Gly-88 to Thr-104, Thr-123 to Ser-128.

25 The tissue distribution of this gene indicates that it could be used in the detection and/or treatment of neurological disorders such as such as Alzheimer's Disease, Parkinson's Disease, Huntington's Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, and panic disorder.

30 **FEATURES OF PROTEIN ENCODED BY GENE NO: 15**

This gene is expressed primarily in adrenal gland tumor and osteoclastoma.

Therefore, polynucleotides and polypeptides of the invention are useful as
 reagents for differential identification of the tissue(s) or cell type(s) present in a
 biological sample and for diagnosis of diseases and conditions, which include, but are
 35 not limited to, endocrine and bone disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for

differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine system and in bone, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., adrenal gland, and bone, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:139 as residues: Ile-52 to Trp-57.

- 10 The tissue distribution of this gene indicates that it may be involved in the treatment and/or detection of adrenal gland tumors, osteosarcomas, endocrine disorders and bone disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 16

- 15 The translation product of this gene shares sequence homology with the FK506 binding protein, a protein which plays an important role in immunosuppression. (See Accession No. M75099.) Specifically, a 12-kDa FK506-binding protein (FKBP-12) is a cytosolic receptor for the immunosuppressants FK506 and rapamycin. (See, Proc. Natl. Acad. Sci. 88: 6677-6681 (1991).) Thus, based on homology, it is likely that this gene also has immunosuppression activity. Preferred polypeptides comprise the amino acid sequence: GRIDTSLTRDPLVIELGQKQVIPGLEQSLLDMCVGEKRRRAIIPSH LAYGKRGFPSPVADAVVQYDVELIALIR (SEQ ID NO:267); and/or IHYTGSLV DGR IIDTS (SEQ ID NO:268). Also preferred are the polynucleotide fragments encoding these polypeptides.

- 25 This gene is expressed primarily in melanocytes.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer and other hyperproliferative disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and cancer, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., melanocytes, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to

the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:140 as residues: Ala-118 to Phe-124, Arg-178 to Lys-201.

- 5 The tissue distribution and homology to the FK506 binding proteins which are believed to a role in immunosuppression mediated by the immunosuppressant drugs rapamycin and cyclosporin, indicates that this gene could serve as a novel target for the identification of novel immunosuppressant drugs.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 17**

- The translation product of this gene shares sequence homology with the rat calcium-activated potassium channel rSK3, which is thought to be important in regulating vascular tone. (See Accession No. gil2564072, gil1575663, and
15 gil1575661.) Although homologous to these proteins, this gene contains an 18 amino acid insert, not previously identified in the homologs. Preferred polypeptide fragments comprise the amino acid sequence: CESPESPAQPSGSSLP AWYH (SEQ ID NO:269). Also preferred are the polynucleotide fragments encoding these polypeptides.

 This gene is expressed primarily in B-cells, frontal cortex and endothelial cells.

- Therefore, polynucleotides and polypeptides of the invention are useful as
20 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cardiovascular (hyper/hypotension, asthma, pulmonary edema, pneumonia, heart disease, restenosis, atherosclerosis, stroke, angina and thrombosis) and neurological disorders. Similarly, polypeptides and antibodies directed to these
25 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cardiovascular and nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, brain and other tissue of the nervous system, and endothelium,
30 and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID
35 NO:141 as residues: Glu-72 to Gly-82, His-90 to Val-95, Gln-168 to Lys-174, Val-202 to Ser-212.

The tissue distribution and homology to calcium-activated potassium channels indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of vascular disorders (hyper/hypotension, athesma, pulmonary edema, pneumonia, heart disease, restenosis, atherosclerosis, stoke, angina and thrombosis).

FEATURES OF PROTEIN ENCODED BY GENE NO: 18

This gene is expressed primarily in smooth muscle and to a lesser extent in brain (amygdala, corpus colosum, hippocampus).

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cardiovascular (hypertension, heart disease, athesma, pulmonary edema, restenosis, atherosclerosis, stoke, angina, thrombosis, and wound healing), and neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cardiovascular and neurological systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., smooth muscle, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:142 as residues: Lys-43 to Arg-49, Tyr-58 to Glu-65.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of cardiovascular disorders (hypertension, heart disease, athesma, pulmonary edema, restenosis, atherosclerosis, stoke, angina, thrombosis, and wound healing). Expression in brain indicates a role in the treatment and diagnosis of behavioral or neurological disorders, such as depression, schizophrenia, Alzheimer's disease, mania, dementia, paranoia, and addictive behavior.

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 19

This gene is expressed primarily in T-cells (Jurkats, resting, activated, and

anergic T-cells), endothelial cells, pineal gland, and to a lesser extent in a variety of other tissues and cell types. Preferred polypeptide fragments comprise the amino acid sequence: EEAGAGRRCSHGARPAGLGLNEGLGLGGDPDHTDTGSRSKQRINN WKESKHKVIMASASARGNQDKDAHFPFPPSKQSLLFCPKSKLHIHRAEISK (SEQ ID NO:270); and/or SKQRINNWKESKHKVIMASASAR (SEQ ID NO:271).
 5 Also preferred are the polynucleotide fragments encoding these polypeptides.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation, immune and cardiovascular disorders. Similarly,
 10 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, neurological and vascular systems, expression of this gene at significantly higher or
 15 lower levels may be routinely detected in certain tissues and cell types (e.g., T-cells and other blood cells, endothelial cells, and pineal gland, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily
 20 fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:143 as residues: Phe-71 to Arg-76, Pro-82 to His-87, Glu-103 to Ala-111.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of immune
 25 disorders including: leukemias, lymphomas, auto-immune, immuno-suppressive (e.g. transplantation) and immunodeficiencies (e.g. AIDS) and hematopoietic disorders. In addition, expression in the pineal gland might suggest a role in the diagnosis of specific brain tumors and treatment of neurological disorders. Endothelial cell expression might suggest a role in cardiovascular or respiratory/pulmonary disorders or infections
 30 (athesma, pulmonary edema, pneumonia).

FEATURES OF PROTEIN ENCODED BY GENE NO: 20

This gene is expressed primarily in brain and embryo and to a lesser extent in leukocytes. This gene maps to chromosome 15, and therefore can be used as a marker
 35 in linkage analysis to chromosome 15.

Therefore, polynucleotides and polypeptides of the invention are useful as

reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental and neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 144 as residues: Met-1 to Gly-8.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of immune disorders including: leukemias, lymphomas, auto-immune, immuno-suppressive (e.g. transplantation) and immunodeficiencies (e.g. AIDS) and hematopoietic disorders. The expression in the brain -- and in particular the fetal brain -- would suggest a possible role in the treatment and diagnosis of developmental and neurodegenerative diseases of the brain and nervous system (depression, schizophrenia, Alzheimer's disease, mania, dementia, paranoia, and addictive behavior).

FEATURES OF PROTEIN ENCODED BY GENE NO: 21

This gene is expressed primarily in brain, kidney, lung, liver, spleen, and a variety of leukocytes (especially T-cells) and to a lesser extent in a variety of other tissues and cell types.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, leukemias, lymphomas, autoimmune, immunosuppressive, and immunodeficiencies, hematopoietic disorders, as well as renal disorders, and neoplasms. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the renal, pulmonary, immune, and central nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.,

brain and other tissue of the nervous system, kidney, pulmonary tissue, liver, spleen, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of renal conditions, such as acute renal failure, kidney fibrosis, and kidney tubule regeneration.

The expression in leukocytes and other immune tissues indicates a role in immune disorders including: leukemias, lymphomas, auto-immune, immuno-suppressive (e.g. transplantation) and immunodeficiencies (e.g. AIDS) and hematopoietic disorders. The expression in the brain -- and in particular the fetal brain -- indicates a possible role in the treatment and diagnosis of developmental and neurodegenerative diseases of the brain and nervous system (depression, schizophrenia, Alzheimer's disease, mania, dementia, paranoia, and addictive behavior).

FEATURES OF PROTEIN ENCODED BY GENE NO: 22

This gene is expressed primarily in skin (fetal epithelium, keratinocytes and skin). This gene also maps to chromosome 19, and therefore can be used in linkage analysis as a marker for chromosome 19.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, skin cancers (e.g., melanomas), eczema, psoriasis or other disorders of the skin. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skin, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., skin and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:146 as residues: Pro-28 to Glu-35, Ser-39 to Phe-44, Ala-94 to Gln-99.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of skin cancers (e.g., melanomas), eczema, psoriasis or other disorders of the skin.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 23

This gene maps to chromosome 11. Another group recently isolated this same gene, associating the sequence to the region thought to harbor the gene involved in Multiple Endocrine Neoplasia Type 1, or MEN 1. (See Accession No. 2529721 and Genome Res. 7(7), 725-735 (1997), incorporated herein by reference in its entirety.)

10 Preferred polypeptide fragments comprise the amino acid sequence: LFHWACLNERA AQLPRNTAXAGYQCPSCNGPS (SEQ ID NO:272).

This gene is expressed primarily in epididymus, pineal gland, T-cells, as well as fetal epithelium, lung and kidney.

Therefore, polynucleotides and polypeptides of the invention are useful as
15 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune, metabolic mediated disorders, and MEN. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a
20 number of disorders of the above tissues or cells, particularly of the immune, renal, neurological and pulmonary systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., epididymus and other reproductive tissue, pineal gland, T-cells and other blood cells, epithelium, lung, and kidney, and cancerous and wounded tissues) or bodily fluids
25 (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
30 corresponding to this gene are useful for the treatment and diagnosis of developmental deficiencies or abnormalities as well as a host of different disorders which arise as a result of conditions in the indicated tissues or cell types. An area of particular interest is in the treatment and diagnosis of immune disorders including: leukemias, lymphomas, auto-immune, immuno-suppressive (e.g. transplantation) and immunodeficiencies (e.g.
35 AIDS) and hematopoietic disorders. The expression in the brain, and in particular the fetal brain, would suggest a possible role in the treatment and diagnosis of

developmental and neurodegenerative diseases of the brain and nervous system (depression, schizophrenia, Alzheimer's disease, mania, dementia, paranoia, and addictive behavior). Respiratory/pulmonary disorders, such as atesma, pulmonary edema are also potential therapeutic areas, as well as renal conditions such as acute renal failure, kidney fibrosis and kidney tubule regeneration. Moreover, this gene can be used in the treatment and/or detection of MEN I.

FEATURES OF PROTEIN ENCODED BY GENE NO: 24

This gene is expressed primarily in fetal spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, leukemia, lymphoma, AIDS, hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., spleen and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of immune disorders including: leukemias, lymphomas, auto-immune, immuno-suppressive (e.g. transplantation) and immunodeficiencies (e.g. AIDS) and hematopoietic disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 25

A closely related homolog of this gene was recently cloned by another group, calling the gene CDO, an oncogene-, serum-, and anchorage-regulated member of the Ig/fibronectin type III repeat family. (See Accession No. 2406628, and J. Cell Biol. 138(1): 203-213 (1997), herein incorporated by reference in its entirety.) Preferred polypeptide fragments comprise the amino acid sequence: FYIYYRPTDSDNDSYKK DMVEGDKYWHSISHLQPETS YDIKMQCFNEGGESEFSNVMICETKARKSSGQP GRLPPPTLAPPQPPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIVLIIVTFIPF CLWRAWKSKQKHTTDLGFRSALPPSCPYTMVPLGGLPGHQA VDSPTS VASVD

GPVLM (SEQ ID NO:273); or YIYYRPTDSDNDSYKKDMVEGDKYWSHSLQ
PETSYDIKMQCFNEGGESEFSNVMICETKARKS (SEQ ID NO:274).

This gene is expressed primarily in fetal lung and kidney, human embryo and osteoclastoma stromal cells and to a lesser extent in a variety of other tissues and cell
5 types.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental disorders and cancers, as well as pulmonary and renal
10 disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the respiratory/pulmonary, skeletal and renal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell
15 types (e.g., lung, kidney, embryonic tissue, and bone cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include
20 those comprising a sequence shown in SEQ ID NO:149 as residues: Thr-5 to Pro-18, Ala-76 to Thr-84.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of: osteoporosis, fracture, osteosarcoma, ossification, and osteonecrosis, as well as
25 respiratory/pulmonary disorders, such as atesma, pulmonary edema, and renal conditions such as acute renal failure, kidney fibrosis and kidney tubule regeneration.

FEATURES OF PROTEIN ENCODED BY GENE NO: 26

This gene is homologous to the HIV envelope glycoprotein. (See Accession
30 No. 2641463.) Preferred polypeptide fragments comprise the amino acid sequence: NVRALLHRMPEPPKINTAKFNNNKRKNLSL (SEQ ID NO:275).

This gene is expressed primarily in pineal gland and skin, and to a lesser extent in lung.

Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, neurological and behavior disorders: respiratory/pulmonary disorders, such as atesma, pulmonary edema; skin conditions such as eczema, psoriasis, acne and skin cancer, as well as AIDS. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential
 5 identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous and respiratory systems, as well as skin and AIDS, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, pineal gland, epidermis, and pulmonary tissue, and cancerous and wounded tissues) or bodily fluids
 10 (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:150 as residues: Gln-15 to Gln-20.

15 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of conditions which affect the above tissues, such as: skin cancer, eczema, psoriasis, acne, atesma, pulmonary edema, neuro-degenerative or developmental disorders such as Alzheimer's, depression, schizophrenia, dementia, and AIDS.

20

FEATURES OF PROTEIN ENCODED BY GENE NO: 27

Preferred polypeptide encoded by this gene comprise the following amino acid sequence: NTNQREALQYAKNFQPFALNHQKDIQVLMGSLVYLRQGIENSPYVHL
 LDANQWADICDIFTRDACALLGLSVESPLSVSFSAGCVALPALINIKAVIEQRQC
 25 TGVWNQKDELPIEVDLGKKCWYHSIFACPILRQQTTDNNPPMKLVCGHIISRD
 ALNKMFGSKLKCPYCPMEQSPGDAKQIFF (SEQ ID NO:276). Polynucleotides encoding such polypeptides are also provided as are complementary polynucleotides thereto.

This gene is expressed primarily in liver (adult and fetal) and spleen tissue, and
 30 to a lesser extent in placenta, T helper cells, kidney tumor, ovarian tumor, melanocytes and fetal heart.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
 35 not limited to, immune and developmental diseases and disorders and liver diseases such as liver cancer. Similarly, polypeptides and antibodies directed to these

polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, circulatory and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, placenta, blood cells, kidney, ovary and other reproductive tissue, melanocytes, and heart, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful for study, diagnosis and treatment of growth, hematopoietic and immune system disorders particularly related to the liver.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 28**

The translation product of this gene shares sequence homology with prostaglandin transporter which is thought to be important in metabolic and endocrine disorders. See, for example, Gastroenterology Oct:109(4):1274-1282 (1995). Preferred polypeptides encoded by this gene comprise the following amino acid sequence:

20 SYLSACFAGCNSTNLTGACLTTPAENATVVPKGKPSPGCQEAFLTFLCVMCI
CSLIGAMARHP (SEQ ID NO:277); and/or PSVILIRTVSPELKSYALGVLFLLRL
LGFIPPPLIFGAGIDSTCLFWSTFCGEQGACVLYDENVVYRYLYVSIAIALKSFAFI
(SEQ ID NO:278).

This gene is expressed primarily in hematopoietic and brain tissues.

25 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, metabolic, immune and endocrine diseases and disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing

30 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the metabolic, immune and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., endocrine tissue, hematopoietic tissue, and brain and other tissue of the nervous system, and cancerous and wounded

35 tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to

the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to prostaglandin (and anion) transporter indicates that polynucleotides and polypeptides corresponding to this gene are useful for
5 study, diagnosis and treatment of endocrine, metabolic, immune and kidney disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 29

This gene is expressed primarily in early stage human lung.

Therefore, polynucleotides and polypeptides of the invention are useful as
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, growth and respiratory disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of
15 the above tissues or cells, particularly of the developmental and respiratory systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., pulmonary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the
20 standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:153 as residues: Val-50 to Trp-55.

The tissue distribution indicates that the protein products of this gene are useful for study, diagnosis and treatment of respiratory and growth diseases and disorders.
25

FEATURES OF PROTEIN ENCODED BY GENE NO: 30

The translation product of this gene shares sequence homology with human DNA helicase which is thought to be important in accurate and complete DNA replication in creation of new cells. Preferred polypeptides encoded by this gene
30 comprise the following amino acid sequence: QSLFTRFVRVGVPTVDLDAQGRARA SLCXXYNWRYKNLGNLPHVQLLPEFSTANAGLLYDFQLINVEDFQGVGESEPN PYFYQNLGAEYVVALFMYMCLLGYPADKISILTTYNGQKHLIRDIINRRCGNN PLIGRPNKVTTVDRFQGGQNDYILLSVRTRA VGH LRDVRRLLV VAMSRAR (SEQ ID NO:279); and/or LVKEAKIIAMTCTHAALKRHDLVKLGFKYDNILMEE
35 AAQILEIETFIPLLLQNPQDGF SRLKRWIMIGDHHQLPPVI (SEQ ID NO:280).

This gene is expressed primarily in testes tumor and to a lesser extent in adrenal

gland tumor and placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancers and endocrine/growth disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine, developmental, and reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., testes and other reproductive tissue, adrenal gland, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to DNA helicase indicates that the protein products of this gene are useful for study, treatment, and diagnosis of many cancer types, including testicular cancer; as well as disorders involving endocrine function and normal growth and development.

FEATURES OF PROTEIN ENCODED BY GENE NO: 31

The translation product of this gene shares sequence homology with BID-apoptotic death gene (mouse), Genbank accession no. PID g1669514, which is thought to be important in programmed cell death.

This gene is expressed primarily in jurkat membrane bound polysomes and activated neutrophils and to a lesser extent in endothelial cells and human cerebellum.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancers and other proliferative disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, endothelium, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,

urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID
 5 NO:155 as residues: Glu-4 to Leu-11, Cys-28 to Arg-35, Gln-50 to His-66, Glu-73 to Gln-79, Gly-94 to Ser-100, Arg-114 to Asp-126, Pro-139 to Lys-146.

The tissue distribution and homology to BID-apoptotic death gene indicates that the protein products of this gene are useful for study of cell death, and treatment and diagnosis of proliferative disorders and cancers. Apoptosis - programmed cell death - is
 10 a physiological mechanism involved in the deletion of peripheral T lymphocytes of the immune system, and its dysregulation can lead to a number of different pathogenic processes. Diseases associated with increased cell survival, or the inhibition of apoptosis, include cancers (such as follicular lymphomas, carcinomas with p53 mutations, and hormone-dependent tumors, such as breast cancer, prostate cancer,
 15 Kaposi's sarcoma and ovarian cancer); autoimmune disorders (such as systemic lupus erythematosus and immune-related glomerulonephritis rheumatoid arthritis) and viral infections (such as herpes viruses, pox viruses and adenoviruses), inflammation; graft vs. host disease, acute graft rejection, and chronic graft rejection. Diseases associated with increased apoptosis include AIDS; neurodegenerative disorders (such as
 20 Alzheimer's disease, Parkinson's disease, Amyotrophic lateral sclerosis, Retinitis pigmentosa, Cerebellar degeneration); myelodysplastic syndromes (such as aplastic anemia), ischemic injury (such as that caused by myocardial infarction, stroke and reperfusion injury), toxin-induced liver disease (such as that caused by alcohol), septic shock, cachexia and anorexia. Thus, the invention provides a method of enhancing
 25 apoptosis in an individual by treating the individual with a polypeptide encoded by this gene.

FEATURES OF PROTEIN ENCODED BY GENE NO: 32

30 The translation product of this gene shares sequence homology with human fructose transporter which is thought to be important in normal metabolic function and activity.

This gene is expressed primarily in T-cell lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as
 35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, leukemia and other cancers, and metabolic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic, lymph and metabolic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., T-cells and other blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:156 as residues: Pro-22 to Gly-48, Ser-54 to Pro-61.

The tissue distribution indicates that the protein products of this gene are useful for study of mechanisms leading to cancer, treatment and diagnosis of cancerous and pre-cancerous conditions; as well as the study and treatment of various metabolic diseases and disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 33

This gene is expressed primarily in human meningioma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation and other disorders of the CNS. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the CNS and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., meningioma and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:157 as residues: Asn-23 to Pro-31.

The tissue distribution indicates that the protein products of this gene are useful for study, diagnosis and treatment of disorders of the CNS and inflammatory responses.

FEATURES OF PROTEIN ENCODED BY GENE NO: 34

This gene is expressed primarily in activated monocytes and wound healing tissues and to a lesser extent in fetal epithelium.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune and inflammatory disorders and wound healing and tissue repair dysfunctions. Similarly, polypeptides and antibodies directed to these polypeptides are
10 useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, epithelial and gastrointestinal systems, and healing wounds, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., monocytes and other blood cells, and epithelium, and
15 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:158 as residues:
20 Ala-28 to Ala-33, Gly-35 to Glu-45.

The tissue distribution indicates that the protein products of this gene are useful for diagnosis, study and treatment of immune and inflammatory disorders and wound healing dysfunctions.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 35

This gene is expressed primarily in human osteosarcoma and prostate cancer.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
30 not limited to, skeletal and neoplastic conditions such as bone and prostate cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and skeletal systems, expression of this gene at significantly higher or lower
35 levels may be routinely detected in certain tissues (e.g., bone, and prostate, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial

fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:159 as residues:

5 Ser-14 to Gly-22, Leu-37 to Gln-43.

The tissue distribution indicates that the protein products of this gene are useful for diagnosis and treatment of skeletal disorders and cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 36

10 This gene encodes a protein which is highly homologous to a protein called congenital heart disease protein 5, presumably implicated in congenital heart disease (see Genbank PID g2810996).

This gene is expressed primarily in Hodgkin's lymphoma, erythroleukemia cells, and TNF activated synovial fibroblasts, to a lesser extent in ovarian cancer,
15 cerebellum, spleen, fetal liver and placenta and finally to a lesser extent in various other mesenchymal tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
20 not limited to, cancer, immune, hematopoietic and cardiovascular disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, hematopoietic and cardiovascular systems, expression of this gene at significantly
25 higher or lower levels may be routinely detected in certain tissues and cell types (e.g., heart and other cardiovascular tissue, lymphoid tissue, blood cells, bone marrow, ovary and other reproductive tissue, brain and other tissue of the nervous system, spleen, liver, and mesenchymal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell
30 sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:160 as residues: Lys-41 to Met-49, Gln-54 to Glu-59, Glu-76 to Thr-88.

35 The homology of this gene and translation product to congenital heart disease protein 5 indicates a role for this protein in the diagnosis, prognosis and/or treatment of

heart disease or other cardiovascular related disorders. In addition, predominant expression in cells associated with the immune and hematopoietic system indicates a role for this protein in the treatment, diagnosis and/or prognosis of immune and autoimmune diseases, such as lupus, transplant rejection, allergic reactions, arthritis, asthma, immunodeficiency diseases, leukemia, AIDS, thymus disorders such as Graves Disease, lymphocytic thyroiditis, hyperthyroidism and hypothyroidism, graft versus host reaction, graft versus host disease, transplant rejection, myelogenous leukemia, bone marrow fibrosis, and myeloproliferative disease. The protein could also be used to enhance or protect proliferation, differentiation and functional activation of hematopoietic progenitor cells such as bone marrow cells, which could be useful for cancer patients undergoing chemotherapy or patients undergoing bone marrow transplantation. The protein may also be useful to increase the proliferation of peripheral blood leukocytes, which could be useful in the combat of a range of hematopoietic disorders including immunodeficiency diseases, leukemia, and septicemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 37

This gene is expressed primarily in ovarian cancer.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, urogenital neoplasias. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., ovary and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:161 as residues: Asn-22 to Asn-27.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis and treatment of ovarian and other tumors.

FEATURES OF PROTEIN ENCODED BY GENE NO: 38

The translation product of this gene shares sequence homology with zinc finger proteins.

This gene is expressed primarily in various fetal, cancer, and endothelial lines.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune and growth disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for
10 differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cardiovascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., fetal tissue, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
15 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful for study, diagnosis and treatment of immune and developmental conditions and cancer.

20

FEATURES OF PROTEIN ENCODED BY GENE NO: 39

This gene is expressed primarily in fetal, infant, and adult brain and to a lesser extent in other brain and endocrine organs and blastomas.

Therefore, polynucleotides and polypeptides of the invention are useful as
25 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, brain tumors and neurodegenerative conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of
30 disorders of the above tissues or cells, particularly of the nervous and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., brain and other tissue of the nervous system, endocrine tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an
35 individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the

disorder.

The tissue distribution indicates that the protein products of this gene are useful for the study, diagnosis and treatment of brain cancer and other neurological disorders.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 40

The translation product of this gene shares sequence homology with vesicular glycoproteins and lectins. Preferred polypeptides encoded by this gene comprise the following amino acid sequence: DTYPNEEKQQERVFPXXSAMVNNNGSLSYDHER DGRPTELGGCXAIVRNLHYDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGV
 10 RLPRGYFFGTSSITGDLSDNHDVISLKLFEFTVERTPEEE (SEQ ID NO:281);
 and/or LKREHSLSKPYQGVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQGA
 LWNRVPCFLRDWELQVHFQKHGQKKNLHGDGLAIWYT (SEQ ID NO:282).

This gene is expressed primarily in infant brain and to a lesser extent in various normal and transformed neural, endocrine, and immune organs.

15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological and neurodevelopmental conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological
 20 probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and hormonal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., brain and other tissue of the nervous system, endocrine tissue, and tissue and cells of the immune system, and cancerous and wounded tissues)
 25 or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:164 as residues: Pro-64 to Gly-71, Gly-
 30 94 to Leu-100, Thr-110 to Pro-116, Thr-135 to Arg-145, Glu-164 to Glu-171, Asp-204 to Asp-211, Arg-253 to His-261, Asn-312 to Tyr-323.

The tissue distribution indicates that the protein products of this gene are useful for the study, diagnosis and treatment of mental retardation and other neurological disorders and neoplasias.

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 41

This gene displays homology to the glycosyltransferase family, which catalyze the addition of sialic acids to carbohydrate groups which are present on glycoproteins.

This gene is expressed primarily in smooth muscle and to a lesser extent in
5 pineal gland, fetal liver, and infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, gastrointestinal injury, inflammatory and neurodegenerative conditions.
10 Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., smooth muscle, pineal gland,
15 liver, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those
20 comprising a sequence shown in SEQ ID NO:165 as residues: Ser-12 to Trp-21, Arg-24 to Pro-32, Asp-73 to Lys-82, Lys-90 to Ala-97.

The tissue distribution indicates that the protein products of this gene are useful for the study, diagnosis and treatment of neurodegenerative and growth disorders and gastrointestinal repair.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 42

The translation product of this gene shares sequence similarity with metallothionein polypeptides. See, for example, Proc. Natl. Acad. Sci. U S A 1992 Jul 15;89(14):6333-6337. Metallothioneins are believed to inhibit neuronal survival among
30 other biological functions. Based on the sequence similarity (especially the conserved cysteine motifs characteristic of the metallothionein family) the translation product of this gene is expected to share certain biological activities with other members of the metallothionein polypeptide family. Preferred polypeptides encoded by this gene comprise the following amino acid sequence: PGTLQCSALHHDPGCANCSRFCRD
35 CSPPACQC (SEQ ID NO:283).

This gene is expressed exclusively in placenta and fetal liver.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hematopoietic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., placenta, liver, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to metallothionein indicates that the protein products of this gene are useful for diagnosis and treatment of immune and hematopoietic system disorders and neurological diseases, especially in fetal development.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 43

Preferred polypeptides encoded by this gene comprise the following amino acid sequence: FLYDVLMXHEAVMRTHQIQLPDPEFPS (SEQ ID NO:284).

This gene is expressed primarily in T-cells and synovial tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune system disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., synovial tissue, and T-cells and other blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful for treatment and diagnosis of disorders of the immune system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 44

- 5 The translation product of this gene shares sequence similarity with several methyltransferases (e.g., see Genbank gill065505).
- This gene is expressed primarily in ovary, thymus, infant adrenal gland, tissues of the nervous system and the hematopoietic tissue, and to a lesser extent in adipose tissue and many other tissues.
- 10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders of the reproductive system, the endocrine system, the hematopoietic system and the CNS. Similarly, polypeptides and antibodies directed to
- 15 these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, endocrine, CNS and reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., ovary and other reproductive tissue, thymus, adrenal gland,
- 20 brain and other tissue of the nervous system, hematopoietic tissue, and adipose tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the
- 25 disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:168 as residues: Ser-3 to Gly-12, Asp-19 to Arg-31, Tyr-70 to Tyr-77, Asn-130 to Lys-140, Pro-165 to Gln-170, Pro-192 to Lys-199, Leu-216 to Glu-227, Glu-254 to Phe-281.
- The tissue distribution and homology to methyltransferase indicates that the
- 30 protein products of this gene are useful for diagnosis and treatment of disorders of the CNS, the hematopoietic system and reproductive organs and tissues. For example, the abundant expression in the ovary may indicate that the gene product can be used as a hormone with either systemic or reproductive functions; as growth factors for germ cell maintenance and in vitro culture; as a fertility control agent; remedy for sexual
- 35 dysfunction or sex development disorders; diagnostics/treatment for ovarian tumors, such as serous adenocarcinoma, dysgerminoma, embryonal carcinoma,

choriocarcinoma, teratoma, etc; The expression in thymus may indicate its utilities in T-cell development and thus its applications in immune related medical conditions, such as infection, allergy, immune deficiency, tissue/organ transplantation, etc.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 45

The translation product of this gene shares sequence homology with cytochrome C oxidase which is thought to be important in metabolic function of cells. This gene has now recently been published as estrogen response gene. See Genbank accession no. AB007618 and Mol. Cell. Biol. 18 (1), 442-449 (1998). See also J Immunol. Mar 1:154(5): 2384-2392 (1995), where the mouse homologue was published and implicated in siliocis.

This gene is expressed primarily in adipose tissue, kidney and fetal brain and to a lesser extent in several other tissues and organs.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, metabolic diseases involving especially adipose tissue, brain and kidney. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the CNS and vascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., adipose tissue, kidney, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:169 as residues: Thr-5 to Ser-14.

The tissue distribution and homology to cytochrome C oxidase, estrogen response gene product and siliocis related gene product indicates that the protein products of this gene are useful for diagnosis and treatment of metabolic disorders in the CNS, adipose tissue and kidney, particularly siliocis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 46

The translation product of this gene shares sequence homology with reticulocalbin. See, for example, J. Biochem. 117 (5), 1113-1119 (1995). Based on the

sequence similarity, the translation product of this gene is expected to share certain biological activities with reticulocalbin, e.g., Ca^{++} binding activities. This gene product is sometimes hereinafter referred to as "Reticulocalbin-2".

5 This gene is expressed primarily in breast, endothelial cells, synovial, heart and smooth muscle cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the breast, vascular and skeletal/cardiac muscular system.

10 Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the breast, vascular and skeleto-muscular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g.,

15 mammary tissue, endothelial cells, synovial tissue, heart and other cardiovascular tissue, and smooth muscle, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an

20 individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:170 as residues: Gly-16 to Arg-32, Ala-42 to Asn-50, Glu-66 to Gln-76, Arg-85 to Gly-94, Thr-108 to Asp-115, Trp-121 to Gly-130. Leu-137 to His-144, Glu-155 to Lys-161, Asp-175 to Ser-180, Glu-209 to Gly-217, Glu-232 to Glu-237, Thr-243 to Asp-261, Glu-287 to Arg-295.

25 The tissue distribution indicates that the protein products of this gene are useful for diagnosis and treatment of diseases of the vascular and skeletal/cardiac muscular system. The homology of the gene with reticulocalbin indicates its biological function in regulating calcium store, a particularly important function in muscular cell types. The gene expression in the heart may indicate its utilities in diagnosis and remedy in heart

30 failure, ischemic heart diseases, cardiomyopathy, hypertension, arrhythmia, etc. The abundant expression in the breast may indicate its applications in breast neoplasia and breast cancers, such as fibroadenoma, papillary carcinoma, ductal carcinoma, Paget's disease, medullary carcinoma, mucinous carcinoma, tubular carcinoma, secretory carcinoma and apocrine carcinoma; juvenile hypertrophy and gynecomastia, mastitis

35 and abscess, duct ectasia, fat necrosis and fibrocystic diseases, etc.

FEATURES OF PROTEIN ENCODED BY GENE NO: 47

The translation product of this gene shares weak sequence homology with H⁺-transporting ATP synthase which is thought to be important in cell metabolism or signal transduction.

5 This gene is expressed only in testis.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of some types of diseases and conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in
10 providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and hematopoietic tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., testes and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine,
15 synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

 Since only one out of about a million expressed sequence tag is found in testes
20 indicates that its expression is low and selectively in testes. Since some of the genes only expressed in testes are usually expressed in brain or in certain induced hematopoietic cells/tissues, it is speculated that this gene to be expressed in brain or hematopoietic cells/tissues and is useful for diagnosis and treatment of disorders these systems.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 48

 The translation product of this gene shares sequence homology with human polymeric immunoglobulin receptor (accession No.X73079) which is thought to be important in antibody recognition and immune defenses. In one embodiment,
30 polypeptides of the invention comprise the sequence GWYWCG (SEQ ID NO:285). Polynucleotides encoding these polypeptides are also encompassed by the invention.

 This gene is expressed primarily in placenta and to a lesser extent in corpus callosum and fetal liver and spleen.

 Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, disorders of the immune system, e.g. autoimmune diseases and immunodeficiency. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., placenta, liver, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:172 as residues: Tyr-37 to Cys-49, Gly-51 to Tyr-56, Lys-88 to Trp-93, Leu-130 to Glu-136.

The tissue distribution and homology to human polymeric immunoglobulin receptor indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of immune disorders, e.g. autoimmune diseases and immunodeficiencies.

FEATURES OF PROTEIN ENCODED BY GENE NO: 49

This gene is expressed in thymus.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune disorder. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., thymus and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of immune disorders, e.g. autoimmunity and immunodeficiency.

FEATURES OF PROTEIN ENCODED BY GENE NO: 50

Preferred polypeptide encoded by this gene comprise the following amino acid sequence: MKVGARIRVKMSVNKAHPVVSTHWRWPAEWPQMFLHLAQEP RTE
 5 VKSRPLGLAGFIRQDSKTRKPLEQETIMSAADTALWPYGHGNREHQENELQKY
 LQYKDMHLLDSGQSLGHTHTLQGSHNLTALNI (SEQ ID NO:286).

Polynucleotides encoding this polypeptide are also provided as are complementary polynucleotides thereto.

10 This gene is expressed primarily in adrenal gland, pituitary, T helper cells, and breast cells and to a lesser extent in a wide variety of tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of the some diseases and conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
 15 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., adrenal gland, pituitary, T-cells and other blood cells, and mammary tissue, and cancerous and wounded tissues) or bodily fluids
 20 (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:174 as residues: Gln-39 to Ser-47, Arg-57 to Glu-67,
 25 Tyr-82 to Gln-95.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of a wide range of disorders, such as immune and endocrine disorders.

30 FEATURES OF PROTEIN ENCODED BY GENE NO: 51

The translation product of this gene shares sequence homology with human Sop2p-like protein which is important in cytoskeleton structure. In one embodiment, polypeptides of the invention comprise the sequence SLHKNSVSQISVLSGGKAKCS
 35 QFCTTGMDGGMSIWDVKSLESALKDLKI (SEQ ID NO:287). Polynucleotides encoding this polypeptide are also encompassed by the invention. This gene maps to chromosome 7. Therefore, polynucleotides of the invention can be used in linkage

analysis as a marker for chromosome 7.

This gene is expressed primarily in immune and hematopoietic tissues/cells and to a lesser extent in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immunological and hematopoietic disorders and inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a
10 number of disorders of the above tissues or cells, particularly of the immune and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., immune and hematopoietic tissue/cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample
15 taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:175 as residues: Lys-49 to Gln-54, Ala-61 to Arg-66, Lys-82 to Lys-87, Glu-126 to Val-133, His-136 to Ile-141, Glu-175 to Ser-187, Asp-
20 286 to Leu-296, Ala-298 to Ser-310.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of immunological, hematopoietic, and inflammatory disorders, e.g, immunodeficiency, autoimmunity, inflammation.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 52

The translation product of this gene shares sequence homology with *Caenorhabditis elegans* R53.5 gene encoding a putative secreted protein without known function.

30 This gene is expressed primarily in endothelial cells, brain and several highly vascularized, and tumor tissues and to a lesser extent in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
35 not limited to, aberrant angiogenesis and tumorigenesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes

for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vascular and brain system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endothelial cells, brain and other tissue of the nervous system, and vascular tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:176 as residues: Thr-43 to Asn-60, Thr-106 to Phe-115, Asp-122 to Arg-133, Arg-186 to Asp-192, Leu-211 to Lys-216.

The tissue distribution and homology to a *C. elegans* secreted protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis or treatment of disorders in vascular or brain system, e.g. aberrant angiogenesis, ischemia, neurodegeneration, etc.

FEATURES OF PROTEIN ENCODED BY GENE NO: 53

In one embodiment, polypeptides of the invention comprise the sequence EASKSSHAGLDLFSVAACHRF (SEQ ID NO:288). Polynucleotides encoding this polypeptide are also encompassed by the invention.

This gene is expressed primarily in T-cells and to a lesser extent in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, lymphocytic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the lymphoid system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., T-cells and other blood cells, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:177 as residues: Pro-3 to Thr-8, Arg-37 to Asp-46.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis, treatment, and cure of lymphocytic disorders.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 54

The translation product of this gene shares sequence homology with secreted cartilage matrix protein, a major component of the extracellular matrix of nonarticular cartilage which is thought to be important in cartilage structure. In specific embodiments, polypeptides of the invention comprise the sequence: RCKKCTEGPI
 10 DLVFVIDGSKSLGEENFEVVKQF (SEQ ID NO:297); VTGIIDSLTISPKAARVGL
 LQYSTQVH (SEQ ID NO:290); TEFTLRNFNSAKDMKKAVAHEMKYM (SEQ ID
 NO:291); GKGSMTGLALKHMFERSFTQGEARPF (SEQ ID NO:292); STRVP
 RAAIVFTDGRAQDDVSEWASKAKANGITMYAVGVGKAIE (SEQ ID NO:293);
 15 EELQEIASEPTNKHLYAEDFSTMDEISEKLKKGICEALED (SEQ ID NO:294);
 TQRLEEMTQRM (SEQ ID NO:295); PQGCPEQLH (SEQ ID NO:296); and/or
 YMGKGSMTGLALKHMFERSFT (SEQ ID NO:289). Polynucleotides encoding these
 polypeptides are also encompassed by the invention.

This gene is expressed primarily in placenta, infant brain, prostate, fetal lung and to a lesser extent in endometrium and fetal tissues.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, abnormal placenta and pregnancy, disorder and injury in brain, prostate, and vasculature. Similarly, polypeptides and antibodies directed to these polypeptides
 25 are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproduction, neuronal, and vascular systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., placenta, brain and other tissue of the nervous system, prostate, lung and
 30 endometrium, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

35 The tissue distribution and homology to cartilage matrix protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis,

treatment, and cure of abnormalities in placenta and pregnancy, disorder and injury in brain, prostate, and vasculature.

FEATURES OF PROTEIN ENCODED BY GENE NO: 55

5 The translation product of this gene is the human ortholog of bovine and hamster CII-3, a succinate-ubiquinone oxidoreductase complex II membrane-intrinsic subunit, which is thought to be important in mitochondrial electron transport chain during metabolism. In specific embodiments, the polypeptides of the invention comprise MAALLLRHVGRHCLRAHFSPQLCIRNAVPLGTTAKEEMERFWNKNIG
10 SNRPLSPHITIYS (SEQ ID NO:298); VFPLMYHTWNGIRHLMWDLGKGLKIPQL YQSG (SEQ ID NO:299); MAALLLRHVGRHCLRAH (SEQ ID NO:300); VKSLCL GPALIHTAKFAL (SEQ ID NO:301); VFPLMYHTWNGIRHLMWDLGKGL (SEQ ID NO:302).

 This gene is expressed in 8-week old early stage human.

15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, metabolism disorder. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential
20 identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the [insert system where a related disease state is likely, e.g., immune], expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or
25 cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

 The tissue distribution and homology to indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis, treatment, and cure of
30 metabolism disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 56

 This gene is expressed primarily in umbilical vein endothelial cells, human ovarian tumor cells, human meningioma cells, and human Jurkat membrane bound
35 polysomes. In specific embodiments, polypeptides of the invention comprise the amino acid sequence: RVWDVRPFAPKERCVKIFQGNV (SEQ ID NO:303); HNFENLL

RCSWSPDGSKIAAGSADRFVYV (SEQ ID NO:304); and/or WDTTSRRILYKLPG HAGSINEVAFHPDEPI (SEQ ID NO:305). Polynucleotides encoding these polypeptides are also encompassed by the invention.

Therefore, polynucleotides and polypeptides of the invention are useful as
 5 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation, immune and cardiovascular disorders and urogenital neoplasias. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these
 10 tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, neurological, urogenital, reproductive system and vascular systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, cells, endothelial cells, ovary and other reproductive tissue, meningima, and cancerous and wounded tissues) or
 15 bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:143 as residues: Phe-71 to Arg-76, Pro-
 20 82 to His-87, Glu-103 to Ala-111.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of immune disorders including: leukemias, lymphomas, auto-immune, immuno-suppressive (e.g. transplantation) and immunodeficiencies (e.g. AIDS) and hematopoietic disorders. In
 25 addition, expression in ovarian tumor cells suggests that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis, and treatment of ovarian tumors, and other tumors and neoplasias. Further, endothelial cell expression suggests a role in cardiovascular or respiratory/pulmonary disorders or infections (athsma, pulmonary edema, pneumonia).
 30

FEATURES OF PROTEIN ENCODED BY GENE NO: 57

The translation product of this gene shares sequence homology with type I collagen. In specific embodiments, the polypeptides of the invention comprise the
 35 sequence: GRIPAPAPSVPAGPDSR (SEQ ID NO:309); VRGRTVLRPGLDAEPE LSPE (SEQ ID NO:306); EQRVLERKCLKKERKKEERQ (SEQ ID NO:307); ARRS

AELAWDYLCRWAQKHKNWRFQKTRQTWLLHMYDSDKVPDEHFSTLLAYLE
GLQGR (SEQ ID NO:255); and/or RLREAGLVAQHPP (SEQ ID NO:308).

Polynucleotides encoding these polypeptides are also encompassed by the invention.

5 This gene is expressed primarily in epididymus, prostate cell line (LNCAP),
and pituitary gland; and to a lesser extent in many other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
not limited to, abnormalities of the epididymus, prostate (especially prostate cancer),
10 and pituitary gland. Similarly, polypeptides and antibodies directed to these
polypeptides are useful in providing immunological probes for differential identification
of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
particularly of the male reproductive system and neuroendocrine system, expression of
this gene at significantly higher or lower levels may be routinely detected in certain
15 tissues (e.g., epididymus and other reproductive tissue, prostate, and pituitary gland,
and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine,
synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual
having such a disorder, relative to the standard gene expression level, i.e., the
expression level in healthy tissue or bodily fluid from an individual not having the
20 disorder.

The tissue distribution and homology to type I collagen, indicates that
polynucleotides and polypeptides corresponding to this gene are useful for diagnosis
and treatment of abnormalities of the epididymus, prostate (especially prostate cancer),
and pituitary gland.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 58

This gene is expressed primarily in the frontal cortex of the brain from a
schizophrenic individual.

Therefore, polynucleotides and polypeptides of the invention are useful as
30 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
not limited to, schizophrenia. Similarly, polypeptides and antibodies directed to these
polypeptides are useful in providing immunological probes for differential identification
of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
35 particularly of the nervous system, expression of this gene at significantly higher or
lower levels may be routinely detected in certain tissues (e.g., brain and other tissue of

the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of schizophrenia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 59

The polypeptide encoded by Gene 59 is homologous to human surface 4 integral membrane protein. In specific embodiments, the polypeptides of the invention comprise the sequence: TGCVLVLSRNFVQYACFGLFGIILQTIAYSILWDLKF LMRN (SEQ ID NO:310); SRSEGKSMFAGVPTMRESSPKQYMLGGRVLLV LMFMTLLHFDASFFSIVQNIVG (SEQ IDNO:311); GTAEDFADQFLRVTKQYLP HVARLCLISTFLEDGIRMFQWSEQRDYIDTTWNCGYLLAS (SEQ ID NO:312); LMRNESRS (SEQ ID NO:314); ASFLLSRTSWGTA (SEQ ID NO:315); and/or ASFLLSRTSWG TALMIL (SEQ ID NO:313). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in Hodgkin's lymphoma and lung; and to a lesser extent in many other human tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, Hodgkin's lymphoma, tumors or other abnormalities of the lung. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and respiratory systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., lymphoid tissue, and pulmonary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:183 as residues: Met-20 to Trp-27.

The tissue distribution indicates that polynucleotides and polypeptides

corresponding to this gene are useful for diagnosis and treatment of Hodgkin's lymphoma, tumors or other abnormalities of the lung.

FEATURES OF PROTEIN ENCODED BY GENE NO: 60

5 This gene is expressed primarily in bone cancer and stomach cancer, and to a lesser extent in many other tissues.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
10 not limited to, bone cancer and stomach cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the bone, and the stomach, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues
15 (e.g., bone, and stomach, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

20 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of bone cancer and stomach cancer and possibly other cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 61

25 This gene is expressed primarily in epididymus, and lymph node of breast cancer, and to a lesser extent in many other tissues.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
30 not limited to, abnormalities of the epididymus, and breast cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the epididymus and breast, expression of this gene at significantly higher or lower levels may be routinely
35 detected in certain tissues (e.g., epididymus and other reproductive tissue, lymphoid tissue, and mammary tissue, and cancerous and wounded tissues) or bodily fluids

(e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:185 as residues: Arg-57 to Ser-65.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of abnormalities of the epididymus, and breast cancer.

10 FEATURES OF PROTEIN ENCODED BY GENE NO: 62

The translation product of this gene appears to be the human homolog of bovine NADH dehydrogenase which is thought to be important in cellular metabolism. In specific embodiments, the polypeptides of the invention comprise the amino acid sequence: SMSALTRLASFARVGGRLFRSGCARTAGDGGVRHAGGGVHIEPRY
15 RQFPQLTRSQVFQSEFFSGLMFWILWRFWHDSEEVLGHFPYPDPSQWTDEEL
GIPPDDDED (SEQ ID NO:323), or fragments thereof. Polynucleotides encoding this polypeptide are also encompassed by the invention.

This gene is expressed in larynx tumor, lymph node, brain amygdala, human cardiomyopathy, and retina.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases affecting cellular metabolism. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes
25 for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., larynx, lymphoid tissue, brain and other tissue of the nervous system, heart and cardiovascular tissue, and retina, and cancerous and wounded tissues) or
30 bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:208 as residues: Pro-27 to Gln-32, Arg-
35 42 to Glu-51.

The tissue distribution and homology to NADH dehydrogenase indicates that

polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of diseases involving cellular metabolism.

FEATURES OF PROTEIN ENCODED BY GENE NO: 63

5 This gene is expressed primarily in amygdala, and to a lesser extent in many other tissues.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
10 not limited to, abnormalities of the amygdala. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the amygdala, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.,
15 amygdala, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a
20 sequence shown in SEQ ID NO:187 as residues: Gln-17 to Glu-29, Pro-41 to Phe-46, Ser-59 to Ile-70, Thr-97 to Leu-105.

 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of abnormalities of amygdala.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 64

 This gene is expressed primarily in female bladder, and to a lesser extent in chronic synovitis and hemangiopericytoma.

 Therefore, polynucleotides and polypeptides of the invention are useful as
30 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, bladder cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
35 particularly of the urinary tract, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., bladder, synovial tissue, and

vascular tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:188 as residues: Pro-2 to Gln-7, Pro-27 to Phe-34.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatments of defects of the urinary tract, especially bladder cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 65

This gene is expressed primarily in fetal spleen, and to a lesser extent in hemangiopericytoma, thymus, and synovial sarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, defects of immune or hematopoietic systems. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., spleen, vascular tissue, thymus, blood cells, and synovial tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The protein product of this gene is useful for treatment of defects of the immune or hematopoietic systems, because of the gene's expression in thymus and spleen.

FEATURES OF PROTEIN ENCODED BY GENE NO: 66

This gene is expressed primarily in human pituitary and to a lesser extent in placenta and fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, endocrine growth disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., 5 pituitary and other endocrine tissue, placenta, and pulmonary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue 10 or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:190 as residues: Val-38 to Asn-44, Gly-53 to Ser-65.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of growth disorders related to 15 pituitary dysfunction.

FEATURES OF PROTEIN ENCODED BY GENE NO: 67

The translation product of this gene shares sequence homology with a *Caenorhabditis elegans* gene of unknown function. In specific embodiments, the 20 polypeptides of the invention comprise the sequence: DPRRPNKVLRYPKPPSE CNPALDDPTP (SEQ ID NO:317); DYMNLLGMIFSMCGLMLKLKWCWVA VYCS (SEQ ID NO:318); FISFANSRSEDTKQMMSSF (SEQ ID NO:316); and/or MLSISAVVMSYLQNPQPMTPPW (SEQ ID NO:319). Polynucleotides encoding these polypeptides are also encompassed by the invention.

25 This gene is expressed primarily in primary breast cancer and lymph node breast cancer and to a lesser extent in adult brain, lung cancer, colon cancer, epithelioid sarcoma, and Caco-2 cell line.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a 30 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cancer and tumor tissues, expression of this gene at significantly 35 higher or lower levels may be routinely detected in certain tissues (e.g., mammary tissue, lymphoid tissue, brain and other tissue of the nervous system, lung, colon, and

epithelium, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:191 as residues: Asn-34 to Lys-42.

The tissue distribution in a variety of cancer tissues indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of a variety of cancer and tumor types.

10

FEATURES OF PROTEIN ENCODED BY GENE NO: 68

The translation product of this gene shares sequence homology with steroid membrane binding protein. The translation product of this gene has recently been published as progesterone binding protein. See Genbank AJ002030. Preferred polypeptides encoded by this gene comprise the following amino acid sequence: AAGDGDVKLGLTSGSGSESSNDGGSESPGDAGAAAXGGGWAAAALALLTG GGE (SEQ ID NO:320).

This gene is expressed primarily in breast, and to a lesser extent in placenta and fetal tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, breast cancer or developmental disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of breast or fetal tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., mammary tissue, placenta, and fetal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:192 as residues: Pro-43 to Asp-49, Gln-54 to Pro-64, Asp-110 to Asp-118, Lys-138 to Tyr-143, Pro-150 to Asp-170.

The tissue distribution and homology to steroid membrane binding protein and to progesterone binding protein indicates that the protein products of this gene are

useful for treatment of breast cancers, especially those caused by estrogen and progesterone binding.

FEATURES OF PROTEIN ENCODED BY GENE NO: 69

5 Preferred polypeptides encoded by this gene comprise the following amino acid sequence: AADNYGIPRACRNSARSYGAAWLLXPAGSSRVEPTQDISISDQLGG QDVPVFRNLSLLVVGVGAVFSLLFHLGTRERRRRPHAXEPGEHTPLLAPATAQPL LLWKHWLREXAFYQVGILYMTTRLIVNLSQTYMAMYLTYSLHLPKKFIATIPLV MYLSGFLSSFLMKPINKCIGRN (SEQ ID NO:321).

10 This gene is expressed primarily in macrophage (GM-CSF treated), and to a lesser extent in monocytes and dendritic cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation and infection. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., macrophages and other blood cells, and dendritic cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

25 The tissue distribution indicates that the protein products of this gene are useful for treatment of infection or inflammation or other events or defects involving the immune system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 70

30 This gene is expressed primarily in adult brain and to a lesser extent in thyroid, 12 week old early stage human, and stromal cell TF274.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological or neuro-endocrine diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes

for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous or endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, thyroid, and stromal cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:194 as residues: Pro-65 to Cys-71.

The tissue distribution indicates that the protein products of this gene are useful for treatment and diagnosis of neurological diseases or metabolic conditions involving the neuro-endocrine system.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 71**

This gene is expressed in T-cell helper and to a lesser extent in adult brain and adult testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune disorders, meningitis or reproductive problems. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, neural and reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., T-cells and other blood cells, brain and other tissue of the nervous system, testes and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:195 as residues: Val-18 to Tyr-24, Ala-89 to Asp-99, Asp-104 to Ala-117, Leu-121 to Pro-136.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis immune and

reproductive disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 72

5 The translated polypeptide of this contig has a high degree of identity with the Ob Receptor-Associated Protein deposited as GenBank Accession No. 2266638. No function has been determined for the Ob Receptor-Associated Protein, however it is expressed upon stimulation of the Ob Receptor by Leptin.

This gene is expressed in T-cells and to a lesser extent in endothelial and bone marrow cells.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, acute lymphoblastic leukemia, hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
15 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., T-cells and other blood cells, endothelial cells, and bone marrow, and cancerous and wounded tissues) or
20 bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:196 as residues: Ser-61 to Trp-70.

25 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of leukemia and other disorders of the primary immune system. In addition, since this gene appears to be related to the Ob Receptor-Related Protein, it is likely that this polypeptide is also involved in the Ob/Leptin signal transduction cascade. As a result, this protein may be
30 of use in the molecular diagnosis and therapeutic intervention of obesity and related disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 73

35 The translation product of this contig has homology with furin, a protein thought to be a key endopeptidase in the constitutive secretory pathway. The identification and initial characterization of Furin was reported by Takahasi and

colleagues (Biochem Biophys Res Commun 1993 Sep 15;195(2):1019-1026).

This gene is expressed in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the immune system such as allergies, wound healing and antigen recognition. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., neutrophils and other blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of allergies or other immune disorders since neutrophils are an important part of an allergic response. Further, since this protein appears to be related to Furin, it can be used diagnostically and therapeutically to treat secretory protein processing disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 74

This gene is expressed in the frontal cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, of the motor activity and sensory functions that involve the central nervous system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene

expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of neural disorders that affect cognitive functions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 75

The translation product of this gene shares sequence homology with inorganic pyrophosphatase which is thought to be important in the catalysis the hydrolysis of diphosphate bonds, chiefly in nucleoside di- and triphosphates and essential enzymes that are important for controlling the cellular levels of inorganic pyrophosphate (PPi). The bovine homolog of this gene has been identified by Yang and Wensel (J. Biol. Chem. 267:24641-24647 (1992)).

This gene is expressed in osteoclastoma cells and to a lesser extent in epithelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, osteoporosis and other bone weakening diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone, and epithelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:199 as residues: Lys-22 to Tyr-28, Asp-64 to Lys-77, Pro-86 to Ile-91, Gln-99 to Pro-119, Tyr-169 to Asp-174, Lys-176 to Gly-181, Trp-189 to Asn-202, Lys-233 to Gly-239, Ser-250 to Asp-257.

The tissue distribution and homology to inorganic pyrophosphatase indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of osteoporosis through the removal of bone by demineralization.

FEATURES OF PROTEIN ENCODED BY GENE NO: 76

The translation product of this gene shares exact sequence homology with ATP sulfurylase/APS kinase (GenBank Accession No. 2673862) which is thought to be important in biosynthesis of the activated sulfate donor, adenosine 3'-phosphate 5'-phosphosulfate, involves the sequential action of two enzyme activities: ATP sulfurylase, which catalyzes the formation of adenosine 5'-phosphosulfate (APS) from ATP and free sulfate, and APS kinase, which subsequently phosphorylates APS to produce adenosine 3'-phosphate 5'-phosphosulfate.

This gene is expressed in osteoclastoma cells and to a lesser extent in developmental tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, antibiotic resistant bacterial infections, osteoarthritis and other autoimmune diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or skeletal structure expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., bone, and developmental tissues, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:200 as residues: Asn-15 to Trp-20, Ser-36 to Gly-41, Pro-103 to Val-110, Pro-134 to Arg-143, Leu-173 to Arg-178, Ser-190 to Ala-197, His-314 to Arg-319, Arg-354 to Asn-362, Asp-391 to Arg-397, Glu-402 to Asp-409, Asp-434 to Leu-439, Glu-441 to Arg-446, Gly-455 to Asp-462, Pro-528 to His-541, Asn-566 to Arg-571, Tyr-574 to Glu-581, Thr-589 to Glu-603.

The tissue distribution and homology to ATP sulfurylase/APS kinase indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment or detection of autoimmune diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 77

This polypeptide is identical to the SLP-76-associated protein reported by Musci and colleagues (J. Biol. Chem. 272 (18), 11674-11677 (1997)) and to the FYB protein

reported by da Silva and coworkers (Proc. Natl. Acad. Sci. U.S.A. (1997) In press).

These proteins have been reported to be novel T-cell Proteins which bind FYN and SLP-76 and regulate IL-2 production. Preferred polypeptides encoded by this gene

comprise the following amino acid sequence: RITDNPEGKWLGRARGSYGYIK

5 TTAVEIXYDSLKLKKDSLKGAPSRPIEDDQEVYDDVAEQDDISSHSQSGSGGIFPP
PPDDDIYDGIEEEDADDGFPAPPKQLDMGDEVYDDVDTSDFPVSSAEMSQGTNV
GKAKTEEKDLKKLKKQXKEXKDFRKKFKYDGEIRVLVSTKVTTTSITSKKWGT
RDLQVKPGESLEVIQTDDTKVLCRNEEGKYGYVLRSLADNDGEIYDDIADGC
IYDND (SEQ ID NO:322).

10 This gene is expressed in CD34 positive cells (hematopoietic progenitor cells) and to a lesser extent in adult spleen derived from a chronic lymphocytic leukemia patient.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

15 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, chronic lymphocytic leukemia; hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and

20 hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., T-cells and other blood cells, bone marrow, hematopoietic cells, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the

25 standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Further, nucleic acids and polypeptides of the present invention are useful both diagnostically and therapeutically in the intervention of immune and other disorders in which the ability to alter IL-2 expression is desired. Preferred epitopes include those comprising a sequence shown in

30 SEQ ID NO:201 as residues: Ala-17 to Lys-37, Val-39 to Ser-45, Lys-59 to His-70, Arg-90 to Leu-95, Lys-97 to Lys-107, Ser-117 to Leu-124, Phe-133 to Ser-138, Trp-146 to Leu-167, Pro-175 to Asn-185, Lys-190 to Ser-211, Pro-213 to Ser-222, His-230 to Pro-235, Pro-240 to Pro-246, Pro-253 to Gly-261, Leu-271 to Leu-303, Leu-305 to Leu-326, Lys-343 to Leu-349, Thr-363 to Leu-371, Arg-373 to Tyr-381, Tyr-

35 391 to Leu-401, Pro-404 to Val-414, Ser-426 to Ser-432, Ile-448 to Ser-457, Gln-462 to Trp-468, Lys-477 to Ser-501, Asp-518 to Ser-523, Ala-541 to Gln-554.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of a variety of hematopoietic disorders. The noted expression of this gene in the hematopoietic progenitor cell compartment - as determined by its expression on CD34 positive hematopoietic stem and progenitor cells - indicates that it plays a critical role in the expansion or proliferation of hematopoietic stem/progenitor cells, as well as in the differentiation of the various blood cell lineages. Thus it could be useful in the reconstitution of the hematopoietic system of patients with leukemias and other hematopoietic diseases.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 78**

This gene is homologous to heparin cofactor II (HCII) which is a 66-kDa plasma glycoprotein that inhibits thrombin rapidly in the presence of dermatan sulfate or heparin.

This gene is expressed in apoptotic and anergic T-cells.

15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, thrombopenia T-cell lymphomas; Hodgkin's lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system - most notably the T-cell compartment, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., T-cells and other blood cells, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

25 The homology to heparin cofactor II (HCII) and the tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoietic disorders particularly in thrombopoiesis, most notably of the T-cell compartment. This could include immune modulation, inflammation, immune surveillance, graft rejection, and autoimmunity.

35 **FEATURES OF PROTEIN ENCODED BY GENE NO: 79**

The translation product of this gene shares sequence homology with a mouse

protein believed to represent an integral membrane protein.

This gene is expressed in fetal cochlea and epididymus and to a lesser extent in adult spleen and osteoclastoma.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, osteoclastoma; disorders of the inner ear; male fertility disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell
10 type(s). For a number of disorders of the above tissues or cells, particularly of the inner ear; male reproductive tract; bone; and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cochlea, epididymus and other reproductive tissue, spleen, and bone, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or
15 spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:203 as residues: Lys-13 to Gly-23, Cys-38 to Asp-43, Gly-48 to Trp-53, Cys-223 to Ile-237, Ile-240 to
20 Ser-246.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of hearing and fertility disorders. Likewise, it may have a role in the modulation of immune function and in the treatment of osteoporosis.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 80

The translation product of this gene shares sequence homology with reticulocalbin which is thought to be important in the binding of calcium, particularly within the endoplasmic reticulum.

30 This gene is expressed in endothelial cells and stromal cells and to a lesser extent in osteoblasts, osteoclasts, and T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
35 not limited to, osteoporosis; osteoclastomas; T-cell lymphomas; Hodgkin's disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in

providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vasculature, bone, and immune systems - particularly the T-cell compartments, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endothelial cells, stromal cells, bone, T-cells and other blood cells, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:204 as residues: Lys-20 to Arg-27, Pro-32 to Asp-48, Leu-64 to Arg-72, Asp-108 to Lys-114, Glu-128 to Thr-133, Asp-139 to Phe-147, Thr-196 to Ala-204, Tyr-218 to Glu-228, Val-230 to Gln-236, Arg-241 to Lys-255, Glu-276 to Lys-287.

The tissue distribution and homology to reticulocalbin indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of bone disorders such as osteoporosis; the diagnosis and treatment of T-cell lymphomas and Hodgkin's lymphoma; and the treatment of diseases and defects of the vasculature, such as vascular leak syndrome and aberrant angiogenesis that accompanies tumor growth.

FEATURES OF PROTEIN ENCODED BY GENE NO: 81

The translation product of this gene shares sequence homology with a family of peptide transport genes - particularly the AtPTR2-B gene from *Arabidopsis* - which are thought to be important in the uptake of small peptides.

This gene is expressed in a number of fetal tissues, most notably lung, brain, cochlea, and liver/spleen, and to a lesser extent in osteoclastoma and endometrial tumors.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, osteoclastoma; endometrial tumors; cancer; leukemias. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the bone and endometrium, expression of this gene at significantly higher or lower levels may be

5 routinely detected in certain tissues (e.g., fetal tissue, pulmonary tissue, bone, brain and other tissue of the nervous system, cochlea, liver, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:205 as residues: Lys-186 to Asn-199, Pro-202 to Ala-207.

10 The tissue distribution and homology to peptide transport genes indicates that polynucleotides and polypeptides corresponding to this gene are useful for the control of cell proliferation, owing to its strong expression in fetal tissues undergoing active cell division, as well as its expression in a variety of tumors or cancers of adult tissues. Potentially, it may regulate the uptake of peptides that stimulate cell proliferation. This gene product may also be useful in stimulating the uptake of a variety of peptide-based
15 drug compounds.

FEATURES OF PROTEIN ENCODED BY GENE NO: 82

This gene is expressed in fetal liver and spleen and to a lesser extent in endothelial cells.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer and tumors of a hematopoietic and/or endothelial cell origin; leukemias. Similarly, polypeptides and antibodies directed to these polypeptides
25 are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and/or vasculature, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, endothelial cells, vascular tissue, and tissue and cells of the immune system,
30 and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID
35 NO:206 as residues: Met-1 to Asp-9, Arg-66 to Gly-76, Asp-164 to Arg-171.

The tissue distribution indicates that polynucleotides and polypeptides

corresponding to this gene are useful for the treatment of disorders of the immune system. Expression of this gene product in both fetal liver/spleen and endothelial cells indicates that it may be expressed in the hemangioblast, the progenitor cell for both the immune system and the vasculature. Thus, it is most likely expressed in hematopoietic stem cells, and may be useful for the expansion of hematopoietic stem and progenitor cells in conjunction with cancer treatment for a variety of leukemias.

FEATURES OF PROTEIN ENCODED BY GENE NO: 84

The translation product of this gene shares sequence homology with NADH dehydrogenase which is thought to be important in cellular metabolism.

This gene is expressed in fetal dura mater and to a lesser extent in T-cells and hypothalamus.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases affecting cellular metabolism. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., fetal tissue, T-cells and other blood cells, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:208 as residues: Pro-27 to Gln-32, Arg-42 to Glu-51.

The tissue distribution and homology to NADH dehydrogenase indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of diseases involving cellular metabolism.

FEATURES OF PROTEIN ENCODED BY GENE NO: 85

The translation product of this gene shares sequence homology with I-TRAF, a novel TNF receptor associated factor (TRAF)-interacting protein that regulates TNF receptor-mediated signal transduction. This protein is thought to be important in
5 regulating the cellular response to tumor necrosis factor (TNF), which is an important mediator of inflammation.

This gene is expressed in endothelial cells and to a lesser extent in glioblastoma and osteoblastoma.

Therefore, polynucleotides and polypeptides of the invention are useful as
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation; glioblastoma and osteoblastoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of
15 disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endothelial cells, bone, and glial cells and tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from
20 an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:209 as residues: Glu-15 to Thr-22, Glu-46 to Leu-62, Arg-103 to Glu-119, Gln-127 to Glu-132, Asn-152 to Trp-158, Gln-191 to Gln-210, Glu-264 to Thr-271, Tyr-282 to Leu-288, Trp-319 to Thr-331, Glu-335 to Ser-348, Ser-353 to Ser-358, Asp-382 to Asn-392.
25

The tissue distribution and homology to I-TRAF indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of inflammatory diseases, including rheumatoid arthritis, sepsis, inflammatory bowel
30 disease, and psoriasis, particularly where tumor necrosis factor is known to be involved.

FEATURES OF PROTEIN ENCODED BY GENE NO: 86

This gene has homology with a candidate gene involved in X-linked Retinopathy reported by Wong and colleagues (Genomics 15:467-471 (1993)).

This gene is expressed in a T-cell line.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation and autoimmune diseases; T-cell lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
10 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., T-cells and other blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
15 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of inflammatory
20 disorders such as sepsis, inflammatory bowel disease, psoriasis, and rheumatoid arthritis as well as autoimmune disease such as lupus. It could also be useful in immune modulation and in the process of immune surveillance. The present invention can be used diagnostically and therapeutically to treat X-linked Retinopathy.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 87

This gene is expressed in human brain tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
30 not limited to, brain disorders; neurodegenerative disorders; tumors of a brain origin. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels
35 may be routinely detected in certain tissues (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,

urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID

5 NO:211 as residues: Cys-32 to Tyr-38.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of CNS disorders such as epilepsy, paranoia, depression, Alzheimer's disease, and schizophrenia. It could be useful in the survival and/or proliferation of neurons and could effect neuronal

10 regeneration.

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
1	HAGEW82	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	11	1679	247	1607	353	353	125	1			30
2	HAGFY16	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	12	1830	87	1786	128	128	126	1	26	27	44
2	HBMCF37	xxxxx 03/19/98	pBluescript	98	1487	79	1487	170	170	212	1	44	45	69
2	HFLQB16	209641 02/25/98	Uni-ZAP XR	99	1653	394	1637	413	413	213	1	25	26	81
3	HALAA60	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	13	1212	1	1212	99	99	127	1	24	25	38
4	HAPBL78	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	14	2061	882	2061	900	900	128	1	22	23	22
5	HASAV70	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	15	1412	10	733	103	103	129	1	20	21	109

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
6	HBNAF22	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	16	1052	276	880	538	538	130	1	17	18	62
7	HBNBL77	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	17	683	1	683	181	181	131	1			29
8	HCDDR90	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	18	1054	86	1007	86	86	132	1	23	24	52
9	HCEEF50	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	19	1393	132	1393	192	192	133	1	17	18	56
10	HCEMU42	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	20	1215	277	1070	401	401	134	1	18	19	215
11	HCENE16	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	21	2042	614	2011	793	793	135	1	26	27	48

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
12	HMSJJ74	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	22	1872	21	1872	69	69	136	1	23	24	67
13	HCUBF15	97923 03/07/97 209071 05/22/97	ZAP Express	23	289	1	289	89	89	137	1	29	30	51
14	HE2DE47	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	24	3533	2821	3532	808	808	138	1	30	31	539
14	HE2DE47	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	100	1145	435	1115	515	515	214	1	22	23	80
15	HKMLH01	209179 07/24/97	pBluescript	25	1148	171	907	196	196	139	1	26	27	56
15	HE6DGG34	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	101	734	25	734	295	295	215	1	36	37	48
16	HE9DGG49	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	26	717	1	717	70	70	140	1	27	28	200

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
16	HE9DG49	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	102	713	17	713	78	78	216	1	28	29	202
17	HELBA06	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	27	1099	1	1099	38	38	141	1	22	23	215
17	HELBA06	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	103	1080	1	1080	149	149	217	1	25	26	185
18	HSLFM29	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	28	941	171	941	128	128	142	1	42	43	101
19	HELBW38	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	29	756	62	756	294	294	143	1	30	31	111
20	HEITHN28	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	30	2100	408	2093	496	496	144	1			19

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
21	HFCDK17	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	31	1448	475	1392	567	567	145	1			29
22	HFEAF41	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	32	456	1	409	21	21	146	1	28	29	98
23	HFKFL13	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	33	1326	1	1322	210	210	147	1			7
24	HFSBG13	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	34	710	1	710	242	242	148	1	16	17	38
25	HFTBE43	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	35	1188	110	1161	178	178	149	1	26	27	130
26	HFTDJ36	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	36	956	1	938	144	144	150	1	21	22	31
27	HKTAC77	97924 03/07/97	Uni-ZAP XR	37	1603	974	1581	1104	1104	151	1			13

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
28	HLHSH36	97924 03/07/97	pBluescript	38	1089	55	1067		209	152	1			7
29	HLHSV96	97924 03/07/97	pBluescript	39	629	1	629	119	119	153	1	32	33	67
30	HLQBQ86	97924 03/07/97	Lambda ZAP II	40	1964	408	1793	581	581	154	1			25
31	HLTBX31	97924 03/07/97	Uni-ZAP XR	41	1522	13	1123	126	126	155	1	32	33	194
32	HLTCJ63	97924 03/07/97	Uni-ZAP XR	42	875	1	875	43	43	156	1	18	19	90
33	HMIKAH44	97924 03/07/97	pSport1	43	843	1	843	171	171	157	1	30	31	30
34	HMQAJ64	97924 03/07/97	Uni-ZAP XR	44	489	3	489	55	55	158	1	19	20	89
34	HMQAJ64	97924 03/07/97	Uni-ZAP XR	104	489	6	489	58	58	218	1	22	23	89
35	HOABG65	97924 03/07/97	Uni-ZAP XR	45	534	1	534	17	17	159	1	18	19	88
36	HODCL36	97924 03/07/97	Uni-ZAP XR	46	1374	1	1374	15	15	160	1	20	21	173
36	HODCL36	97924 03/07/97	Uni-ZAP XR	105	640	58	640	72	72	219	1	20	21	137
36	HODCL36	97924 03/07/97	Uni-ZAP XR	106	1529	40	1399	54	54	220	1	27	28	47
37	HODCL50	97924 03/07/97	Uni-ZAP XR	47	596	1	596	269	269	161	1	27	28	44

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
38	HODCV74	97924 03/07/97	Uni-ZAP XR	48	851	99	822	170	170	162	1			22
39	HODCZ16	97924 03/07/97	Uni-ZAP XR	49	2020	569	2020	638	638	163	1	17	18	69
40	HTOEU03	97924 03/07/97	Uni-ZAP XR	50	2432	848	2432	99	99	164	1	19	20	322
40	HTOEU03	97924 03/07/97	Uni-ZAP XR	107	2435	849	2435	928	928	221	1	31	32	69
41	HPBCJ74	97924 03/07/97	pBluescript SK-	51	2340	1627	2340	150	150	165	1	60	61	319
41	HPBCJ74	97924 03/07/97	pBluescript SK-	108	805	92	791	239	239	222	1	21	22	82
42	HPMBU33	97924 03/07/97	Uni-ZAP XR	52	601	188	601	432	432	166	1			30
43	HSAUL66	97924 03/07/97	Uni-ZAP XR	53	359	1	337	142	142	167	1	18	19	71
44	HSIDQ18	97924 03/07/97	Uni-ZAP XR	54	1141	1	1141	25	25	168	1	30	31	280
44	HSIDQ18	97924 03/07/97	Uni-ZAP XR	109	1166	21	1166	433	433	223	1	30	31	42
45	HSJBB37	97924 03/07/97	Uni-ZAP XR	55	1560	63	1148	217	217	169	1			22
46	HSJBQ79	97924 03/07/97	Uni-ZAP XR	56	1507	164	608	57	57	170	1	19	20	326
46	HSJBQ79	97924 03/07/97	Uni-ZAP XR	110	586	4	586	35	35	224	1	23	24	183

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
47	HTEGA76	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	57	450	1	450	83	83	171	1	35	36	68
48	HTEJN13	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	58	1147	1	1147	163	163	172	1	15	16	158
48	HTEJN13	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	111	1134	1	1134	155	155	225	1	19	20	70
49	HTHBL86	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	59	777	1	777	115	115	173	1	18	19	122
50	HTSFO71	97958 03/13/97 209072 05/22/97	pBluescript	60	1191	48	598	52	52	174	1	30	31	128
50	HTSFO71	97958 03/13/97 209072 05/22/97	pBluescript	112	1333	594	1333	829	829	226	1			9
51	HAPNO80	209235 09/04/97	Uni-ZAP XR	61	1580	443	1554	114	114	175	1	1	2	371

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
51	HAUCC47	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	113	1015	249	708	244	244	227	1	28	29	137
52	HBMCL41	97958 03/13/97 209072 05/22/97	pBluescript	62	1117	105	1034	182	182	176	1	28	29	215
53	HCFLD84	97958 03/13/97 209072 05/22/97	pSport1	63	361	1	361	97	97	177	1	32	33	54
54	HE8EM69	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	64	1668	1	1638	150	150	178	1	20	21	22
55	HE8EZ48	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	65	1353	35	1303	231	231	179	1	33	34	102
56	HEBGF73	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	66	1011	655	1011	703	703	180	1	38	39	47

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
57	HFEBF41	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	67	1193	267	1090	459	181	1	35	36	95
58	HFRBU14	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	68	560	1	560	63	182	1	29	30	94
59	HFVGZ79	97958 03/13/97 209072 05/22/97	pBluescript	69	1657	765	1581	839	183	1	21	22	26
60	HHGCM76	97958 03/13/97 209072 05/22/97	Lambda ZAP II	70	711	8	711	270	184	1			10
61	HHGCO88	97958 03/13/97 209072 05/22/97	Lambda ZAP II	71	935	111	935	272	185	1	19	20	64
62	HHGCP52	97958 03/13/97 209072 05/22/97	Lambda ZAP II	72	504	113	484	127	186	1	21	22	21

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
63	HHGDB72	97958 03/13/97 209072 05/22/97	Lambda ZAP II	73	620	1	620	96	96	187	1	18	19	131
64	HHGDI71	97958 03/13/97 209072 05/22/97	Lambda ZAP II	74	581	156	581	248	248	188	1	32	33	68
65	HHSDI45	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	75	1843	537	1786	630	630	189	1	27	28	44
66	HHSEB66	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	76	1441	116	800	167	167	190	1	36	37	64
67	HJPAZ83	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	114	1076	398	1076		575	228	1	11	12	22
68	HLDBO49	97958 03/13/97 209072 05/22/97	pCMVSPORT 3.0	78	2776	18	1888	187	187	192	1	14	15	169

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
69	HLDBQ19	97958 03/13/97 209072 05/22/97	pCMVSPORT 3.0	79	1525	401	1480	534	534	193	1	22	23	65
69	HLDBQ19	209226 08/28/97	pCMVSPORT 3.0	115	1487	401	1487	534	534	229	1	22	23	131
70	HMSGT42	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	80	1563	33	1077	40	40	194	1	32	33	91
71	HMWIC78	97957 03/13/97 209073 05/22/97	Uni-Zap XR	81	1020	18	780	238	238	195	1	23	24	175
72	HTTCT79	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	82	770	101	770	286	286	196	1	26	27	69
73	HNGJU84	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	83	481	1	481	58	58	197	1	20	21	24
74	HNTAC73	97957 03/13/97 209073 05/22/97	pCMVSPORT 3.0	84	644	1	623	14	14	198	1	25	26	72

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
75	HOSEI45	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	85	1351	435	1284	98	98	199	1	12	13	288
75	HOSEI45	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	116	1350	428	1283		545	230	1			27
76	HOSFD58	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	86	2527	290	1747	56	56	200	1	30	31	623
76	HOSFD58	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	117	2527	288	1747	477	477	231	1	32	33	60
77	HSAUM95	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	87	2566	1843	2566	251	251	201	1	30	31	648
77	HSAUM95	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	118	1098	375	1098	677	677	232	1	21	22	28

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
78	HSAUR67	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	88	540	1	540	83	83	202	1	32	33	54
79	HSKDI81	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	89	1863	152	1165	188	188	203	1	11	12	265
79	HSKDI81	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	119	1679	152	1166	315	315	233	1			17
80	HSKDW91	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	90	2478	1149	2449	92	92	204	1	19	20	314
81	HTLEX50	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	91	2058	476	2058	414	414	205	1	20	21	206
82	HSKHL65	97957 03/13/97 209073 05/22/97	pBluescript	92	1411	345	1411	157	157	206	1	69	70	194

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
82	HSKHL65	97957 03/13/97 209073 05/22/97	pBluescript	121	1411	345	1411	526	526	235	1	37	38	71
83	HHFGA11	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	93	2187	147	2184	397	397	207	1	30	31	329
83	HHFGA11	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	122	2256	138	2063	228	228	236	1	19	20	95
84	HWTBL40	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	94	757	524	608	445	445	208	1	20	21	57
85	HBXFG80	97957 03/13/97 209073 05/22/97	ZAP Express	95	2394	481	2394	523	523	209	1	1	2	391
86	HCACY32	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	96	672	1	672	117	117	210	1	21	22	25

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
87	HCEDO21	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	97	1419	1	1419	207	207	211	1	20	21	37

Table 1 summarizes the information corresponding to each "Gene No." described above. The nucleotide sequence identified as "NT SEQ ID NO:X" was assembled from partially homologous ("overlapping") sequences obtained from the "cDNA clone ID" identified in Table 1 and, in some cases, from additional related DNA clones. The overlapping sequences were assembled into a single contiguous sequence of high redundancy (usually three to five overlapping sequences at each nucleotide position), resulting in a final sequence identified as SEQ ID NO:X.

The cDNA Clone ID was deposited on the date and given the corresponding deposit number listed in "ATCC Deposit No:Z and Date." Some of the deposits contain multiple different clones corresponding to the same gene. "Vector" refers to the type of vector contained in the cDNA Clone ID.

"Total NT Seq." refers to the total number of nucleotides in the contig identified by "Gene No." The deposited clone may contain all or most of these sequences, reflected by the nucleotide position indicated as "5' NT of Clone Seq." and the "3' NT of Clone Seq." of SEQ ID NO:X. The nucleotide position of SEQ ID NO:X of the putative start codon (methionine) is identified as "5' NT of Start Codon." Similarly, the nucleotide position of SEQ ID NO:X of the predicted signal sequence is identified as "5' NT of First AA of Signal Pep."

The translated amino acid sequence, beginning with the methionine, is identified as "AA SEQ ID NO:Y," although other reading frames can also be easily translated using known molecular biology techniques. The polypeptides produced by these alternative open reading frames are specifically contemplated by the present invention.

The first and last amino acid position of SEQ ID NO:Y of the predicted signal peptide is identified as "First AA of Sig Pep" and "Last AA of Sig Pep." The predicted first amino acid position of SEQ ID NO:Y of the secreted portion is identified as "Predicted First AA of Secreted Portion." Finally, the amino acid position of SEQ ID NO:Y of the last amino acid in the open reading frame is identified as "Last AA of ORF."

SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, SEQ ID NO:X is useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in the deposited clone. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to the secreted proteins encoded by the cDNA clones identified in Table 1.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X and the predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing a human cDNA of the invention deposited with the ATCC, as set forth in Table 1. The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, or the deposited clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are species homologs. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for the desired homologue.

The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below).

It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

- 5 The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified by the one-step method described in Smith and Johnson, *Gene* 67:31-40 (1988). Polypeptides of the invention also can be purified from natural or recombinant sources
- 10 using antibodies of the invention raised against the secreted protein in methods which are well known in the art.

Signal Sequences

- 15 Methods for predicting whether a protein has a signal sequence, as well as the cleavage point for that sequence, are available. For instance, the method of McGeoch, *Virus Res.* 3:271-286 (1985), uses the information from a short N-terminal charged region and a subsequent uncharged region of the complete (uncleaved) protein. The method of von Heinje, *Nucleic Acids Res.* 14:4683-4690 (1986) uses the information from the residues surrounding the cleavage site, typically residues -13 to +2, where +1
- 20 indicates the amino terminus of the secreted protein. The accuracy of predicting the cleavage points of known mammalian secretory proteins for each of these methods is in the range of 75-80%. (von Heinje, *supra*.) However, the two methods do not always produce the same predicted cleavage point(s) for a given protein.

- 25 In the present case, the deduced amino acid sequence of the secreted polypeptide was analyzed by a computer program called SignalP (Henrik Nielsen et al., *Protein Engineering* 10:1-6 (1997)), which predicts the cellular location of a protein based on the amino acid sequence. As part of this computational prediction of localization, the methods of McGeoch and von Heinje are incorporated. The analysis of the amino acid sequences of the secreted proteins described herein by this program provided the results
- 30 shown in Table 1.

- As one of ordinary skill would appreciate, however, cleavage sites sometimes vary from organism to organism and cannot be predicted with absolute certainty. Accordingly, the present invention provides secreted polypeptides having a sequence shown in SEQ ID NO:Y which have an N-terminus beginning within 5 residues (i.e., +
- 35 or - 5 residues) of the predicted cleavage point. Similarly, it is also recognized that in some cases, cleavage of the signal sequence from a secreted protein is not entirely

uniform, resulting in more than one secreted species. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

Moreover, the signal sequence identified by the above analysis may not necessarily predict the naturally occurring signal sequence. For example, the naturally occurring signal sequence may be further upstream from the predicted signal sequence. However, it is likely that the predicted signal sequence will be capable of directing the secreted protein to the ER. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

10 **Polynucleotide and Polypeptide Variants**

"Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. The query sequence may be an entire sequence shown in Table 1, the ORF (open reading frame), or any fragment specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. (1990) 6:237-245). In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization

Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 bases at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query

amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions,

- 5 interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequences shown in Table 1 or to the amino acid sequence encoded by deposited DNA clone can be
10 determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. (1990) 6:237-245). In a sequence alignment the query and
15 subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window
20 Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity.
25 For subject sequences truncated at the N- and C-termini, relative to the the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of
30 the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are
35 considered for the purposes of manually adjusting the percent identity score. That is, only query residue positions outside the farthest N- and C-terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired
5 residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence.
10 This time the deletions are internal deletions so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query
15 sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or
20 activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in
25 the human mRNA to those preferred by a bacterial host such as *E. coli*).

Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level.
30 Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, one or more amino acids can be
35 deleted from the N-terminus or C-terminus of the secreted protein without substantial loss of biological function. The authors of Ron et al., J. Biol. Chem. 268: 2984-2988 (1993), reported variant KGF proteins having heparin binding activity even after

deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

Moreover, ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See, Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

Furthermore, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

Thus, the invention further includes polypeptide variants which show substantial biological activity. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity. For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie, J. U. et al., Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham and Wells, Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly.

Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues, where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino acids, such as an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

Polynucleotide and Polypeptide Fragments

In the present invention, a "polynucleotide fragment" refers to a short polynucleotide having a nucleic acid sequence contained in the deposited clone or shown in SEQ ID NO:X. The short nucleotide fragments are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length. A fragment "at least 20 nt in length," for example, is intended to include 20 or more contiguous bases from the cDNA sequence contained in the deposited clone or the nucleotide sequence shown in SEQ ID NO:X. These nucleotide fragments are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., 50, 150, 500, 600, 2000 nucleotides) are preferred.

Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments having a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700, or 701 to the end of SEQ ID NO:X or the cDNA contained in the deposited clone. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has biological activity.

In the present invention, a "polypeptide fragment" refers to a short amino acid sequence contained in SEQ ID NO:Y or encoded by the cDNA contained in the deposited clone. Protein fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, or 161 to the end of the coding region. Moreover, polypeptide fragments can be about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either extreme or at both extremes.

Preferred polypeptide fragments include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or the mature form having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any

combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotide fragments encoding these polypeptide fragments are also preferred.

- Also preferred are polypeptide and polynucleotide fragments characterized by
- 5 structural or functional domains, such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions.
- 10 Polypeptide fragments of SEQ ID NO:Y falling within conserved domains are specifically contemplated by the present invention. Moreover, polynucleotide fragments encoding these domains are also contemplated.

- Other preferred fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an
- 15 activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

Epitopes & Antibodies

- In the present invention, "epitopes" refer to polypeptide fragments having
- 20 antigenic or immunogenic activity in an animal, especially in a human. A preferred embodiment of the present invention relates to a polypeptide fragment comprising an epitope, as well as the polynucleotide encoding this fragment. A region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." In contrast, an "immunogenic epitope" is defined as a part of a protein that elicits an
- 25 antibody response. (See, for instance, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998- 4002 (1983).)

Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

- 30 In the present invention, antigenic epitopes preferably contain a sequence of at least seven, more preferably at least nine, and most preferably between about 15 to about 30 amino acids. Antigenic epitopes are useful to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. (See, for instance, Wilson et al., Cell 37:767-778 (1984); Sutcliffe, J. G. et al., Science 219:660-666 (1983).)

- 35 Similarly, immunogenic epitopes can be used to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., supra; Wilson et al., supra; Chow, M. et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle, F. J. et

al., J. Gen. Virol. 66:2347-2354 (1985).) A preferred immunogenic epitope includes the secreted protein. The immunogenic epitopes may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier. However,
5 immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting.)

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules as well as antibody fragments (such as, for example,
10 Fab and F(ab')₂ fragments) which are capable of specifically binding to protein. Fab and F(ab')₂ fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding than an intact antibody. (Wahl et al., J. Nucl. Med. 24:316-325 (1983).) Thus, these fragments are preferred, as well as the products of a FAB or other immunoglobulin expression library.
15 Moreover, antibodies of the present invention include chimeric, single chain, and humanized antibodies.

Fusion Proteins

Any polypeptide of the present invention can be used to generate fusion
20 proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular locations based on trafficking signals, the polypeptides of the present invention can be
25 used as targeting molecules once fused to other proteins.

Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

30 Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties may be added to the
35 polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

Moreover, polypeptides of the present invention, including fragments, and specifically epitopes, can be combined with parts of the constant domain of immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life in vivo. One reported example
5 describes chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EP A 394,827; Traunecker et al., Nature 331:84-86 (1988).) Fusion proteins having disulfide-linked dimeric structures (due to the IgG) can also be more efficient in binding and neutralizing other molecules, than the
10 monomeric secreted protein or protein fragment alone. (Fountoulakis et al., J. Biochem. 270:3958-3964 (1995).)

Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a
15 fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP-A 0232 262.) Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified, would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for
20 example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, D. Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol. Chem. 270:9459-9471 (1995).)

Moreover, the polypeptides of the present invention can be fused to marker
25 sequences, such as a peptide which facilitates purification of the fused polypeptide. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for
30 instance, hexa-histidine provides for convenient purification of the fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein. (Wilson et al., Cell 37:767 (1984).)

Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the present invention.

Vectors, Host Cells, and Protein Production

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral
5 vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is
10 a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to
15 name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or
20 UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples of
25 appropriate hosts include, but are not limited to, bacterial cells, such as E. coli, Streptomyces and Salmonella typhimurium cells; fungal cells, such as yeast cells; insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS, 293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1
35 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., Basic Methods
5 In Molecular Biology (1986). It is specifically contemplated that the polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography,
10 phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention, and preferably the secreted form, can also
15 be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production
20 procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein
25 after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

30 **Uses of the Polynucleotides**

Each of the polynucleotides identified herein can be used in numerous ways as reagents. The following description should be considered exemplary and utilizes known techniques.

The polynucleotides of the present invention are useful for chromosome
35 identification. There exists an ongoing need to identify new chromosome markers, since few chromosome marking reagents, based on actual sequence data (repeat

polymorphisms), are presently available. Each polynucleotide of the present invention can be used as a chromosome marker.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp) from the sequences shown in SEQ ID NO:X. Primers can be
5 selected using computer analysis so that primers do not span more than one predicted exon in the genomic DNA. These primers are then used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the SEQ ID NO:X will yield an amplified fragment.

Similarly, somatic hybrids provide a rapid method of PCR mapping the
10 polynucleotides to particular chromosomes. Three or more clones can be assigned per day using a single thermal cycler. Moreover, sublocalization of the polynucleotides can be achieved with panels of specific chromosome fragments. Other gene mapping strategies that can be used include in situ hybridization, prescreening with labeled flow-sorted chromosomes, and preselection by hybridization to construct chromosome
15 specific-cDNA libraries.

Precise chromosomal location of the polynucleotides can also be achieved using fluorescence in situ hybridization (FISH) of a metaphase chromosomal spread. This technique uses polynucleotides as short as 500 or 600 bases; however, polynucleotides 2,000-4,000 bp are preferred. For a review of this technique, see Verma et al.,
20 "Human Chromosomes: a Manual of Basic Techniques," Pergamon Press, New York (1988).

For chromosome mapping, the polynucleotides can be used individually (to mark a single chromosome or a single site on that chromosome) or in panels (for marking multiple sites and/or multiple chromosomes). Preferred polynucleotides
25 correspond to the noncoding regions of the cDNAs because the coding sequences are more likely conserved within gene families, thus increasing the chance of cross hybridization during chromosomal mapping.

Once a polynucleotide has been mapped to a precise chromosomal location, the physical position of the polynucleotide can be used in linkage analysis. Linkage
30 analysis establishes coinheritance between a chromosomal location and presentation of a particular disease. (Disease mapping data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library) .) Assuming 1 megabase mapping resolution and one gene per 20 kb, a cDNA precisely localized to a chromosomal region associated with the disease
35 could be one of 50-500 potential causative genes.

Thus, once coinheritance is established, differences in the polynucleotide and the corresponding gene between affected and unaffected individuals can be examined.

First, visible structural alterations in the chromosomes, such as deletions or translocations, are examined in chromosome spreads or by PCR. If no structural alterations exist, the presence of point mutations are ascertained. Mutations observed in some or all affected individuals, but not in normal individuals, indicates that the mutation may cause the disease. However, complete sequencing of the polypeptide and the corresponding gene from several normal individuals is required to distinguish the mutation from a polymorphism. If a new polymorphism is identified, this polymorphic polypeptide can be used for further linkage analysis.

Furthermore, increased or decreased expression of the gene in affected individuals as compared to unaffected individuals can be assessed using polynucleotides of the present invention. Any of these alterations (altered expression, chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

In addition to the foregoing, a polynucleotide can be used to control gene expression through triple helix formation or antisense DNA or RNA. Both methods rely on binding of the polynucleotide to DNA or RNA. For these techniques, preferred polynucleotides are usually 20 to 40 bases in length and complementary to either the region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxy-nucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988).) Triple helix formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques are effective in model systems, and the information disclosed herein can be used to design antisense or triple helix polynucleotides in an effort to treat disease.

Polynucleotides of the present invention are also useful in gene therapy. One goal of gene therapy is to insert a normal gene into an organism having a defective gene, in an effort to correct the genetic defect. The polynucleotides disclosed in the present invention offer a means of targeting such genetic defects in a highly accurate manner. Another goal is to insert a new gene that was not present in the host genome, thereby producing a new trait in the host cell.

The polynucleotides are also useful for identifying individuals from minute biological samples. The United States military, for example, is considering the use of restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identifying

personnel. This method does not suffer from the current limitations of "Dog Tags" which can be lost, switched, or stolen, making positive identification difficult. The polynucleotides of the present invention can be used as additional DNA markers for RFLP.

5 The polynucleotides of the present invention can also be used as an alternative to RFLP, by determining the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, individuals can be identified because each individual will have a unique set
10 of DNA sequences. Once an unique ID database is established for an individual, positive identification of that individual, living or dead, can be made from extremely small tissue samples.

 Forensic biology also benefits from using DNA-based identification techniques as disclosed herein. DNA sequences taken from very small biological samples such as
15 tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, etc., can be amplified using PCR. In one prior art technique, gene sequences amplified from polymorphic loci, such as DQa class II HLA gene, are used in forensic biology to identify individuals. (Erlich, H., PCR Technology, Freeman and Co. (1992).) Once these specific polymorphic loci are amplified, they are digested with one or more
20 restriction enzymes, yielding an identifying set of bands on a Southern blot probed with DNA corresponding to the DQa class II HLA gene. Similarly, polynucleotides of the present invention can be used as polymorphic markers for forensic purposes.

 There is also a need for reagents capable of identifying the source of a particular tissue. Such need arises, for example, in forensics when presented with tissue of
25 unknown origin. Appropriate reagents can comprise, for example, DNA probes or primers specific to particular tissue prepared from the sequences of the present invention. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

30 In the very least, the polynucleotides of the present invention can be used as molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, as a probe to "subtract-out" known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers for attachment to a "gene chip" or other support, to raise anti-DNA antibodies using
35 DNA immunization techniques, and as an antigen to elicit an immune response.

Uses of the Polypeptides

Each of the polypeptides identified herein can be used in numerous ways. The following description should be considered exemplary and utilizes known techniques.

5 A polypeptide of the present invention can be used to assay protein levels in a biological sample using antibody-based techniques. For example, protein expression in tissues can be studied with classical immunohistological methods. (Jalkanen, M., et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, M., et al., J. Cell . Biol. 105:3087-3096 (1987).) Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known 10 in the art and include enzyme labels, such as, glucose oxidase, and radioisotopes, such as iodine (^{125}I , ^{121}I), carbon (^{14}C), sulfur (^{35}S), tritium (^3H), indium (^{112}In), and technetium ($^{99\text{m}}\text{Tc}$), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

15 In addition to assaying secreted protein levels in a biological sample, proteins can also be detected in vivo by imaging. Antibody labels or markers for in vivo imaging of protein include those detectable by X-radiography, NMR or ESR. For X-radiography, suitable labels include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for 20 NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma.

A protein-specific antibody or antibody fragment which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example, ^{131}I , 25 ^{112}In , $^{99\text{m}}\text{Tc}$), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously, or intraperitoneally) into the mammal. It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human 30 subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of $^{99\text{m}}\text{Tc}$. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments." (Chapter 13 in Tumor Imaging: The Radiochemical Detection of Cancer, S.W. Burchiel and B. A. Rhodes, eds., Masson 35 Publishing Inc. (1982).)

Thus, the invention provides a diagnostic method of a disorder, which involves (a) assaying the expression of a polypeptide of the present invention in cells or body fluid of an individual; (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a disorder.

Moreover, polypeptides of the present invention can be used to treat disease. For example, patients can be administered a polypeptide of the present invention in an effort to replace absent or decreased levels of the polypeptide (e.g., insulin), to supplement absent or decreased levels of a different polypeptide (e.g., hemoglobin S for hemoglobin B), to inhibit the activity of a polypeptide (e.g., an oncogene), to activate the activity of a polypeptide (e.g., by binding to a receptor), to reduce the activity of a membrane bound receptor by competing with it for free ligand (e.g., soluble TNF receptors used in reducing inflammation), or to bring about a desired response (e.g., blood vessel growth).

Similarly, antibodies directed to a polypeptide of the present invention can also be used to treat disease. For example, administration of an antibody directed to a polypeptide of the present invention can bind and reduce overproduction of the polypeptide. Similarly, administration of an antibody can activate the polypeptide, such as by binding to a polypeptide bound to a membrane (receptor).

At the very least, the polypeptides of the present invention can be used as molecular weight markers on SDS-PAGE gels or on molecular sieving gel filtration columns using methods well known to those of skill in the art. Polypeptides can also be used to raise antibodies, which in turn are used to measure protein expression from a recombinant cell, as a way of assessing transformation of the host cell. Moreover, the polypeptides of the present invention can be used to test the following biological activities.

Biological Activities

The polynucleotides and polypeptides of the present invention can be used in assays to test for one or more biological activities. If these polynucleotides and polypeptides do exhibit activity in a particular assay, it is likely that these molecules may be involved in the diseases associated with the biological activity. Thus, the polynucleotides and polypeptides could be used to treat the associated disease.

Immune Activity

A polypeptide or polynucleotide of the present invention may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the

proliferation, differentiation, or mobilization (chemotaxis) of immune cells. Immune cells develop through a process called hematopoiesis, producing myeloid (platelets, red blood cells, neutrophils, and macrophages) and lymphoid (B and T lymphocytes) cells from pluripotent stem cells. The etiology of these immune deficiencies or disorders
5 may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or infectious. Moreover, a polynucleotide or polypeptide of the present invention can be used as a marker or detector of a particular immune system disease or disorder.

A polynucleotide or polypeptide of the present invention may be useful in
10 treating or detecting deficiencies or disorders of hematopoietic cells. A polypeptide or polynucleotide of the present invention could be used to increase differentiation and proliferation of hematopoietic cells, including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain (or many) types hematopoietic cells. Examples of immunologic deficiency syndromes include, but are not limited to:
15 blood protein disorders (e.g. agammaglobulinemia, dysgammaglobulinemia), ataxia telangiectasia, common variable immunodeficiency, Digeorge Syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency (SCIDs), Wiskott-Aldrich Disorder, anemia, thrombocytopenia, or hemoglobinuria.

Moreover, a polypeptide or polynucleotide of the present invention could also
20 be used to modulate hemostatic (the stopping of bleeding) or thrombolytic activity (clot formation). For example, by increasing hemostatic or thrombolytic activity, a polynucleotide or polypeptide of the present invention could be used to treat blood coagulation disorders (e.g., afibrinogenemia, factor deficiencies), blood platelet
25 disorders (e.g. thrombocytopenia), or wounds resulting from trauma, surgery, or other causes. Alternatively, a polynucleotide or polypeptide of the present invention that can decrease hemostatic or thrombolytic activity could be used to inhibit or dissolve clotting. These molecules could be important in the treatment of heart attacks (infarction), strokes, or scarring.

A polynucleotide or polypeptide of the present invention may also be useful in
30 treating or detecting autoimmune disorders. Many autoimmune disorders result from inappropriate recognition of self as foreign material by immune cells. This inappropriate recognition results in an immune response leading to the destruction of the host tissue. Therefore, the administration of a polypeptide or polynucleotide of the
35 present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing autoimmune disorders.

Examples of autoimmune disorders that can be treated or detected by the present invention include, but are not limited to: Addison's Disease, hemolytic anemia, antiphospholipid syndrome, rheumatoid arthritis, dermatitis, allergic encephalomyelitis, glomerulonephritis, Goodpasture's Syndrome, Graves' Disease, Multiple Sclerosis, Myasthenia Gravis, Neuritis, Ophthalmia, Bullous Pemphigoid, Pemphigus, Polyendocrinopathies, Purpura, Reiter's Disease, Stiff-Man Syndrome, Autoimmune Thyroiditis, Systemic Lupus Erythematosus, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitus, and autoimmune inflammatory eye disease.

Similarly, allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated by a polypeptide or polynucleotide of the present invention. Moreover, these molecules can be used to treat anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility.

A polynucleotide or polypeptide of the present invention may also be used to treat and/or prevent organ rejection or graft-versus-host disease (GVHD). Organ rejection occurs by host immune cell destruction of the transplanted tissue through an immune response. Similarly, an immune response is also involved in GVHD, but, in this case, the foreign transplanted immune cells destroy the host tissues. The administration of a polypeptide or polynucleotide of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing organ rejection or GVHD.

Similarly, a polypeptide or polynucleotide of the present invention may also be used to modulate inflammation. For example, the polypeptide or polynucleotide may inhibit the proliferation and differentiation of cells involved in an inflammatory response. These molecules can be used to treat inflammatory conditions, both chronic and acute conditions, including inflammation associated with infection (e.g., septic shock, sepsis, or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, or resulting from over production of cytokines (e.g., TNF or IL-1.)

Hyperproliferative Disorders

A polypeptide or polynucleotide can be used to treat or detect hyperproliferative disorders, including neoplasms. A polypeptide or polynucleotide of the present invention may inhibit the proliferation of the disorder through direct or indirect

interactions. Alternatively, a polypeptide or polynucleotide of the present invention may proliferate other cells which can inhibit the hyperproliferative disorder.

For example, by increasing an immune response, particularly increasing antigenic qualities of the hyperproliferative disorder or by proliferating, differentiating, or mobilizing T-cells, hyperproliferative disorders can be treated. This immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, decreasing an immune response may also be a method of treating hyperproliferative disorders, such as a chemotherapeutic agent.

Examples of hyperproliferative disorders that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but are not limited to neoplasms located in the: abdomen, bone, breast, digestive system, liver, pancreas, peritoneum, endocrine glands (adrenal, parathyroid, pituitary, testicles, ovary, thymus, thyroid), eye, head and neck, nervous (central and peripheral), lymphatic system, pelvic, skin, soft tissue, spleen, thoracic, and urogenital.

Similarly, other hyperproliferative disorders can also be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of such hyperproliferative disorders include, but are not limited to: hypergammaglobulinemia, lymphoproliferative disorders, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenstrom's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease, besides neoplasia, located in an organ system listed above.

Infectious Disease

A polypeptide or polynucleotide of the present invention can be used to treat or detect infectious agents. For example, by increasing the immune response, particularly increasing the proliferation and differentiation of B and/or T cells, infectious diseases may be treated. The immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, the polypeptide or polynucleotide of the present invention may also directly inhibit the infectious agent, without necessarily eliciting an immune response.

Viruses are one example of an infectious agent that can cause disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of viruses, include, but are not limited to the following DNA and RNA viral families: Arbovirus, Adenoviridae, Arenaviridae, Arterivirus, Birnaviridae, Bunyaviridae, Caliciviridae, Circoviridae, Coronaviridae, Flaviviridae, Hepadnaviridae (Hepatitis), Herpesviridae (such as, Cytomegalovirus, Herpes

Simplex, Herpes Zoster), Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae), Orthomyxoviridae (e.g., Influenza), Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g., Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g., Rubivirus). Viruses falling within these families can cause a variety of diseases or symptoms, including, but not limited to: arthritis, bronchiolitis, encephalitis, eye infections (e.g., conjunctivitis, keratitis), chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), meningitis, opportunistic infections (e.g., AIDS), pneumonia, Burkitt's Lymphoma, chickenpox, hemorrhagic fever, Measles, Mumps, Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's, warts), and viremia. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Similarly, bacterial or fungal agents that can cause disease or symptoms and that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following Gram-Negative and Gram-positive bacterial families and fungi: Actinomycetales (e.g., Corynebacterium, Mycobacterium, Norcardia), Aspergillosis, Bacillaceae (e.g., Anthrax, Clostridium), Bacteroidaceae, Blastomycosis, Bordetella, Borrelia, Brucellosis, Candidiasis, Campylobacter, Coccidioidomycosis, Cryptococcosis, Dermatocycoses, Enterobacteriaceae (Klebsiella, Salmonella, Serratia, Yersinia), Erysipelothrix, Helicobacter, Legionellosis, Leptospirosis, Listeria, Mycoplasmatales, Neisseriaceae (e.g., Acinetobacter, Gonorrhea, Meningococcal), Pasteurellaceae Infections (e.g., Actinobacillus, Haemophilus, Pasteurella), Pseudomonas, Rickettsiaceae, Chlamydiaceae, Syphilis, and Staphylococcal. These bacterial or fungal families can cause the following diseases or symptoms, including, but not limited to: bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis), gingivitis, opportunistic infections (e.g., AIDS related infections), paronychia, prosthesis-related infections, Reiter's Disease, respiratory tract infections, such as Whooping Cough or Empyema, sepsis, Lyme Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning, Typhoid, pneumonia, Gonorrhea, meningitis, Chlamydia, Syphilis, Diphtheria, Leprosy, Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus, impetigo, Rheumatic Fever, Scarlet Fever, sexually transmitted diseases, skin diseases (e.g., cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Moreover, parasitic agents causing disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following families: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis, Dourine, Ectoparasitic, Giardiasis, Helminthiasis, Leishmaniasis, Theileriasis, Toxoplasmosis, Trypanosomiasis, and Trichomonas. These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), Malaria, pregnancy complications, and toxoplasmosis. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Preferably, treatment using a polypeptide or polynucleotide of the present invention could either be by administering an effective amount of a polypeptide to the patient, or by removing cells from the patient, supplying the cells with a polynucleotide of the present invention, and returning the engineered cells to the patient (ex vivo therapy). Moreover, the polypeptide or polynucleotide of the present invention can be used as an antigen in a vaccine to raise an immune response against infectious disease.

Regeneration

A polynucleotide or polypeptide of the present invention can be used to differentiate, proliferate, and attract cells, leading to the regeneration of tissues. (See, Science 276:59-87 (1997).) The regeneration of tissues could be used to repair, replace, or protect tissue damaged by congenital defects, trauma (wounds, burns, incisions, or ulcers), age, disease (e.g. osteoporosis, osteoarthritis, periodontal disease, liver failure), surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, or systemic cytokine damage.

Tissues that could be regenerated using the present invention include organs (e.g., pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac), vascular (including vascular endothelium), nervous, hematopoietic, and skeletal (bone, cartilage, tendon, and ligament) tissue. Preferably, regeneration occurs without or decreased scarring. Regeneration also may include angiogenesis.

Moreover, a polynucleotide or polypeptide of the present invention may increase regeneration of tissues difficult to heal. For example, increased tendon/ligament regeneration would quicken recovery time after damage. A polynucleotide or polypeptide of the present invention could also be used prophylactically in an effort to avoid damage. Specific diseases that could be treated include of tendinitis, carpal tunnel syndrome, and other tendon or ligament defects. A further example of tissue

regeneration of non-healing wounds includes pressure ulcers, ulcers associated with vascular insufficiency, surgical, and traumatic wounds.

Similarly, nerve and brain tissue could also be regenerated by using a polynucleotide or polypeptide of the present invention to proliferate and differentiate
5 nerve cells. Diseases that could be treated using this method include central and peripheral nervous system diseases, neuropathies, or mechanical and traumatic disorders (e.g., spinal cord disorders, head trauma, cerebrovascular disease, and stroke). Specifically, diseases associated with peripheral nerve injuries, peripheral neuropathy (e.g., resulting from chemotherapy or other medical therapies), localized
10 neuropathies, and central nervous system diseases (e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome), could all be treated using the polynucleotide or polypeptide of the present invention.

15 **Chemotaxis**

A polynucleotide or polypeptide of the present invention may have chemotaxis activity. A chemotactic molecule attracts or mobilizes cells (e.g., monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells) to a particular site in the body, such as inflammation, infection, or site of
20 hyperproliferation. The mobilized cells can then fight off and/or heal the particular trauma or abnormality.

A polynucleotide or polypeptide of the present invention may increase chemotactic activity of particular cells. These chemotactic molecules can then be used to treat inflammation, infection, hyperproliferative disorders, or any immune system
25 disorder by increasing the number of cells targeted to a particular location in the body. For example, chemotactic molecules can be used to treat wounds and other trauma to tissues by attracting immune cells to the injured location. Chemotactic molecules of the present invention can also attract fibroblasts, which can be used to treat wounds.

It is also contemplated that a polynucleotide or polypeptide of the present
30 invention may inhibit chemotactic activity. These molecules could also be used to treat disorders. Thus, a polynucleotide or polypeptide of the present invention could be used as an inhibitor of chemotaxis.

Binding Activity

35 A polypeptide of the present invention may be used to screen for molecules that bind to the polypeptide or for molecules to which the polypeptide binds. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit

(antagonist), or decrease activity of the polypeptide or the molecule bound. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural or functional mimetic. (See, Coligan et al., Current Protocols in Immunology 1(2):Chapter 5 (1991).) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or at least, a fragment of the receptor capable of being bound by the polypeptide (e.g., active site). In either case, the molecule can be rationally designed using known techniques.

Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, *Drosophila*, or *E. coli*. Cells expressing the polypeptide (or cell membrane containing the expressed polypeptide) are then preferably contacted with a test compound potentially containing the molecule to observe binding, stimulation, or inhibition of activity of either the polypeptide or the molecule.

The assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a label, or in an assay involving competition with a labeled competitor. Further, the assay may test whether the candidate compound results in a signal generated by binding to the polypeptide.

Alternatively, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

Preferably, an ELISA assay can measure polypeptide level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The antibody can measure polypeptide level or activity by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptide from suitably manipulated cells or tissues.

Therefore, the invention includes a method of identifying compounds which bind to a polypeptide of the invention comprising the steps of: (a) incubating a candidate binding compound with a polypeptide of the invention; and (b) determining if binding has occurred. Moreover, the invention includes a method of identifying
5 agonists/antagonists comprising the steps of: (a) incubating a candidate compound with a polypeptide of the invention, (b) assaying a biological activity, and (b) determining if a biological activity of the polypeptide has been altered.

Other Activities

10 A polypeptide or polynucleotide of the present invention may also increase or decrease the differentiation or proliferation of embryonic stem cells, besides, as discussed above, hematopoietic lineage.

A polypeptide or polynucleotide of the present invention may also be used to modulate mammalian characteristics, such as body height, weight, hair color, eye color,
15 skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery). Similarly, a polypeptide or polynucleotide of the present invention may be used to modulate mammalian metabolism affecting catabolism, anabolism, processing, utilization, and storage of energy.

A polypeptide or polynucleotide of the present invention may be used to change
20 a mammal's mental state or physical state by influencing biorhythms, circadian rhythms, depression (including depressive disorders), tendency for violence, tolerance for pain, reproductive capabilities (preferably by Activin or Inhibin-like activity), hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities.

25 A polypeptide or polynucleotide of the present invention may also be used as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components.

Other Preferred Embodiments

Other preferred embodiments of the claimed invention include an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 50 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1.

35 Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of

positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Clone Sequence and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous
5 nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Start Codon and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Similarly preferred is a nucleic acid molecule wherein said sequence of
10 contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide
15 sequence which is at least 95% identical to a sequence of at least about 150 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

Further preferred is an isolated nucleic acid molecule comprising a nucleotide
20 sequence which is at least 95% identical to a sequence of at least about 500 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

A further preferred embodiment is a nucleic acid molecule comprising a
nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ
ID NO:X beginning with the nucleotide at about the position of the 5' Nucleotide of the
First Amino Acid of the Signal Peptide and ending with the nucleotide at about the
25 position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in
Table 1.

A further preferred embodiment is an isolated nucleic acid molecule comprising
a nucleotide sequence which is at least 95% identical to the complete nucleotide
sequence of SEQ ID NO:X.

Also preferred is an isolated nucleic acid molecule which hybridizes under
30 stringent hybridization conditions to a nucleic acid molecule, wherein said nucleic acid molecule which hybridizes does not hybridize under stringent hybridization conditions to a nucleic acid molecule having a nucleotide sequence consisting of only A residues or of only T residues.

Also preferred is a composition of matter comprising a DNA molecule which
35 comprises a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the material deposited with the American Type

Culture Collection and given the ATCC Deposit Number shown in Table 1 for said cDNA Clone Identifier.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in the nucleotide sequence of a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the deposit given the ATCC Deposit Number shown in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said sequence of at least 50 contiguous nucleotides is included in the nucleotide sequence of the complete open reading frame sequence encoded by said human cDNA clone.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 150 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 500 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is a method for detecting in a biological sample a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing a nucleotide sequence of at least one nucleic acid molecule in said sample with a sequence selected from said group and determining whether the sequence of said nucleic acid molecule in said sample is at least 95% identical to said selected sequence.

Also preferred is the above method wherein said step of comparing sequences comprises determining the extent of nucleic acid hybridization between nucleic acid molecules in said sample and a nucleic acid molecule comprising said sequence selected from said group. Similarly, also preferred is the above method wherein said step of comparing sequences is performed by comparing the nucleotide sequence determined from a nucleic acid molecule in said sample with said sequence selected from said group. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

A further preferred embodiment is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting nucleic acid molecules in said sample, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for identifying the species, tissue or cell type of a biological sample can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject nucleic acid molecules, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for diagnosing a pathological condition can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1.

Also preferred is a polypeptide, wherein said sequence of contiguous amino acids is included in the amino acid sequence of SEQ ID NO:Y in the range of positions beginning with the residue at about the position of the First Amino Acid of the Secreted Portion and ending with the residue at about the Last Amino Acid of the Open Reading Frame as set forth for SEQ ID NO:Y in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the complete amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is a polypeptide wherein said sequence of contiguous amino acids is included in the amino acid sequence of a secreted portion of the secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in
5 Table 1.

Further preferred is an isolated antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as
10 defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method for detecting in a biological sample a polypeptide comprising an amino acid sequence which is at least 90% identical to a sequence of at
15 least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method
20 comprises a step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group and determining whether the sequence of said polypeptide molecule in said sample is at least 90% identical to said sequence of at least 10 contiguous amino acids.

Also preferred is the above method wherein said step of comparing an amino
25 acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group comprises determining the extent of specific binding of polypeptides in said sample to an antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an
30 amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method wherein said step of comparing sequences is
35 performed by comparing the amino acid sequence determined from a polypeptide molecule in said sample with said sequence selected from said group.

Also preferred is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting polypeptide molecules in said sample, if any, comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method for identifying the species, tissue or cell type of a biological sample, which method comprises a step of detecting polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the above group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

In any of these methods, the step of detecting said polypeptide molecules includes using an antibody.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a nucleotide sequence encoding a polypeptide wherein said polypeptide comprises an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said nucleotide sequence encoding a polypeptide has been optimized for expression of said polypeptide in a prokaryotic host.

Also preferred is an isolated nucleic acid molecule, wherein said polypeptide
5 comprises an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

10 Further preferred is a method of making a recombinant vector comprising inserting any of the above isolated nucleic acid molecule into a vector. Also preferred is the recombinant vector produced by this method. Also preferred is a method of making a recombinant host cell comprising introducing the vector into a host cell, as well as the recombinant host cell produced by this method.

15 Also preferred is a method of making an isolated polypeptide comprising culturing this recombinant host cell under conditions such that said polypeptide is expressed and recovering said polypeptide. Also preferred is this method of making an isolated polypeptide, wherein said recombinant host cell is a eukaryotic cell and said polypeptide is a secreted portion of a human secreted protein comprising an amino acid
20 sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y beginning with the residue at the position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y wherein Y is an integer set forth in Table 1 and said position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y is defined in Table 1; and an amino acid sequence of a secreted portion of a protein encoded by a human
25 cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The isolated polypeptide produced by this method is also preferred.

Also preferred is a method of treatment of an individual in need of an increased level of a secreted protein activity, which method comprises administering to such an
30 individual a pharmaceutical composition comprising an amount of an isolated polypeptide, polynucleotide, or antibody of the claimed invention effective to increase the level of said protein activity in said individual.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of
35 illustration and are not intended as limiting.

Examples

Example 1: Isolation of a Selected cDNA Clone From the Deposited Sample

5 Each cDNA clone in a cited ATCC deposit is contained in a plasmid vector. Table 1 identifies the vectors used to construct the cDNA library from which each clone was isolated. In many cases, the vector used to construct the library is a phage vector from which a plasmid has been excised. The table immediately below correlates the related plasmid for each phage vector used in constructing the cDNA library. For
10 example, where a particular clone is identified in Table 1 as being isolated in the vector "Lambda Zap," the corresponding deposited clone is in "pBluescript."

	<u>Vector Used to Construct Library</u>	<u>Corresponding Deposited Plasmid</u>
	Lambda Zap	pBluescript (pBS)
	Uni-Zap XR	pBluescript (pBS)
15	Zap Express	pBK
	lafmid BA	plafmid BA
	pSport1	pSport1
	pCMVSPORT 2.0	pCMVSPORT 2.0
	pCMVSPORT 3.0	pCMVSPORT 3.0
20	pCR [®] 2.1	pCR [®] 2.1

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Altling-Mees, M. A. and Short, J. M., Nucleic Acids Res. 17:9494 (1989)) and pBK (Altling-Mees, M. A. et al., Strategies 5:58-61 (1992)) are
25 commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Both can be transformed into E. coli strain XL-1 Blue, also available from Stratagene. pBS comes in 4 forms SK+, SK-, KS+ and KS. The S and K refers to the orientation of the polylinker to the T7 and T3 primer
30 sequences which flank the polylinker region ("S" is for SacI and "K" is for KpnI which are the first sites on each respective end of the linker). "+" or "-" refer to the orientation of the f1 origin of replication ("ori"), such that in one orientation, single stranded rescue initiated from the f1 ori generates sense strand DNA and in the other, antisense.

35 Vectors pSport1, pCMVSPORT 2.0 and pCMVSPORT 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into E. coli strain

DH10B, also available from Life Technologies. (See, for instance, Gruber, C. E., et al., *Focus* 15:59 (1993).) Vector lafmid BA (Bento Soares, Columbia University, NY) contains an ampicillin resistance gene and can be transformed into *E. coli* strain XL-1 Blue. Vector pCR[®]2.1, which is available from Invitrogen, 1600 Faraday Avenue,
5 Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, available from Life Technologies. (See, for instance, Clark, J. M., *Nuc. Acids Res.* 16:9677-9686 (1988) and Mead, D. et al., *Bio/Technology* 9: (1991).) Preferably, a polynucleotide of the present invention does not comprise the phage vector sequences identified for the particular clone in Table 1, as well as the
10 corresponding plasmid vector sequences designated above.

The deposited material in the sample assigned the ATCC Deposit Number cited in Table 1 for any given cDNA clone also may contain one or more additional plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing the same ATCC Deposit Number contain at least a plasmid for each cDNA clone
15 identified in Table 1. Typically, each ATCC deposit sample cited in Table 1 comprises a mixture of approximately equal amounts (by weight) of about 50 plasmid DNAs, each containing a different cDNA clone; but such a deposit sample may include plasmids for more or less than 50 cDNA clones, up to about 500 cDNA clones.

Two approaches can be used to isolate a particular clone from the deposited
20 sample of plasmid DNAs cited for that clone in Table 1. First, a plasmid is directly isolated by screening the clones using a polynucleotide probe corresponding to SEQ ID NO:X.

Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported.
25 The oligonucleotide is labeled, for instance, with ³²P-γ-ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press, Cold Spring, NY (1982).) The plasmid mixture is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as
30 those provided by the vector supplier or in related publications or patents cited above. The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening (e.g., Sambrook et al., *Molecular Cloning: A Laboratory*
35 *Manual*, 2nd Edit., (1989), Cold Spring Harbor Laboratory Press, pages 1.93 to 1.104), or other techniques known to those of skill in the art.

Alternatively, two primers of 17-20 nucleotides derived from both ends of the SEQ ID NO:X (i.e., within the region of SEQ ID NO:X bounded by the 5' NT and the 3' NT of the clone defined in Table 1) are synthesized and used to amplify the desired cDNA using the deposited cDNA plasmid as a template. The polymerase chain reaction is carried out under routine conditions, for instance, in 25 μ l of reaction mixture with 0.5 μ g of the above cDNA template. A convenient reaction mixture is 1.5-5 mM MgCl_2 , 0.01% (w/v) gelatin, 20 μ M each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

Several methods are available for the identification of the 5' or 3' non-coding portions of a gene which may not be present in the deposited clone. These methods include but are not limited to, filter probing, clone enrichment using specific probes, and protocols similar or identical to 5' and 3' "RACE" protocols which are well known in the art. For instance, a method similar to 5' RACE is available for generating the missing 5' end of a desired full-length transcript. (Fromont-Racine et al., Nucleic Acids Res. 21(7):1683-1684 (1993).)

Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcripts. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest is used to PCR amplify the 5' portion of the desired full-length gene. This amplified product may then be sequenced and used to generate the full length gene.

This above method starts with total RNA isolated from the desired source, although poly-A+ RNA can be used. The RNA preparation can then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase should then be inactivated and the RNA treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

This modified RNA preparation is used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction is

used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the desired gene.

5

Example 2: Isolation of Genomic Clones Corresponding to a Polynucleotide

A human genomic P1 library (Genomic Systems, Inc.) is screened by PCR using primers selected for the cDNA sequence corresponding to SEQ ID NO:X.,
10 according to the method described in Example 1. (See also, Sambrook.)

Example 3: Tissue Distribution of Polypeptide

Tissue distribution of mRNA expression of polynucleotides of the present invention is determined using protocols for Northern blot analysis, described by,
15 among others, Sambrook et al. For example, a cDNA probe produced by the method described in Example 1 is labeled with P³² using the rediprime™ DNA labeling system (Amersham Life Science), according to manufacturer's instructions. After labeling, the probe is purified using CHROMA SPIN-100™ column (Clontech Laboratories, Inc.), according to manufacturer's protocol number PT1200-1. The purified labeled probe is
20 then used to examine various human tissues for mRNA expression.

Multiple Tissue Northern (MTN) blots containing various human tissues (H) or human immune system tissues (IM) (Clontech) are examined with the labeled probe using ExpressHyb™ hybridization solution (Clontech) according to manufacturer's protocol number PT1190-1. Following hybridization and washing, the blots are
25 mounted and exposed to film at -70°C overnight, and the films developed according to standard procedures.

Example 4: Chromosomal Mapping of the Polynucleotides

An oligonucleotide primer set is designed according to the sequence at the 5'
30 end of SEQ ID NO:X. This primer preferably spans about 100 nucleotides. This primer set is then used in a polymerase chain reaction under the following set of conditions : 30 seconds, 95°C; 1 minute, 56°C; 1 minute, 70°C. This cycle is repeated 32 times followed by one 5 minute cycle at 70°C. Human, mouse, and hamster DNA is used as template in addition to a somatic cell hybrid panel containing individual
35 chromosomes or chromosome fragments (Bios, Inc). The reactions is analyzed on

either 8% polyacrylamide gels or 3.5 % agarose gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR fragment in the particular somatic cell hybrid.

5 **Example 5: Bacterial Expression of a Polypeptide**

A polynucleotide encoding a polypeptide of the present invention is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 1, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as
10 BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Amp^r), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site
15 (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning sites.

The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the E. coli strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, which expresses
20 the lacI repressor and also confers kanamycin resistance (Kan^r). Transformants are identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis.

Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml).
25 The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells are grown to an optical density 600 (O.D.⁶⁰⁰) of between 0.4 and 0.6. IPTG (Isopropyl-B-D-thiogalacto pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

30 Cells are grown for an extra 3 to 4 hours. Cells are then harvested by centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic agent 6 Molar Guanidine HCl by stirring for 3-4 hours at 4°C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from
35 QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high

affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995) QIAGEN, Inc., *supra*).

5 Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with 6 M guanidine-HCl, pH 5.

10 The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein can be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins are eluted by the addition of 250 mM imidazole. Imidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4° C or frozen at -80° C.

15 In addition to the above expression vector, the present invention further includes an expression vector comprising phage operator and promoter elements operatively linked to a polynucleotide of the present invention, called pHE4a. (ATCC Accession Number 209645, deposited on February 25, 1998.) This vector contains: 1) a 20 neomycinphosphotransferase gene as a selection marker, 2) an E. coli origin of replication, 3) a T5 phage promoter sequence, 4) two lac operator sequences, 5) a Shine-Delgarno sequence, and 6) the lactose operon repressor gene (*lacIq*). The origin of replication (*oriC*) is derived from pUC19 (LTI, Gaithersburg, MD). The promoter sequence and operator sequences are made synthetically.

25 DNA can be inserted into the pHEa by restricting the vector with NdeI and XbaI, BamHI, XhoI, or Asp718, running the restricted product on a gel, and isolating the larger fragment (the stuffer fragment should be about 310 base pairs). The DNA insert is generated according to the PCR protocol described in Example 1, using PCR primers having restriction sites for NdeI (5' primer) and XbaI, BamHI, XhoI, or 30 Asp718 (3' primer). The PCR insert is gel purified and restricted with compatible enzymes. The insert and vector are ligated according to standard protocols.

The engineered vector could easily be substituted in the above protocol to express protein in a bacterial system.

Example 6: Purification of a Polypeptide from an Inclusion Body

The following alternative method can be used to purify a polypeptide expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

- 5 Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50
10 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

- The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by
15 centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

- The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is discarded and the polypeptide containing supernatant is incubated at 4°C
20 overnight to allow further GuHCl extraction.

- Following high speed centrifugation (30,000 xg) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing
25 for 12 hours prior to further purification steps.

- To clarify the refolded polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive
30 Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant polypeptide should exhibit greater than 95% purity after the above refolding and purification steps. No major contaminant bands should be observed from Commassie blue stained 16% SDS-PAGE gel when 5 μ g of purified protein is loaded. The purified protein can also be tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

Example 7: Cloning and Expression of a Polypeptide in a Baculovirus Expression System

In this example, the plasmid shuttle vector pA2 is used to insert a polynucleotide into a baculovirus to express a polypeptide. This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus (AcMNPV) followed by convenient restriction sites such as BamHI, Xba I and Asp718. The polyadenylation site of the simian virus 40 ("SV40") is used for efficient polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene from *E. coli* under control of a weak *Drosophila* promoter in the same orientation, followed by the polyadenylation signal of the polyhedrin gene. The inserted genes are flanked on both sides by viral sequences for cell-mediated homologous recombination with wild-type viral DNA to generate a viable virus that express the cloned polynucleotide.

Many other baculovirus vectors can be used in place of the vector above, such as pAc373, pVL941, and pAcIM1, as one skilled in the art would readily appreciate, as long as the construct provides appropriately located signals for transcription, translation, secretion and the like, including a signal peptide and an in-frame AUG as required. Such vectors are described, for instance, in Luckow et al., *Virology* 170:31-39 (1989).

Specifically, the cDNA sequence contained in the deposited clone, including the AUG initiation codon and the naturally associated leader sequence identified in Table 1, is amplified using the PCR protocol described in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the pA2 vector does not need a second signal peptide. Alternatively, the vector can be modified (pA2 GP) to include a baculovirus leader sequence, using the standard methods described in Summers et al., "A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures," Texas Agricultural Experimental Station Bulletin No. 1555 (1987).

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The plasmid is digested with the corresponding restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("GeneClean" BIO 101 Inc., La Jolla, Ca.).

The fragment and the dephosphorylated plasmid are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing.

Five μg of a plasmid containing the polynucleotide is co-transfected with 1.0 μg of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., Proc. Natl. Acad. Sci. USA 84:7413-7417 (1987). One μg of BaculoGold™ virus DNA and 5 μg of the plasmid are mixed in a sterile well of a microtiter plate containing 50 μl of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 μl Lipofectin plus 90 μl Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is then incubated for 5 hours at 27° C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27° C for four days.

After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life

Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.)

5 After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 μ l of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested
10 and then they are stored at 4° C.

To verify the expression of the polypeptide, Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus containing the polynucleotide at a multiplicity of infection ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is
15 removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc., Rockville, MD). After 42 hours, 5 μ Ci of 35 S-methionine and 5 μ Ci 35 S-cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE
20 followed by autoradiography (if radiolabeled).

Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the produced protein.

Example 8: Expression of a Polypeptide in Mammalian Cells

The polypeptide of the present invention can be expressed in a mammalian cell.
25 A typical mammalian expression vector contains a promoter element, which mediates the initiation of transcription of mRNA, a protein coding sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription is achieved
30 with the early and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLV, HIV and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter).

Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden),
35 pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSPORT 2.0, and pCMVSPORT 3.0. Mammalian host cells that could be used

include, human HeLa, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the polypeptide can be expressed in stable cell lines containing the polynucleotide integrated into a chromosome. The co-transfection with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that carry several hundred or even several thousand copies of the gene of interest. (See, e.g., Alt, F. W., et al., J. Biol. Chem. 253:1357-1370 (1978); Hamlin, J. L. and Ma, C., Biochem. et Biophys. Acta, 1097:107-143 (1990); Page, M. J. and Sydenham, M. A., Biotechnology 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., Biochem J. 227:277-279 (1991); Bebbington et al., Bio/Technology 10:169-175 (1992). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

Derivatives of the plasmid pSV2-dhfr (ATCC Accession No. 37146), the expression vectors pC4 (ATCC Accession No. 209646) and pC6 (ATCC Accession No.209647) contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen et al., Molecular and Cellular Biology, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart et al., Cell 41:521-530 (1985).) Multiple cloning sites, e.g., with the restriction enzyme cleavage sites BamHI, XbaI and Asp718, facilitate the cloning of the gene of interest. The vectors also contain the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene, and the mouse DHFR gene under control of the SV40 early promoter.

Specifically, the plasmid pC6, for example, is digested with appropriate restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

A polynucleotide of the present invention is amplified according to the protocol outlined in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the vector does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

5 The amplified fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC6 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene is used for
10 transfection. Five μ g of the expression plasmid pC6 is cotransfected with 0.5 μ g of the plasmid pSVneo using lipofectin (Felgner et al., *supra*). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are
15 trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of
20 methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μ M, 2 μ M, 5 μ M, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 - 200 μ M. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

25

Example 9: Protein Fusions

The polypeptides of the present invention are preferably fused to other proteins. These fusion proteins can be used for a variety of applications. For example, fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG domains, and maltose
30 binding protein facilitates purification. (See Example 5; see also EP A 394,827; Traunecker, et al., Nature 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and albumin increases the halflife time in vivo. Nuclear localization signals fused to the polypeptides of the present invention can target the protein to a specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the
35 activity of a fusion protein. Fusion proteins can also create chimeric molecules having more than one function. Finally, fusion proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion

proteins described above can be made by modifying the following protocol, which outlines the fusion of a polypeptide to an IgG molecule, or the protocol described in Example 5.

5 Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an expression vector, preferably a mammalian expression vector.

10 For example, if pC4 (Accession No. 209646) is used, the human Fc portion can be ligated into the BamHI cloning site. Note that the 3' BamHI site should be destroyed. Next, the vector containing the human Fc portion is re-restricted with BamHI, linearizing the vector, and a polynucleotide of the present invention, isolated by the PCR protocol described in Example 1, is ligated into this BamHI site. Note that the polynucleotide is cloned without a stop codon, otherwise a fusion protein will not be produced.

15 If the naturally occurring signal sequence is used to produce the secreted protein, pC4 does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

20 Human IgG Fc region:

GGGATCCGGAGCCCAAATCTTCTGACAAAACTCACACATGCCACCGTGCC
CAGCACCTGAATTCGAGGGTGCACCGTCAGTCTTCCTCTTCCCCCAAACC
CAAGGACACCCTCATGATCTCCCGGACTCCTGAGGTCACATGCGTGGTGGT
GGACGTAAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACG
25 GCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC
AGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAACCCCC
ATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCT
30 GACCTGCCTGGTCAAAGGCTTCTATCCAAGCGACATCGCCGTGGAGTGGGA
GAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTGG
ACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA
GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGC
ACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGC
35 GACGGCCGCGACTCTAGAGGAT (SEQ ID NO:1)

Example 10: Production of an Antibody from a Polypeptide

The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) For example, cells expressing a polypeptide of the present invention is administered to an animal to induce the production of sera containing polyclonal antibodies. In a preferred method, a preparation of the secreted protein is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

In the most preferred method, the antibodies of the present invention are monoclonal antibodies (or protein binding fragments thereof). Such monoclonal antibodies can be prepared using hybridoma technology. (Köhler et al., Nature 256:495 (1975); Köhler et al., Eur. J. Immunol. 6:511 (1976); Köhler et al., Eur. J. Immunol. 6:292 (1976); Hammerling et al., in: Monoclonal Antibodies and T-Cell Hybridomas, Elsevier, N.Y., pp. 563-681 (1981).) In general, such procedures involve immunizing an animal (preferably a mouse) with polypeptide or, more preferably, with a secreted polypeptide-expressing cell. Such cells may be cultured in any suitable tissue culture medium; however, it is preferable to culture cells in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at about 56°C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 µg/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (Gastroenterology 80:225-232 (1981).) The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide.

Alternatively, additional antibodies capable of binding to the polypeptide can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the protein-specific antibody can be blocked by the polypeptide.

Such antibodies comprise anti-idiotypic antibodies to the protein-specific antibody and can be used to immunize an animal to induce formation of further protein-specific antibodies.

It will be appreciated that Fab and F(ab')₂ and other fragments of the antibodies of the present invention may be used according to the methods disclosed herein. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂ fragments). Alternatively, secreted protein-binding fragments can be produced through the application of recombinant DNA technology or through synthetic chemistry.

For in vivo use of antibodies in humans, it may be preferable to use "humanized" chimeric monoclonal antibodies. Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric antibodies are known in the art. (See, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

Example 11: Production Of Secreted Protein For High-Throughput Screening Assays

The following protocol produces a supernatant containing a polypeptide to be tested. This supernatant can then be used in the Screening Assays described in Examples 13-20.

First, dilute Poly-D-Lysine (644 587 Boehringer-Mannheim) stock solution (1mg/ml in PBS) 1:20 in PBS (w/o calcium or magnesium 17-516F Biowhittaker) for a working solution of 50ug/ml. Add 200 ul of this solution to each well (24 well plates) and incubate at RT for 20 minutes. Be sure to distribute the solution over each well (note: a 12-channel pipetter may be used with tips on every other channel). Aspirate off the Poly-D-Lysine solution and rinse with 1ml PBS (Phosphate Buffered Saline). The PBS should remain in the well until just prior to plating the cells and plates may be poly-lysine coated in advance for up to two weeks.

Plate 293T cells (do not carry cells past P+20) at 2×10^5 cells/well in .5ml DMEM(Dulbecco's Modified Eagle Medium)(with 4.5 G/L glucose and L-glutamine (12-604F Biowhittaker))/10% heat inactivated FBS(14-503F Biowhittaker)/1x Penstrep(17-602E Biowhittaker). Let the cells grow overnight.

The next day, mix together in a sterile solution basin: 300 ul Lipofectamine (18324-012 Gibco/BRL) and 5ml Optimem I (31985070 Gibco/BRL)/96-well plate. With a small volume multi-channel pipetter, aliquot approximately 2ug of an expression vector containing a polynucleotide insert, produced by the methods described in

5 Examples 8 or 9, into an appropriately labeled 96-well round bottom plate. With a multi-channel pipetter, add 50ul of the Lipofectamine/Optimem I mixture to each well. Pipette up and down gently to mix. Incubate at RT 15-45 minutes. After about 20 minutes, use a multi-channel pipetter to add 150ul Optimem I to each well. As a control, one plate of vector DNA lacking an insert should be transfected with each set of

10 transfections.

Preferably, the transfection should be performed by tag-teaming the following tasks. By tag-teaming, hands on time is cut in half, and the cells do not spend too much time on PBS. First, person A aspirates off the media from four 24-well plates of cells, and then person B rinses each well with .5-1ml PBS. Person A then aspirates off

15 PBS rinse, and person B, using a 12-channel pipetter with tips on every other channel, adds the 200ul of DNA/Lipofectamine/Optimem I complex to the odd wells first, then to the even wells, to each row on the 24-well plates. Incubate at 37°C for 6 hours.

While cells are incubating, prepare appropriate media, either 1%BSA in DMEM with 1x penstrep, or CHO-5 media (116.6 mg/L of CaCl₂ (anhyd); 0.00130 mg/L

20 CuSO₄·5H₂O; 0.050 mg/L of Fe(NO₃)₃·9H₂O; 0.417 mg/L of FeSO₄·7H₂O; 311.80 mg/L of KCl; 28.64 mg/L of MgCl₂; 48.84 mg/L of MgSO₄; 6995.50 mg/L of NaCl; 2400.0 mg/L of NaHCO₃; 62.50 mg/L of NaH₂PO₄·H₂O; 71.02 mg/L of Na₂HPO₄; .4320 mg/L of ZnSO₄·7H₂O; .002 mg/L of Arachidonic Acid ; 1.022 mg/L of Cholesterol; .070 mg/L of DL-alpha-Tocopherol-Acetate; 0.0520 mg/L of Linoleic

25 Acid; 0.010 mg/L of Linolenic Acid; 0.010 mg/L of Myristic Acid; 0.010 mg/L of Oleic Acid; 0.010 mg/L of Palmitic Acid; 0.010 mg/L of Palmitic Acid; 100 mg/L of Pluronic F-68; 0.010 mg/L of Stearic Acid; 2.20 mg/L of Tween 80; 4551 mg/L of D-Glucose; 130.85 mg/ml of L- Alanine; 147.50 mg/ml of L-Arginine-HCL; 7.50 mg/ml of L-Asparagine-H₂O; 6.65 mg/ml of L-Aspartic Acid; 29.56 mg/ml of L-Cystine-2HCL-H₂O; 31.29 mg/ml of L-Cystine-2HCL; 7.35 mg/ml of L-Glutamic Acid; 365.0

30 mg/ml of L-Glutamine; 18.75 mg/ml of Glycine; 52.48 mg/ml of L-Histidine-HCL-H₂O; 106.97 mg/ml of L-Isoleucine; 111.45 mg/ml of L-Leucine; 163.75 mg/ml of L-Lysine HCL; 32.34 mg/ml of L-Methionine; 68.48 mg/ml of L-Phenylalanine; 40.0 mg/ml of L-Proline; 26.25 mg/ml of L-Serine; 101.05 mg/ml of L-Threonine; 19.22

35 mg/ml of L-Tryptophan; 91.79 mg/ml of L-Tyrosine-2Na-2H₂O; 99.65 mg/ml of L-Valine; 0.0035 mg/L of Biotin; 3.24 mg/L of D-Ca Pantothenate; 11.78 mg/L of

Choline Chloride; 4.65 mg/L of Folic Acid; 15.60 mg/L of i-Inositol; 3.02 mg/L of Niacinamide; 3.00 mg/L of Pyridoxal HCL; 0.031 mg/L of Pyridoxine HCL; 0.319 mg/L of Riboflavin; 3.17 mg/L of Thiamine HCL; 0.365 mg/L of Thymidine; and 0.680 mg/L of Vitamin B₁₂; 25 mM of HEPES Buffer; 2.39 mg/L of Na Hypoxanthine; 5 0.105 mg/L of Lipoic Acid; 0.081 mg/L of Sodium Putrescine-2HCL; 55.0 mg/L of Sodium Pyruvate; 0.0067 mg/L of Sodium Selenite; 20uM of Ethanolamine; 0.122 mg/L of Ferric Citrate; 41.70 mg/L of Methyl-B-Cyclodextrin complexed with Linoleic Acid; 33.33 mg/L of Methyl-B-Cyclodextrin complexed with Oleic Acid; and 10 mg/L of Methyl-B-Cyclodextrin complexed with Retinal) with 2mm glutamine and 1x 10 penstrep. (BSA (81-068-3 Bayer) 100gm dissolved in 1L DMEM for a 10% BSA stock solution). Filter the media and collect 50 ul for endotoxin assay in 15ml polystyrene conical.

The transfection reaction is terminated, preferably by tag-teaming, at the end of the incubation period. Person A aspirates off the transfection media, while person B 15 adds 1.5ml appropriate media to each well. Incubate at 37°C for 45 or 72 hours depending on the media used: 1%BSA for 45 hours or CHO-5 for 72 hours.

On day four, using a 300ul multichannel pipetter, aliquot 600ul in one 1ml deep well plate and the remaining supernatant into a 2ml deep well. The supernatants from each well can then be used in the assays described in Examples 13-20.

20 It is specifically understood that when activity is obtained in any of the assays described below using a supernatant, the activity originates from either the polypeptide directly (e.g., as a secreted protein) or by the polypeptide inducing expression of other proteins, which are then secreted into the supernatant. Thus, the invention further provides a method of identifying the protein in the supernatant characterized by an 25 activity in a particular assay.

Example 12: Construction of GAS Reporter Construct

One signal transduction pathway involved in the differentiation and proliferation of cells is called the Jaks-STATs pathway. Activated proteins in the Jaks-STATs 30 pathway bind to gamma activation site "GAS" elements or interferon-sensitive responsive element ("ISRE"), located in the promoter of many genes. The binding of a protein to these elements alter the expression of the associated gene.

GAS and ISRE elements are recognized by a class of transcription factors called Signal Transducers and Activators of Transcription, or "STATs." There are six 35 members of the STATs family. Stat1 and Stat3 are present in many cell types, as is Stat2 (as response to IFN-alpha is widespread). Stat4 is more restricted and is not in

many cell types though it has been found in T helper class I, cells after treatment with IL-12. Stat5 was originally called mammary growth factor, but has been found at higher concentrations in other cells including myeloid cells. It can be activated in tissue culture cells by many cytokines.

5 The STATs are activated to translocate from the cytoplasm to the nucleus upon tyrosine phosphorylation by a set of kinases known as the Janus Kinase ("Jaks") family. Jaks represent a distinct family of soluble tyrosine kinases and include Tyk2, Jak1, Jak2, and Jak3. These kinases display significant sequence similarity and are generally catalytically inactive in resting cells.

10 The Jaks are activated by a wide range of receptors summarized in the Table below. (Adapted from review by Schidler and Darnell, Ann. Rev. Biochem. 64:621-51 (1995).) A cytokine receptor family, capable of activating Jaks, is divided into two groups: (a) Class 1 includes receptors for IL-2, IL-3, IL-4, IL-6, IL-7, IL-9, IL-11, IL-12, IL-15, Epo, PRL, GH, G-CSF, GM-CSF, LIF, CNTF, and thrombopoietin; and
15 (b) Class 2 includes IFN- α , IFN- γ , and IL-10. The Class 1 receptors share a conserved cysteine motif (a set of four conserved cysteines and one tryptophan) and a WSXWS motif (a membrane proximal region encoding Trp-Ser-Xxx-Trp-Ser (SEQ ID NO:2)).

20 Thus, on binding of a ligand to a receptor, Jaks are activated, which in turn activate STATs, which then translocate and bind to GAS elements. This entire process is encompassed in the Jaks-STATs signal transduction pathway.

25 Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the GAS or the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. For example, growth factors and cytokines are known to activate the Jaks-STATs pathway. (See Table below.) Thus, by using GAS elements linked to reporter molecules, activators of the Jaks-STATs pathway can be identified.

	<u>Ligand</u>	<u>tyk2</u>	<u>JAKs</u> <u>Jak1</u>	<u>Jak2</u>	<u>Jak3</u>	<u>STATS</u>	<u>GAS(elements) or ISRE</u>
	<u>IFN family</u>						
5	IFN-a/B	+	+	-	-	1,2,3	ISRE
	IFN-g		+	+	-	1	GAS (IRF1>Lys6>IFP)
	Il-10	+	?	?	-	1,3	
	<u>gp130 family</u>						
10	IL-6 (Pleiotrohic)	+	+	+	?	1,3	GAS (IRF1>Lys6>IFP)
	Il-11(Pleiotrohic)	?	+	?	?	1,3	
	OnM(Pleiotrohic)	?	+	+	?	1,3	
	LIF(Pleiotrohic)	?	+	+	?	1,3	
	CNTF(Pleiotrohic)	-/+	+	+	?	1,3	
15	G-CSF(Pleiotrohic)	?	+	?	?	1,3	
	IL-12(Pleiotrohic)	+	-	+	+	1,3	
	<u>g-C family</u>						
20	IL-2 (lymphocytes)	-	+	-	+	1,3,5	GAS
	IL-4 (lymph/myeloid)	-	+	-	+	6	GAS (IRF1 = IFP >>Ly6)(IgH)
	IL-7 (lymphocytes)	-	+	-	+	5	GAS
	IL-9 (lymphocytes)	-	+	-	+	5	GAS
	IL-13 (lymphocyte)	-	+	?	?	6	GAS
	IL-15	?	+	?	+	5	GAS
25	<u>gp140 family</u>						
	IL-3 (myeloid)	-	-	+	-	5	GAS (IRF1>IFP>>Ly6)
	IL-5 (myeloid)	-	-	+	-	5	GAS
	GM-CSF (myeloid)	-	-	+	-	5	GAS
30	<u>Growth hormone family</u>						
	GH	?	-	+	-	5	
	PRL	?	+/-	+	-	1,3,5	
	EPO	?	-	+	-	5	GAS(B-CAS>IRF1=IFP>>Ly6)
35	<u>Receptor Tyrosine Kinases</u>						
	EGF	?	+	+	-	1,3	GAS (IRF1)
	PDGF	?	+	+	-	1,3	
40	CSF-1	?	+	+	-	1,3	GAS (not IRF1)

To construct a synthetic GAS containing promoter element, which is used in the Biological Assays described in Examples 13-14, a PCR based strategy is employed to generate a GAS-SV40 promoter sequence. The 5' primer contains four tandem copies of the GAS binding site found in the IRF1 promoter and previously demonstrated to bind STATs upon induction with a range of cytokines (Rothman et al., Immunity 1:457-468 (1994).), although other GAS or ISRE elements can be used instead. The 5' primer also contains 18bp of sequence complementary to the SV40 early promoter sequence and is flanked with an XhoI site. The sequence of the 5' primer is:

5' : GCGCCTCGAGATTTCCCCGAAATCTAGATTTCCCCGAAATGATTTCCCCG
 10 AAATGATTTCCCCGAAATATCTGCCATCTCAATTAG:3' (SEQ ID NO:3)

The downstream primer is complementary to the SV40 promoter and is flanked with a Hind III site: 5':GCGGCAAGCTTTTGGCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in the B-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI/Hind III and subcloned into BLSK2-. (Stratagene.) Sequencing with forward and reverse primers confirms that the insert contains the following sequence:

5' : CTCGAGATTTCCCCGAAATCTAGATTTCCCCGAAATGATTTCCCCGAAATG
 20 ATTTCCCCGAAATATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCC
 CTAAGTCCGCCCCTAAGTCCGCCCAGTTCCGCCCATTCTCCGC
 CCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCTCGGC
 CTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTT
 TGCAAAAAGCTT:3' (SEQ ID NO:5)

25 With this GAS promoter element linked to the SV40 promoter, a GAS:SEAP2 reporter construct is next engineered. Here, the reporter molecule is a secreted alkaline phosphatase, or "SEAP." Clearly, however, any reporter molecule can be instead of SEAP, in this or in any of the other Examples. Well known reporter molecules that can be used instead of SEAP include chloramphenicol acetyltransferase (CAT), luciferase,
 30 alkaline phosphatase, B-galactosidase, green fluorescent protein (GFP), or any protein detectable by an antibody.

The above sequence confirmed synthetic GAS-SV40 promoter element is subcloned into the pSEAP-Promoter vector obtained from Clontech using HindIII and XhoI, effectively replacing the SV40 promoter with the amplified GAS:SV40 promoter element, to create the GAS-SEAP vector. However, this vector does not contain a
 35 neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

Thus, in order to generate mammalian stable cell lines expressing the GAS-SEAP reporter, the GAS-SEAP cassette is removed from the GAS-SEAP vector using SalI and NotI, and inserted into a backbone vector containing the neomycin resistance gene, such as pGFP-1 (Clontech), using these restriction sites in the multiple cloning
5 site, to create the GAS-SEAP/Neo vector. Once this vector is transfected into mammalian cells, this vector can then be used as a reporter molecule for GAS binding as described in Examples 13-14.

Other constructs can be made using the above description and replacing GAS with a different promoter sequence. For example, construction of reporter molecules
10 containing NFK-B and EGR promoter sequences are described in Examples 15 and 16. However, many other promoters can be substituted using the protocols described in these Examples. For instance, SRE, IL-2, NFAT, or Osteocalcin promoters can be substituted, alone or in combination (e.g., GAS/NF-KB/EGR, GAS/NF-KB, IL-2/NFAT, or NF-KB/GAS). Similarly, other cell lines can be used to test reporter
15 construct activity, such as HELA (epithelial), HUVEC (endothelial), Reh (B-cell), Saos-2 (osteoblast), HUVAC (aortic), or Cardiomyocyte.

Example 13: High-Throughput Screening Assay for T-cell Activity.

The following protocol is used to assess T-cell activity by identifying factors,
20 such as growth factors and cytokines, that may proliferate or differentiate T-cells. T-cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The T-cell used in this assay is Jurkat T-cells (ATCC Accession No. TIB-152), although Molt-3 cells (ATCC Accession No. CRL-1552) and
25 Molt-4 cells (ATCC Accession No. CRL-1582) cells can also be used.

Jurkat T-cells are lymphoblastic CD4+ Th1 helper cells. In order to generate stable cell lines, approximately 2 million Jurkat cells are transfected with the GAS-SEAP/neo vector using DMRIE-C (Life Technologies)(transfection procedure described below). The transfected cells are seeded to a density of approximately
30 20,000 cells per well and transfectants resistant to 1 mg/ml gentamicin selected. Resistant colonies are expanded and then tested for their response to increasing concentrations of interferon gamma. The dose response of a selected clone is demonstrated.

Specifically, the following protocol will yield sufficient cells for 75 wells containing 200 ul of cells. Thus, it is either scaled up, or performed in multiple to
35 generate sufficient cells for multiple 96 well plates. Jurkat cells are maintained in RPMI + 10% serum with 1%Pen-Strep. Combine 2.5 mls of OPTI-MEM (Life Technologies)

with 10 ug of plasmid DNA in a T25 flask. Add 2.5 ml OPTI-MEM containing 50 ul of DMRIE-C and incubate at room temperature for 15-45 mins.

During the incubation period, count cell concentration, spin down the required number of cells (10^7 per transfection), and resuspend in OPTI-MEM to a final
5 concentration of 10^7 cells/ml. Then add 1ml of 1×10^7 cells in OPTI-MEM to T25 flask and incubate at 37°C for 6 hrs. After the incubation, add 10 ml of RPMI + 15% serum.

The Jurkat:GAS-SEAP stable reporter lines are maintained in RPMI + 10% serum, 1 mg/ml Gentamicin, and 1% Pen-Strep. These cells are treated with supernatants containing a polypeptide as produced by the protocol described in Example 11.
10 On the day of treatment with the supernatant, the cells should be washed and resuspended in fresh RPMI + 10% serum to a density of 500,000 cells per ml. The exact number of cells required will depend on the number of supernatants being screened. For one 96 well plate, approximately 10 million cells (for 10 plates, 100 million cells) are required.

15 Transfer the cells to a triangular reservoir boat, in order to dispense the cells into a 96 well dish, using a 12 channel pipette. Using a 12 channel pipette, transfer 200 ul of cells into each well (therefore adding 100, 000 cells per well).

After all the plates have been seeded, 50 ul of the supernatants are transferred directly from the 96 well plate containing the supernatants into each well using a 12
20 channel pipette. In addition, a dose of exogenous interferon gamma (0.1, 1.0, 10 ng) is added to wells H9, H10, and H11 to serve as additional positive controls for the assay.

The 96 well dishes containing Jurkat cells treated with supernatants are placed in an incubator for 48 hrs (note: this time is variable between 48-72 hrs). 35 ul samples
25 from each well are then transferred to an opaque 96 well plate using a 12 channel pipette. The opaque plates should be covered (using sellophane covers) and stored at -20°C until SEAP assays are performed according to Example 17. The plates containing the remaining treated cells are placed at 4°C and serve as a source of material for repeating the assay on a specific well if desired.

30 As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate Jurkat T cells. Over 30 fold induction is typically observed in the positive control wells.

Example 14: High-Throughput Screening Assay Identifying Myeloid Activity

The following protocol is used to assess myeloid activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate myeloid cells.

- 5 Myeloid cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The myeloid cell used in this assay is U937, a pre-monocyte cell line, although TF-1, HL60, or KG1 can be used.

- 10 To transiently transfect U937 cells with the GAS/SEAP/Neo construct produced in Example 12, a DEAE-Dextran method (Kharbanda et. al., 1994, Cell Growth & Differentiation, 5:259-265) is used. First, harvest 2×10^7 U937 cells and wash with PBS. The U937 cells are usually grown in RPMI 1640 medium containing 10% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 mg/ml streptomycin.

- 15 Next, suspend the cells in 1 ml of 20 mM Tris-HCl (pH 7.4) buffer containing 0.5 mg/ml DEAE-Dextran, 8 ug GAS-SEAP2 plasmid DNA, 140 mM NaCl, 5 mM KCl, 375 uM $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$, 1 mM MgCl_2 , and 675 uM CaCl_2 . Incubate at 37°C for 45 min.

- 20 Wash the cells with RPMI 1640 medium containing 10% FBS and then resuspend in 10 ml complete medium and incubate at 37°C for 36 hr.

The GAS-SEAP/U937 stable cells are obtained by growing the cells in 400 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 400 ug/ml G418 for couple of passages.

- 25 These cells are tested by harvesting 1×10^8 cells (this is enough for ten 96-well plates assay) and wash with PBS. Suspend the cells in 200 ml above described growth medium, with a final density of 5×10^5 cells/ml. Plate 200 ul cells per well in the 96-well plate (or 1×10^5 cells/well).

- 30 Add 50 ul of the supernatant prepared by the protocol described in Example 11. Incubate at 37°C for 48 to 72 hr. As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate U937 cells. Over 30 fold induction is typically observed in the positive control wells. SEAP assay the supernatant according to the protocol described in Example 17.

Example 15: High-Throughput Screening Assay Identifying Neuronal Activity.

When cells undergo differentiation and proliferation, a group of genes are activated through many different signal transduction pathways. One of these genes, EGR1 (early growth response gene 1), is induced in various tissues and cell types upon activation. The promoter of EGR1 is responsible for such induction. Using the EGR1 promoter linked to reporter molecules, activation of cells can be assessed.

Particularly, the following protocol is used to assess neuronal activity in PC12 cell lines. PC12 cells (rat phenochromocytoma cells) are known to proliferate and/or differentiate by activation with a number of mitogens, such as TPA (tetradecanoyl phorbol acetate), NGF (nerve growth factor), and EGF (epidermal growth factor). The EGR1 gene expression is activated during this treatment. Thus, by stably transfecting PC12 cells with a construct containing an EGR promoter linked to SEAP reporter, activation of PC12 cells can be assessed.

The EGR/SEAP reporter construct can be assembled by the following protocol. The EGR-1 promoter sequence (-633 to +1)(Sakamoto K et al., Oncogene 6:867-871 (1991)) can be PCR amplified from human genomic DNA using the following primers:

5' GCGCTCGAGGGATGACAGCGATAGAACCCCGG -3' (SEQ ID NO:6)

5' GCGAAGCTTCGCGACTCCCCGGATCCGCCTC-3' (SEQ ID NO:7)

Using the GAS:SEAP/Neo vector produced in Example 12, EGR1 amplified product can then be inserted into this vector. Linearize the GAS:SEAP/Neo vector using restriction enzymes XhoI/HindIII, removing the GAS/SV40 stuffer. Restrict the EGR1 amplified product with these same enzymes. Ligate the vector and the EGR1 promoter.

To prepare 96 well-plates for cell culture, two mls of a coating solution (1:30 dilution of collagen type I (Upstate Biotech Inc. Cat#08-115) in 30% ethanol (filter sterilized)) is added per one 10 cm plate or 50 ml per well of the 96-well plate, and allowed to air dry for 2 hr.

PC12 cells are routinely grown in RPMI-1640 medium (Bio Whittaker) containing 10% horse serum (JRH BIOSCIENCES, Cat. # 12449-78P), 5% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 ug/ml streptomycin on a precoated 10 cm tissue culture dish. One to four split is done every three to four days. Cells are removed from the plates by scraping and resuspended with pipetting up and down for more than 15 times.

Transfect the EGR/SEAP/Neo construct into PC12 using the Lipofectamine protocol described in Example 11. EGR-SEAP/PC12 stable cells are obtained by growing the cells in 300 ug/ml G418. The G418-free medium is used for routine

growth but every one to two months, the cells should be re-grown in 300 ug/ml G418 for couple of passages.

To assay for neuronal activity, a 10 cm plate with cells around 70 to 80% confluent is screened by removing the old medium. Wash the cells once with PBS (Phosphate buffered saline). Then starve the cells in low serum medium (RPMI-1640 containing 1% horse serum and 0.5% FBS with antibiotics) overnight.

The next morning, remove the medium and wash the cells with PBS. Scrape off the cells from the plate, suspend the cells well in 2 ml low serum medium. Count the cell number and add more low serum medium to reach final cell density as 5×10^5 cells/ml.

Add 200 ul of the cell suspension to each well of 96-well plate (equivalent to 1×10^5 cells/well). Add 50 ul supernatant produced by Example 11, 37°C for 48 to 72 hr. As a positive control, a growth factor known to activate PC12 cells through EGR can be used, such as 50 ng/ul of Neuronal Growth Factor (NGF). Over fifty-fold induction of SEAP is typically seen in the positive control wells. SEAP assay the supernatant according to Example 17.

Example 16: High-Throughput Screening Assay for T-cell Activity

NF- κ B (Nuclear Factor κ B) is a transcription factor activated by a wide variety of agents including the inflammatory cytokines IL-1 and TNF, CD30 and CD40, lymphotoxin-alpha and lymphotoxin-beta, by exposure to LPS or thrombin, and by expression of certain viral gene products. As a transcription factor, NF- κ B regulates the expression of genes involved in immune cell activation, control of apoptosis (NF- κ B appears to shield cells from apoptosis), B and T-cell development, anti-viral and antimicrobial responses, and multiple stress responses.

In non-stimulated conditions, NF- κ B is retained in the cytoplasm with I- κ B (Inhibitor κ B). However, upon stimulation, I- κ B is phosphorylated and degraded, causing NF- κ B to shuttle to the nucleus, thereby activating transcription of target genes. Target genes activated by NF- κ B include IL-2, IL-6, GM-CSF, ICAM-1 and class 1 MHC.

Due to its central role and ability to respond to a range of stimuli, reporter constructs utilizing the NF- κ B promoter element are used to screen the supernatants produced in Example 11. Activators or inhibitors of NF- κ B would be useful in treating

diseases. For example, inhibitors of NF- κ B could be used to treat those diseases related to the acute or chronic activation of NF- κ B, such as rheumatoid arthritis.

To construct a vector containing the NF- κ B promoter element, a PCR based strategy is employed. The upstream primer contains four tandem copies of the NF- κ B binding site (GGGGACTTTCCC) (SEQ ID NO:8), 18 bp of sequence complementary to the 5' end of the SV40 early promoter sequence, and is flanked with an XhoI site:
 5':GCGGCCTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGAC
 TTTCCATCCTGCCATCTCAATTAG:3' (SEQ ID NO:9)

The downstream primer is complementary to the 3' end of the SV40 promoter and is flanked with a Hind III site:

5':GCGGCAAGCTTTTGGCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in the pB-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI and Hind III and subcloned into BLSK2-. (Stratagene)

Sequencing with the T7 and T3 primers confirms the insert contains the following sequence:

5':CTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGGACTTTCC
 ATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCCA
 TCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACT
 AATTTTTTTTATTTATGCAGAGGCCGAGGCCGCTCGGCCTCTGAGCTATTC
 CAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTT:
 3' (SEQ ID NO:10)

Next, replace the SV40 minimal promoter element present in the pSEAP2- promoter plasmid (Clontech) with this NF- κ B/SV40 fragment using XhoI and HindIII. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

In order to generate stable mammalian cell lines, the NF- κ B/SV40/SEAP cassette is removed from the above NF- κ B/SEAP vector using restriction enzymes SalI and NotI, and inserted into a vector containing neomycin resistance. Particularly, the NF- κ B/SV40/SEAP cassette was inserted into pGFP-1 (Clontech), replacing the GFP gene, after restricting pGFP-1 with SalI and NotI.

Once NF- κ B/SV40/SEAP/Neo vector is created, stable Jurkat T-cells are created and maintained according to the protocol described in Example 13. Similarly, the method for assaying supernatants with these stable Jurkat T-cells is also described in Example 13. As a positive control, exogenous TNF alpha (0.1, 1, 10 ng) is added to wells H9, H10, and H11, with a 5-10 fold activation typically observed.

Example 17: Assay for SEAP Activity

As a reporter molecule for the assays described in Examples 13-16, SEAP activity is assayed using the Tropix Phospho-light Kit (Cat. BP-400) according to the following general procedure. The Tropix Phospho-light Kit supplies the Dilution, Assay, and Reaction Buffers used below.

Prime a dispenser with the 2.5x Dilution Buffer and dispense 15 μ l of 2.5x dilution buffer into Optiplates containing 35 μ l of a supernatant. Seal the plates with a plastic sealer and incubate at 65°C for 30 min. Separate the Optiplates to avoid uneven heating.

Cool the samples to room temperature for 15 minutes. Empty the dispenser and prime with the Assay Buffer. Add 50 μ l Assay Buffer and incubate at room temperature 5 min. Empty the dispenser and prime with the Reaction Buffer (see the table below). Add 50 μ l Reaction Buffer and incubate at room temperature for 20 minutes. Since the intensity of the chemiluminescent signal is time dependent, and it takes about 10 minutes to read 5 plates on luminometer, one should treat 5 plates at each time and start the second set 10 minutes later.

Read the relative light unit in the luminometer. Set H12 as blank, and print the results. An increase in chemiluminescence indicates reporter activity.

Reaction Buffer Formulation:

# of plates	Rxn buffer diluent (ml)	CSPD (ml)
10	60	3
11	65	3.25
12	70	3.5
13	75	3.75
14	80	4
15	85	4.25
16	90	4.5
17	95	4.75
18	100	5
19	105	5.25
20	110	5.5
21	115	5.75
22	120	6

23	125	6.25
24	130	6.5
25	135	6.75
26	140	7
27	145	7.25
28	150	7.5
29	155	7.75
30	160	8
31	165	8.25
32	170	8.5
33	175	8.75
34	180	9
35	185	9.25
36	190	9.5
37	195	9.75
38	200	10
39	205	10.25
40	210	10.5
41	215	10.75
42	220	11
43	225	11.25
44	230	11.5
45	235	11.75
46	240	12
47	245	12.25
48	250	12.5
49	255	12.75
50	260	13

Example 18: High-Throughput Screening Assay Identifying Changes in Small Molecule Concentration and Membrane Permeability

Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium, sodium, and pH, as well as alter membrane potential. These alterations can be measured in an assay to identify supernatants which bind to receptors of a particular cell. Although the following protocol describes an assay for calcium, this protocol can easily be modified to detect changes in potassium, sodium, pH, membrane potential, or any other small molecule which is detectable by a fluorescent probe.

The following assay uses Fluorometric Imaging Plate Reader ("FLIPR") to measure changes in fluorescent molecules (Molecular Probes) that bind small molecules. Clearly, any fluorescent molecule detecting a small molecule can be used instead of the calcium fluorescent molecule, fluo-3, used here.

For adherent cells, seed the cells at 10,000 -20,000 cells/well in a Co-star black 96-well plate with clear bottom. The plate is incubated in a CO₂ incubator for 20 hours. The adherent cells are washed two times in Biotek washer with 200 ul of HBSS (Hank's Balanced Salt Solution) leaving 100 ul of buffer after the final wash.

A stock solution of 1 mg/ml fluo-3 is made in 10% pluronic acid DMSO. To load the cells with fluo-3, 50 ul of 12 ug/ml fluo-3 is added to each well. The plate is incubated at 37°C in a CO₂ incubator for 60 min. The plate is washed four times in the Biotek washer with HBSS leaving 100 ul of buffer.

5 For non-adherent cells, the cells are spun down from culture media. Cells are re-suspended to 2-5x10⁶ cells/ml with HBSS in a 50-ml conical tube. 4 ul of 1 mg/ml fluo-3 solution in 10% pluronic acid DMSO is added to each ml of cell suspension. The tube is then placed in a 37°C water bath for 30-60 min. The cells are washed twice with HBSS, resuspended to 1x10⁶ cells/ml, and dispensed into a microplate, 100
10 ul/well. The plate is centrifuged at 1000 rpm for 5 min. The plate is then washed once in Denley CellWash with 200 ul, followed by an aspiration step to 100 ul final volume.

For a non-cell based assay, each well contains a fluorescent molecule, such as fluo-3. The supernatant is added to the well, and a change in fluorescence is detected.

To measure the fluorescence of intracellular calcium, the FLIPR is set for the
15 following parameters: (1) System gain is 300-800 mW; (2) Exposure time is 0.4 second; (3) Camera F/stop is F/2; (4) Excitation is 488 nm; (5) Emission is 530 nm; and (6) Sample addition is 50 ul. Increased emission at 530 nm indicates an extracellular signaling event which has resulted in an increase in the intracellular Ca⁺⁺ concentration.

20 **Example 19: High-Throughput Screening Assay Identifying Tyrosine Kinase Activity**

The Protein Tyrosine Kinases (PTK) represent a diverse group of transmembrane and cytoplasmic kinases. Within the Receptor Protein Tyrosine Kinase
25 RPTK) group are receptors for a range of mitogenic and metabolic growth factors including the PDGF, FGF, EGF, NGF, HGF and Insulin receptor subfamilies. In addition there are a large family of RPTKs for which the corresponding ligand is unknown. Ligands for RPTKs include mainly secreted small proteins, but also membrane-bound and extracellular matrix proteins.

30 Activation of RPTK by ligands involves ligand-mediated receptor dimerization, resulting in transphosphorylation of the receptor subunits and activation of the cytoplasmic tyrosine kinases. The cytoplasmic tyrosine kinases include receptor associated tyrosine kinases of the src-family (e.g., src, yes, lck, lyn, fyn) and non-receptor linked and cytosolic protein tyrosine kinases, such as the Jak family, members
35 of which mediate signal transduction triggered by the cytokine superfamily of receptors (e.g., the Interleukins, Interferons, GM-CSF, and Leptin).

Because of the wide range of known factors capable of stimulating tyrosine kinase activity, the identification of novel human secreted proteins capable of activating tyrosine kinase signal transduction pathways are of interest. Therefore, the following protocol is designed to identify those novel human secreted proteins capable of activating the tyrosine kinase signal transduction pathways.

Seed target cells (e.g., primary keratinocytes) at a density of approximately 25,000 cells per well in a 96 well Loprodyne Silent Screen Plates purchased from Nalge Nunc (Naperville, IL). The plates are sterilized with two 30 minute rinses with 100% ethanol, rinsed with water and dried overnight. Some plates are coated for 2 hr with 100 ml of cell culture grade type I collagen (50 mg/ml), gelatin (2%) or polylysine (50 mg/ml), all of which can be purchased from Sigma Chemicals (St. Louis, MO) or 10% Matrigel purchased from Becton Dickinson (Bedford, MA), or calf serum, rinsed with PBS and stored at 4°C. Cell growth on these plates is assayed by seeding 5,000 cells/well in growth medium and indirect quantitation of cell number through use of alamarBlue as described by the manufacturer Alamar Biosciences, Inc. (Sacramento, CA) after 48 hr. Falcon plate covers #3071 from Becton Dickinson (Bedford, MA) are used to cover the Loprodyne Silent Screen Plates. Falcon Microtest III cell culture plates can also be used in some proliferation experiments.

To prepare extracts, A431 cells are seeded onto the nylon membranes of Loprodyne plates (20,000/200ml/well) and cultured overnight in complete medium. Cells are quiesced by incubation in serum-free basal medium for 24 hr. After 5-20 minutes treatment with EGF (60ng/ml) or 50 ul of the supernatant produced in Example 11, the medium was removed and 100 ml of extraction buffer ((20 mM HEPES pH 7.5, 0.15 M NaCl, 1% Triton X-100, 0.1% SDS, 2 mM Na₃VO₄, 2 mM Na₄P₂O₇ and a cocktail of protease inhibitors (# 1836170) obtained from Boehringer Mannheim (Indianapolis, IN) is added to each well and the plate is shaken on a rotating shaker for 5 minutes at 4°C. The plate is then placed in a vacuum transfer manifold and the extract filtered through the 0.45 mm membrane bottoms of each well using house vacuum. Extracts are collected in a 96-well catch/assay plate in the bottom of the vacuum manifold and immediately placed on ice. To obtain extracts clarified by centrifugation, the content of each well, after detergent solubilization for 5 minutes, is removed and centrifuged for 15 minutes at 4°C at 16,000 x g.

Test the filtered extracts for levels of tyrosine kinase activity. Although many methods of detecting tyrosine kinase activity are known, one method is described here.

Generally, the tyrosine kinase activity of a supernatant is evaluated by determining its ability to phosphorylate a tyrosine residue on a specific substrate (a

biotinylated peptide). Biotinylated peptides that can be used for this purpose include PSK1 (corresponding to amino acids 6-20 of the cell division kinase cdc2-p34) and PSK2 (corresponding to amino acids 1-17 of gastrin). Both peptides are substrates for a range of tyrosine kinases and are available from Boehringer Mannheim.

- 5 The tyrosine kinase reaction is set up by adding the following components in order. First, add 10ul of 5uM Biotinylated Peptide, then 10ul ATP/Mg₂₊ (5mM ATP/50mM MgCl₂), then 10ul of 5x Assay Buffer (40mM imidazole hydrochloride, pH7.3, 40 mM beta-glycerophosphate, 1mM EGTA, 100mM MgCl₂, 5 mM MnCl₂, 0.5 mg/ml BSA), then 5ul of Sodium Vanadate(1mM), and then 5ul of water. Mix the
- 10 components gently and preincubate the reaction mix at 30°C for 2 min. Initiate the reaction by adding 10ul of the control enzyme or the filtered supernatant.

The tyrosine kinase assay reaction is then terminated by adding 10 ul of 120mM EDTA and place the reactions on ice.

- Tyrosine kinase activity is determined by transferring 50 ul aliquot of reaction
- 15 mixture to a microtiter plate (MTP) module and incubating at 37°C for 20 min. This allows the streptavidin coated 96 well plate to associate with the biotinylated peptide. Wash the MTP module with 300ul/well of PBS four times. Next add 75 ul of anti-phosphotyrosine antibody conjugated to horse radish peroxidase(anti-P-Tyr-POD(0.5u/ml)) to each well and incubate at 37°C for one hour. Wash the well as
- 20 above.

- Next add 100ul of peroxidase substrate solution (Boehringer Mannheim) and incubate at room temperature for at least 5 mins (up to 30 min). Measure the absorbance of the sample at 405 nm by using ELISA reader. The level of bound peroxidase activity is quantitated using an ELISA reader and reflects the level of
- 25 tyrosine kinase activity.

Example 20: High-Throughput Screening Assay Identifying Phosphorylation Activity

- As a potential alternative and/or complement to the assay of protein tyrosine
- 30 kinase activity described in Example 19, an assay which detects activation (phosphorylation) of major intracellular signal transduction intermediates can also be used. For example, as described below one particular assay can detect tyrosine phosphorylation of the Erk-1 and Erk-2 kinases. However, phosphorylation of other molecules, such as Raf, JNK, p38 MAP, Map kinase kinase (MEK), MEK kinase,
- 35 Src, Muscle specific kinase (MuSK), IRAK, Tec, and Janus, as well as any other

phosphoserine, phosphotyrosine, or phosphothreonine molecule, can be detected by substituting these molecules for Erk-1 or Erk-2 in the following assay.

Specifically, assay plates are made by coating the wells of a 96-well ELISA plate with 0.1ml of protein G (1ug/ml) for 2 hr at room temp, (RT). The plates are then
5 rinsed with PBS and blocked with 3% BSA/PBS for 1 hr at RT. The protein G plates are then treated with 2 commercial monoclonal antibodies (100ng/well) against Erk-1 and Erk-2 (1 hr at RT) (Santa Cruz Biotechnology). (To detect other molecules, this step can easily be modified by substituting a monoclonal antibody detecting any of the above described molecules.) After 3-5 rinses with PBS, the plates are stored at 4°C
10 until use.

A431 cells are seeded at 20,000/well in a 96-well Loprodyne filterplate and cultured overnight in growth medium. The cells are then starved for 48 hr in basal medium (DMEM) and then treated with EGF (6ng/well) or 50 ul of the supernatants obtained in Example 11 for 5-20 minutes. The cells are then solubilized and extracts
15 filtered directly into the assay plate.

After incubation with the extract for 1 hr at RT, the wells are again rinsed. As a positive control, a commercial preparation of MAP kinase (10ng/well) is used in place of A431 extract. Plates are then treated with a commercial polyclonal (rabbit) antibody (1ug/ml) which specifically recognizes the phosphorylated epitope of the Erk-1 and
20 Erk-2 kinases (1 hr at RT). This antibody is biotinylated by standard procedures. The bound polyclonal antibody is then quantitated by successive incubations with Europium-streptavidin and Europium fluorescence enhancing reagent in the Wallac DELFIA instrument (time-resolved fluorescence). An increased fluorescent signal over background indicates a phosphorylation.

25

Example 21: Method of Determining Alterations in a Gene Corresponding to a Polynucleotide

RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is be isolated. cDNA is then generated from
30 these RNA samples using protocols known in the art. (See, Sambrook.) The cDNA is then used as a template for PCR, employing primers surrounding regions of interest in SEQ ID NO:X. Suggested PCR conditions consist of 35 cycles at 95°C for 30 seconds; 60-120 seconds at 52-58°C; and 60-120 seconds at 70°C, using buffer solutions described in Sidransky, D., et al., Science 252:706 (1991).

35 PCR products are then sequenced using primers labeled at their 5' end with T4 polynucleotide kinase, employing SequiTherm Polymerase. (Epicentre Technologies).

The intron-exon borders of selected exons is also determined and genomic PCR products analyzed to confirm the results. PCR products harboring suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

5 PCR products is cloned into T-tailed vectors as described in Holton, T.A. and Graham, M.W., Nucleic Acids Research, 19:1156 (1991) and sequenced with T7 polymerase (United States Biochemical). Affected individuals are identified by mutations not present in unaffected individuals.

10 Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated according to Example 2 are nick-translated with digoxigenindeoxy-uridine 5'-triphosphate (Boehringer Mannheim), and FISH performed as described in Johnson, Cg. et al., Methods Cell Biol. 35:73-99 (1991). Hybridization with the labeled probe is carried out using a vast excess of human cot-1 DNA for specific hybridization to the corresponding genomic locus.

15 Chromosomes are counterstained with 4,6-diamino-2-phenylidole and propidium iodide, producing a combination of C- and R-bands. Aligned images for precise mapping are obtained using a triple-band filter set (Chroma Technology, Brattleboro, VT) in combination with a cooled charge-coupled device camera (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson, Cv. 20 et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and chromosomal fractional length measurements are performed using the ISee Graphical Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the genomic region hybridized by the probe are identified as insertions, deletions, and translocations. These alterations are used as a diagnostic marker for an associated 25 disease.

Example 22: Method of Detecting Abnormal Levels of a Polypeptide in a Biological Sample

30 A polypeptide of the present invention can be detected in a biological sample, and if an increased or decreased level of the polypeptide is detected, this polypeptide is a marker for a particular phenotype. Methods of detection are numerous, and thus, it is understood that one skilled in the art can modify the following assay to fit their particular needs.

35 For example, antibody-sandwich ELISAs are used to detect polypeptides in a sample, preferably a biological sample. Wells of a microtiter plate are coated with specific antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal or polyclonal and are produced by the method described in Example 10.

The wells are blocked so that non-specific binding of the polypeptide to the well is reduced.

The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to validate results. The plates are then washed three times with deionized or distilled water to remove unbounded polypeptide.

Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove unbounded conjugate.

Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate (NPP) substrate solution to each well and incubate 1 hour at room temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale). Interpolate the concentration of the polypeptide in the sample using the standard curve.

Example 23: Formulating a Polypeptide

The secreted polypeptide composition will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the secreted polypeptide alone), the site of delivery, the method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" for purposes herein is thus determined by such considerations.

As a general proposition, the total pharmaceutically effective amount of secreted polypeptide administered parenterally per dose will be in the range of about 1 µg/kg/day to 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01 mg/kg/day, and most preferably for humans between about 0.01 and 1 mg/kg/day for the hormone. If given continuously, the secreted polypeptide is typically administered at a dose rate of about 1 µg/kg/hour to about 50 µg/kg/hour, either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes and the interval following treatment for responses to occur appears to vary depending on the desired effect.

Pharmaceutical compositions containing the secreted protein of the invention are administered orally, rectally, parenterally, intracisternally, intravaginally,

intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

The secreted polypeptide is also suitably administered by sustained-release systems. Suitable examples of sustained-release compositions include semi-permeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules.

Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman, U. et al., Biopolymers 22:547-556 (1983)), poly (2- hydroxyethyl methacrylate) (R. Langer et al., J. Biomed. Mater. Res. 15:167-277 (1981), and R. Langer, Chem. Tech. 12:98-105 (1982)), ethylene vinyl acetate (R. Langer et al.) or poly-D- (-)-3-hydroxybutyric acid (EP 133,988). Sustained-release compositions also include liposomally entrapped polypeptides. Liposomes containing the secreted polypeptide are prepared by methods known per se: DE 3,218,121; Epstein et al., Proc. Natl. Acad. Sci. USA 82:3688-3692 (1985); Hwang et al., Proc. Natl. Acad. Sci. USA 77:4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008; U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the optimal secreted polypeptide therapy.

For parenteral administration, in one embodiment, the secreted polypeptide is formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form (solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. For example, the formulation preferably does not include oxidizing agents and other compounds that are known to be deleterious to polypeptides.

Generally, the formulations are prepared by contacting the polypeptide uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

The carrier suitably contains minor amounts of additives such as substances that enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, manose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, poloxamers, or PEG.

The secreted polypeptide is typically formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of about 3 to 8. It will be understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

Any polypeptide to be used for therapeutic administration can be sterile. Sterility is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). Therapeutic polypeptide compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Polypeptides ordinarily will be stored in unit or multi-dose containers, for example, sealed ampoules or vials, as an aqueous solution or as a lyophilized formulation for reconstitution. As an example of a lyophilized formulation, 10-ml vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous polypeptide solution, and the resulting mixture is lyophilized. The infusion solution is prepared by reconstituting the lyophilized polypeptide using bacteriostatic Water-for-Injection.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the polypeptides of the present invention may be employed in conjunction with other therapeutic compounds.

Example 24: Method of Treating Decreased Levels of the Polypeptide

It will be appreciated that conditions caused by a decrease in the standard or normal expression level of a secreted protein in an individual can be treated by administering the polypeptide of the present invention, preferably in the secreted form.

5 Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a pharmaceutical composition comprising an amount of the polypeptide to increase the activity level of the polypeptide in such an individual.

10 For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the polypeptide for six consecutive days. Preferably, the polypeptide is in the secreted form. The exact details of the dosing scheme, based on administration and formulation, are provided in Example 23.

Example 25: Method of Treating Increased Levels of the Polypeptide

15 Antisense technology is used to inhibit production of a polypeptide of the present invention. This technology is one example of a method of decreasing levels of a polypeptide, preferably a secreted form, due to a variety of etiologies, such as cancer.

For example, a patient diagnosed with abnormally increased levels of a polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 20 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well tolerated. The formulation of the antisense polynucleotide is provided in Example 23.

Example 26: Method of Treatment Using Gene Therapy

25 One method of gene therapy transplants fibroblasts, which are capable of expressing a polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and separated into small pieces. Small chunks of the tissue are placed on a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is 30 turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS, penicillin and streptomycin) is added. The flasks are then incubated at 37°C for approximately one week.

At this time, fresh media is added and subsequently changed every several days. After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

5 pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

10 The cDNA encoding a polypeptide of the present invention can be amplified using PCR primers which correspond to the 5' and 3' end sequences respectively as set forth in Example 1. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The ligation mixture is then used to
15 transform bacteria HB 101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene of interest properly inserted.

The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is
20 then added to the media and the packaging cells transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media,
25 containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is removed and replaced with fresh media. If the titer of virus is high, then virtually all fibroblasts will be infected and no selection is
30 required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine whether protein is produced.

The engineered fibroblasts are then transplanted onto the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

- 5 The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other disclosures) in the Background of the Invention, Detailed Description, and Examples is hereby incorporated herein by reference.

(1) GENERAL INFORMATION:

(i) APPLICANT: Human Genome Sciences, Inc. et al.
(ii) TITLE OF INVENTION: 87 Human Secreted Proteins
(iii) NUMBER OF SEQUENCES: 323
(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Human Genome Sciences, Inc.
(B) STREET: 9410 Key West Avenue
(C) CITY: Rockville
(D) STATE: Maryland
(E) COUNTRY: USA
(F) ZIP: 20850

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
(B) COMPUTER: HP Vectra 486/33
(C) OPERATING SYSTEM: MSDOS version 6.2
(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: March 19, 1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: A. Anders Brookes
(B) REGISTRATION NUMBER: 36,373
(C) REFERENCE/DOCKET NUMBER: PZ004PCT

(vi) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (301) 309-8504
(B) TELEFAX: (301) 309-8439

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 733 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

164

GGGATCCGGA GCCCAAATCT TCTGACAAAA CTCACACATG CCCACCGTGC CCAGCACCTG 60
AATTCGAGGG TGCACCGTCA GTCTTCCTCT TCCCCCAAA ACCCAAGGAC ACCCTCATGA 120
5 TCTCCCGGAC TCCTGAGGTC ACATGCGTGG TGGTGGACGT AAGCCACGAA GACCCTGAGG 180
TCAAAGTTCAA CTGGTACGTG GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCGCGGG 240
AGGAGCAGTA CAACAGCACG TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT 300
10 GGCTGAATGG CAAGGAGTAC AAGTGCAAGG TCTCCAACAA AGCCCTCCCA ACCCCCATCG 360
AGAAAACCAT CTCCAAAGCC AAAGGGCAGC CCCGAGAACC ACAGGTGTAC ACCCTGCCCC 420
15 CATCCCGGGA TGAGCTGACC AAGAACCAGG TCAGCCTGAC CTGCCTGGTC AAAGGCTTCT 480
ATCCAAGCGA CATCGCCGTG GAGTGGGAGA GCAATGGGCA GCCGAGAAC AACTACAAGA 540
CCACGCCTCC CGTGCTGGAC TCCGACGGCT CTTCTTCCT CTACAGCAAG CTCACCGTGG 600
20 ACAAGAGCAG GTGGCAGCAG GGAACGTCT TCTCATGCTC CGTGATGCAT GAGGCTCTGC 660
ACAACCACTA CACGAGAAG AGCCTCTCCC TGTCTCCGGG TAAATGAGTG CGACGGCCGC 720
25 GACTCTAGAG GAT 733

30 (2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

40 Trp Ser Xaa Trp Ser
1 5

45 (2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 base pairs

(B) TYPE: nucleic acid

50 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

55 GCGCCTCGAG ATTTCCCCGA AATCTAGATT TCCCCGAAAT GATTTCCCCG AAATGATTTT 60
CCCCGAAATAT CTGCCATCTC AATTAG 86

60

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GCGGCAAGCT TTTTGCAAAG CCTAGGC

27

15

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTCGAGATTT CCCCAGAAATC TAGATTTCCT CGAAATGATT TCCCCGAAAT GATTTCCTCCG 60
AAATATCTGC CATCTCAATT AGTCAGCAAC CATAGTCCCG CCCCTAACTC CGCCCATCCC 120
30 GCCCCTAACT CCGCCAGTT CCGCCATTC TCCGCCCAT GGCTGACTAA TTTTITTTAT 180
TTATGCAGAG GCCGAGGCCG CCTCGGCCTC TGAGCTATTC CAGAAGTAGT GAGGAGGCTT 240
35 TTTTGGAGGC CTAGGCTTTT GCAAAAAGCT T 271

40 (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

50 GCGCTCGAGG GATGACAGCG ATAGAACCCC GG

32

55 (2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

5

GCGAAGCTTC GCGACTCCCC GGATCCGCCT C

31

10

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 12 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

20

GGGGACTTTC CC

12

25

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 73 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

35

GCGGCCTCGA GGGGACTTTC CCGGGGACTT TCCGGGACT TTCCGGGACT TTCCATCCTG

60

CCATCTCAAT TAG

73

40

(2) INFORMATION FOR SEQ ID NO: 10:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CTCGAGGGGA CTTTCCCGGG GACTTTCCGG GGACTTTCCG GGACTTTCCA TCTGCCATCT

60

55

CAATTAGTCA GCAACCATAG TCCCGCCCCT AACTCCGCC ATCCCGCCCC TAACTCCGCC

120

CAGTTCCGCC CATCTCCGC CCCATGGCTG ACTAATTTT TTTATTTATG CAGAGGCCGA

180

GGCCGCCTCG GCCTCTGAGC TATTCCAGAA GTAGTGAGGA GGCTTTTGTG GAGGCCTAGG

240

60

167

CTTTTGCAAA AAGCTT

256

5

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1679 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

15 GCAGCGCACC CGGGCGATCG CTTACGCGAT GCGGACGACG TAGCCATCCT TACCTACGTG 60
AAGGAAAATG CCCGCTCGCC CAGCTCCGTC ACCGGTAACG CCTTGTGGAA AGCGATGGAG 120
20 AAGAGCTCGC TCACGCAGCA CTCGTGGCAG TCCCTGAAGG ACCGCTACCT CAAGCACCTG 180
CGGGGCCAGG AGCATAAGTA CCTGCTGGGG GACGCGCCGG TGAGCCCTC CTCCCAGAAG 240
CTCAAGCGGA AGGCGGAGGA GGACCCGGAG GCCGCGGATA GCGGGGAACC ACAGAATAAG 300
25 AGAACTCCAG ATTTGCCTGA AGAAGAGTAT GTGAAGGAAG AAATCCAGGA GAATGAAGAA 360
GCAGTCAAAA AGATGCTTGT GGAAGCCACC CGGGAGTTTG AGGAGGTTGT GGTGGATGAG 420
30 AGCCCTCCTG ATTTTGAAAT ACATATAACT ATGTGTGATG ATGATCCACC CACACCTGAG 480
GAAGACTCAG AAACACAGCC TGATGAGGAG GAAGAAGAAG AAGAAGAAAA AGTTTCTCAA 540
CCAGAGGTGG GAGCTGCCAT TAAGATCATT CGGCAGTTAA TGGAGAAGTT TAACTTGGAT 600
35 CTATCAACAG TTACACAGGC CTTCTAAAAA AATAGTGGTG AGCTGGAGGC TACTTCCGCC 660
TTCTTAGCGT CTGGTCAGAG AGCTGATGGA TATCCCATTT GGTCCCGACA AGATGACATA 720
40 GATTTGCAAA AAGATGATGA GGATACCAGA GAGGCATTGG TCAAAAATT TGGTGCTCAG 780
AATGTAGCTC GGAGGATTGA ATTTGAAAG AAATAATTGG CAAGATAATG AGAAAAGAAA 840
AAAGTCATGG TAGGTGAGGT GGTAAAAA AATTGTGACC AATGAACTTT AGAGAGTTCT 900
45 TGCATTGGAA CTGGCACTTA TTTTCTGACC ATCGCTGCTG TTGCTCTGTG AGTCCTAGAT 960
TTTTGTAGCC AAGCAGAGTT GTAGAGGGGG ATAAAAAGAA AAGAAATTGG ATGTATTTAC 1020
50 AGCTGTCCTT GAACAAGTAT CAATGTGTTT ATGAAAGGAA GATCTAAATC AGACAGGAGT 1080
TGGTCTACAT AGTAGTAATC CATGTGTTGA ATGGAACCCT TGCTATAGTA GTGACAAAGT 1140
GAAAGGAAAT TTAGGAGGCA TAGGCCATTT CAGGCAGCAT AAGTAATCTC CTGTCCTTTG 1200
55 GCAGAAGCTC CTTTAGATG GGATAGATTG CAAATAAAGA ATCTAGAAAT AGGAGAAGAT 1260
TTAATTATGA GGCCTTGAAC ACGGATTATC CCCAAACCCT TGTCAATTCC CCCAGTGAGC 1320
60 TCTGATTTCT AGACTGCTTT GAAAATGCTG TATTCATTTT GCTAACTTAG TATTTGGGTA 1380

5 CCCTGCTCTT TGGCTGTICT TTTTITGGAG CCCTTCTCAG TCAAGTCTGC CGGATGCTTT 1440
 TCTTTACCTA CCCCTCAGTT TTCCTTAAAA CGCGCACACA ACTCTAGAGA GTGTTAAGAA 1500
 TAATGTTACT TGGTTAATGT GTTATTTTAT GAGTATGTGTT TGTGCTAAGC ATTGTGTTAG 1560
 ATTTAAAAAA TTAGTGGATT GACTCCACTT TGTGTGTGTTG TTTTCATTGT TGAAAAATAAA 1620
 10 TATAACTTTG TATTCGAAAA AAAAAAAAAA AAAATNRC TG CGNCCGACA AGGGAATTC 1679

15 (2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1830 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

25 GCGACCGCGC CCTTCAGCTA GCTCGCTCGC TCGCTCTGCT TCCCTGCTGC CGGCTGCGCA 60
 TGGCTTNGGC GTTGGCGGCG CTGGCGGGCG TCGAGCNGCC TGCGSAGCCG GTACCAGCAG 120
 30 TTGCAGAATG AAGAAGAGTC TGGAGAACCT GAACAGGCTG CAGGTGATGC TCCTCCACCT 180
 TACAGCAGCA TTTCTGCAGA GAGCGCACAT NATTTTGA CT ACAAGGATGA GTCTGGGTTT 240
 CCAAAGCCCC CATCTTACAA TGTAGCTACA AACTGCCCCA GTTATGATGA AGCGGAGAGG 300
 35 ACCAAGGCTG AAGCTACTAT CCCTTTGGTT CTTGGGAGAG ATGAGGATTT TGTGGGTCGG 360
 GATGATTTTG ATGATGCTGA CCAGCTGAGG ATAGGAAATG ATGGGATTTT CATGTTAACT 420
 40 TTTTTCATGG CATTCCTCTT TAACTGGATT GGGTTTTTCC TGTCTTTTGG CCTGACCACT 480
 TCAGCTGCAG GAAGGTATGG GGCCATTTCA GGATTTGGTC TCTCTCTAAT TAAATGGATC 540
 CTGATTGTCA GGTMTTCCAC CTATTTCCCT GGATATTTTG ATGGTCAGTA CTGGCTCTGG 600
 45 TGGGTGTTCC TTGTTTTAGG CTTTCTCCTG TTTCTCAGAG GATTTATCAA TTATGCAAAA 660
 GTTCGGAAGA TGCCAGAAAC TTTCTCAAAT CTCCCAGGA CCAGAGTTCT CTTTATTTAT 720
 50 TAAAGATGTT TTCTGGCAAA GGCCTTCCTG CATTTATGAA TTCTCTCTCA AGAAGCAAGA 780
 GAACACCTGC AGGAAGTGAA TCAAGATGCA GAACACAGAG GAATAATCAC CTGCTTTAAA 840
 AAAATAAAGT ACTGTTGAAA AGATCATTTT TCTCTATTTG TTCCTAGGTG TAAAAATTTA 900
 55 ATAGTTAATG CAGAATCTG TAATCATTGA ATCATTAGTG GTTAATGTTT GAAAAAGCTC 960
 TTGCAATCAA GTCTGTGATG TATTAATAAT GCCTTATATA TTGTTTGTAG TCATTTTAAG 1020
 60 TAGCATGAGC CATGTCCCTG TAGTCGGTAG GGGGCAGTCT TGCTTTATTC ATCCTCCATC 1080

	TCAAAATGAA CTTGGAATTA AATATTGTAA GATATGTATA ATGCTGGCCA TTTTAAAGGG	1140
	GTTTTCTCAA AAGTTAAACT TTTGTTATGA CTGTGTTTTT GCACATAATC CATATTTGCT	1200
5	GTTCAAGTTA ATCTAGAAAT TTATTCAATT CTGTATGAAC ACCTGGAAGC AAAATCATAG	1260
	TGCAAAAATA CATTTAAGGT GTGGTCAAAA ATAAGTCTTT AATTGGTAAA TAATAAGCAT	1320
10	TAATTTTTTA TAGCCTGTAT TCACAATTCT GCGGTACCTT ATTGTACCTA AGGGATTCTA	1380
	AAGGTGTTGT CACTGTATAA AACAGAAAGC ACTAGGATAC AAATGAAGCT TAATTACTAA	1440
	AATGTAATTC TTGACACTCT TTCTATAATT AGCGTTCTTC ACCCCCACCC CCACCCCCAC	1500
15	CCCCCTTATT TTCCTTTTGT CTCCTGGTGA TTAGGCCAAA GTCTGGGAGT AAGGAGAGGA	1560
	TTAGGTACTT AGGAGCAAAG AAAGAAGTAG CTTGGAACTT TTGAGATGAT CCCTAACATA	1620
20	CTGTACTACT TGCTTTTACA ATGTGTTAGC AGAAACCACT GGGTTATAAT GTAGAATGAT	1680
	GTGCTTTCTG CCCAAGTGGT AATTCATCTT GGTTTGCTAT GTTAAACTG TAAATACAAC	1740
	AGAACATTAA TAAATATCTC TTGTGTAGCA CCTTTTAAAA AAAAAAAAAA AAAAAAAAAA	1800
25	AAAAAAAAA AANCCCGGGG GGGGGCCCN	1830
30	(2) INFORMATION FOR SEQ ID NO: 13:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1212 base pairs	
	(B) TYPE: nucleic acid	
35	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:	
40	TGTTTGAAGT TGTTACTTTT GTTTACAGCA AAGTTTGATG TAGTGTGCAG TAGTGAGCTC	60
	TAGACTGATC TTTTCTTAAA TCAGAAAGTG ATTAAAGTAT GCACAACCAA AGGCAGGTTT	120
45	TTCTTTTTC A TTTATTCAGC AACTATTAT TAAGCATCAA CTCTGTGCCA GGCACGTTAC	180
	TAGCTGCTAC ATACTGTCTG AACATGACAT ACGGTTAAGT AACTTTACAA TTATTATCAA	240
	ATACTTCAAT GTAGATATTT CTTAAGTTGA AATAGCATTA ACTAGGATAA TGCTTTCATG	300
50	TTATTTTATT TGTCTTGTGA TAGAAATTCA ACTTTGTACC ATCTTAAAAC TAGGTTGCTA	360
	TAAAAATAGG AGGATGAAGT CAATAAAGTT TATGCCAGTT TAAAACTGG AAGGAAAAGG	420
55	TAAGAGCTCT CCATTATAAA ATAGTTGCAT TCGGTTAATT TTTACACATT AGTGCAATTGC	480
	GTATATCAAC TGGCCCTCAA TGAAGCATTT AAGTGCTTGG AATTTTACTA AACTGACTTT	540
	TTTGCAACTT TGGGAGATTT TTGAGGGGAG TGTGAAAAT TGCCAAACAC TCACCTCTTA	600
60	CTCAAACTT CAAATAAAAT ACACATTTTC AAGAGGGAGC ACCTTTTATA TTTGATAAGT	660

	TTTCATTATA AACCTTATAA TACCAGTCAC AAAGAGGTTG TCTGTCTATG GTTTAGCAAA	720
5	CATTTGCTTT TCTTTTGGGA AGTGTGATTG CAATTGCAGA ACAGAAAGTG AGAAAACACT	780
	GCCAGCGGTG ATTGCTACTT GAGGTAGTTT TTTACAATA CCATTTCCCC TCCATGAAAT	840
	TATGTGAAAT TTATTTTATC TTTGGGAAAA GTTGAGAAGA TAGTAAAAGA ATTAGGAATT	900
10	TAAAATTACA GGGAAAAATA TGTAAGTGAA AAGCAATAAA TATTTTGTTT ACTTTGCTAT	960
	CAAGATGTTT ACTATCAGAT ATTTATTATA TGGCAGCAAT TTATATTTTT AATCATTGCC	1020
15	CATTAATAGA CGCAGTAAAA TATTTTGTAA TCAGACATTT GGGGTTTGTA TGTGCATTAA	1080
	AATTGTCTTT TGTACTGTAA GTTACTGTTA ATTTGAATAT TTTATTGAAC TGTCTCCCTG	1140
	TGCCTTTATA ATATAAAGTT GTTCTACAA CTTTAAATGA TCTTAATAAA GAATACTTTA	1200
20	AGAAAAAAA AA	1212
25	(2) INFORMATION FOR SEQ ID NO: 14:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 2061 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:	
35	GGTTTTCCTC CGACTTCGG ACATCTCCCT GGGAGTCGG CAGAGTGGAG TCAAAGGCAA	60
	CCAGTGCTCG CTGCGGTCTC TGGGGATCGG GACCGCGCG GCGGCCCGG AGCGGGATGT	120
40	TCCGGGGCTT GAGCAGTTGG TTGGGCTTGC AGCAGCCGGT GGCAGGCGGT GGCAGCCCA	180
	ATGGAGATGC TCCACCCGAG CAGCCGTCCG AGACGGTGGC TGAGTCTGCG GAGGAGGAGC	240
	TGCAGCAAGC GGGAGACCAG GAGCTCCTCC ACCAGGCCAA AGACTTCGGC AACTATTTAT	300
45	TTAACTTTGC ATCTGCTGCC AAAAAAAGA TAACTGAATC AGTTGCTGAA ACAGCACAAA	360
	CAATAAAGAA ATCCGTAGAA GAAGGAAAA TAGATGGCAT CATTGACAAG ACAATTATAG	420
50	GAGATTTTCA GAAGGAACAG AAAAAATTG TTGAAGAGCA ACATACAAAG AAGTCAGAAG	480
	CAGCTGTGCC CCCATGGGTT GACACTAAG ATGAAGAAAC AATTCAACAA CAAATTTTGG	540
	CCTTATCAGC TGACAAGAGG AATTTCTCTC GTGACCCTCC GGCTGGCGTG CAATTTAATT	600
55	TCGACTTTGA TCAGATGTAC CCCGTGGCCC TGGTCATGCT CCAGGAGGAT GAGCTGCTAR	660
	CAAGATGAGA TTTGCCCTCG TTCCTAACT TGTGAAGGAA GAAGTGTCTT GGAGGAACAA	720
60	CTTTTACCGC GTCTCCCTGA TTAAGCAGTC AGCCAGCTC ACGGCCCTGG CTGCCCAACA	780

	GCAGGCCGCA GGAAGGGAG GAGAAGAGCA ATGGCAGAGA GCAAGATTG CCGCTGGAGA	840
	GGCAGTACGG CCCAAACGC CACCCGTTGT AATCAAATCT CAGCTTAAAA CTCAAGAGGA	900
5	TGAGGAAGAA ATTTCTACTA GCCCAGGTGT TTCTGAGTTT GTCAGTGATG CCTTCGATGC	960
	CTGTAACCTA AATCAGGAAG ATCTAAGGAA AGAAATGGAG CAACTAGTGC TTGACAAAAA	1020
	GCAAGAGGAG ACAGCCGTAC TGGAAGAGGA TTCTGCAGAT TGGGAAAAAG AACTGCAGCA	1080
10	GGAACTTCAA GAATATGAAG TGGTGACAGA ATCTGAAAAA CGAGATGAAA ACTGGGATAA	1140
	GGAAATAGAG AAAATGCTTC AAGAGGAAAA TTAGCTGTTC CTGAAATAGA AGAATAATCC	1200
15	TTAACAGTCT GCAAACGTAC ATTAAATCTT AGATGTTGAC AATTACTGAA TCAGAAGGCA	1260
	TGAAAGAGTA TAATTTTATG AAATTCAAAA TTATTCTTTT TTCAAGTTGA AACTGCCTC	1320
	TTCTACTTTA AAAAAGTATA TAGAACAGTT ACTTCTAATA ATCAGAAAGA GATGTTTTAT	1380
20	AGAACATTTC TTTAATATAA AGTTAGAGAT GTCTTCATAG GCAGTATGGC TATCTTTGCC	1440
	ACAGAAACAT AAGTAAATTT TTAGAGTTCT GTTTTCCATG AGGTCAAAAA TATAATTTAT	1500
25	TCCTCAGTCA TGGTTTTCTA AATATCTGTA CTCCACATTC CATTTTAATT GATATGAGGG	1560
	TGTTAAAGTA CCTACTTAAT GGGTTGATTA CTATCAAAAT GACCAAATTA TACCAAAGAA	1620
	CTTAAGAGGA AGCACTTTCA GAACTATTCA CTGCGCAGGT ATTTTCTAAA ATTCCACCTG	1680
30	AAAGCCAAAA GATAAAATAC ATNAGTTGGA TTTTAATGAT ATAAGCATCA CACAATTTTA	1740
	CATTAAGAAA TACTGTGCAG CCCATGCGTG GTGGCTCAGG CCTGTAATCC CAGCANTTTG	1800
35	GGAGGCCGAG GTGGGCAGAT CACCGGAGGT CAGGAGTTCT AGACCAGCCT TGCCAACATA	1860
	GTGAAACCCT GTCTTTACTA AAAATACAAA AATTAGCCGG GCATGGTGGC AGGCACCTGT	1920
	AATCCAGCT ACTAGGAGG CTTTGAACC CAGGAGGCAG AGGTTGCAGC GAGCTGAGAT	1980
40	CGCGCCACTG CACTCCAGCC TGGGTGATAG AGTGAGATTC AGTCTCAAAA AAAAAAAAAA	2040
	AAAAAAAAAA AATGACCTCG A	2061
45		

(2) INFORMATION FOR SEQ ID NO: 15:

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1412 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

	CCCTTCATCT GCGTTGCCAG GAACCTGTC AGCAGAACT TCTCAAGCCC CATCCTTGCC	60
60	AGGAAGCTCT GTGAAGGTC TGCTGATGAC CCAGATTCCT CCATGGTCCT CCTGTGTCTC	120

	CTGTTGGTGC CCTCTCTGCT CAGTCTCTTT GTACTGGGGC TATTTCTTTG GTTTCCTGAAG	180
5	AGAGAGAGAC AAGAAGAGTA CATTGAAGAG AAGAAGAGAG TGGACATTTG TCGGGAAACT	240
	CCTAACATAT GCCCCCATTC TGGAGAGAAC ACAGAGTACG ACACAATCCC TCACACTAAT	300
	AGAACAATCC TAAAGGAAGA TCCAGCAAAT ACGGTTTACT CCACTGTGGA AATACCGAAA	360
10	AAGATGGAAA ATCCCCACTC ACTGCTCACG ATGCCAGACA CACCAAGGCT ATTTGCCTAT	420
	GAGAATGTTA TCTAGACAGC AGTGCACTCC CCTAAGTCTC TGCTCAAAAA AAAACAATT	480
15	CTCGGCCCAA AGAAAACAAT CAGAAGAATT CACTGATTTG ACTAGAAACA TCAAGGAAGA	540
	ATGAAGAACG TTGACTTTT TCCAGGATAA ATTATCTCTG ATGCTTCTTT AGATTTAAGA	600
	GTTCAATAAT CCATCCACTG CTGAGAAATC TCCTCAAACC CAGAAGGTTT AATCACTTCA	660
20	TCCCAAAAAT GGGATTGTGA ATGTCAGCAA ACCATAAAAA AAGTGCTTAG AAGTATTCCT	720
	ATAAAAATGT AAATGCAAGG TCACACATAT TAATGACAGC CTGTTGTATT AATGATGGCT	780
25	CCAGGTCAGT GTCTGGAGTT TCATTCCATC CCAGGGCTTG GATGTCAGGA TTATACCAAG	840
	AGTCTTGCTA CCAGGAGGGC AAGAAGACCA AACAGACAG ACAAGTCCAG CAGAAGCAGA	900
	TGCACCTGAC AAAAATGGAT GTATTAAATTG GCTCTATAAA CTATGTGCCC AGCAYTATGC	960
30	TGAGCTTACA CTAATTGGTC AGACATGCTG TCTGCCCTCA TGAAATTGGC TCCAAATGAW	1020
	TGAACTACTT TCATGAGCAG TTGTAGCAGG CCTGACCACA GATTCCCAGA GGGCCAGGTG	1080
35	TGGATCCACA GGAATTGAAG GTCAAAGTTC ACAAAGATGA AGAATCAGGG TAGCTGACCA	1140
	TGTTTGGCAG ATACTATAAT GGAGACACAG AAGTGTGCAT GGCCCAAGGA CAAGGACCTC	1200
	CAGCCAGGCT TCATTTATGC ACTTGTCTGC AAAAGAAAAG TCTAGGTTTT AAGGCTGTGC	1260
40	CAGAAGCCAT CCAATAAAG AGACCGAGTC TGAAGTCACA TTGTAAATCT AGTGTAGGAG	1320
	ACTTGGAGTC AGGCAGTGAG ACTGGTGGGG CACGGGGGGC ANTGGGTANT GTAAACCTTT	1380
45	TAAAGATGGT TAATTCNICA TTAGTGTTTT TT	1412

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1052 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TTCTCTCTCT CTCTCTACCC CTCTGTCTC TCCTCCCTC CTCTCTCTC CTCTCTCTC

	TCTCTTCCTC TCCTCTCTCT TCCCTTCCTG TCTCTCTTCC CCTCCTCTCT CTCTTCCTGT	120
	CCTCTATCTC TTCCCTCCT CTATCTCTTC CTCTCCTCTC TCTCTTCCTC TCCTCTCTCT	180
5	CTCTTSCTTT CTTCTCTCTC TCCTGTCTCG GCTGTTGTGG GTTGCAAGTT GGGTGCTGCT	240
	GTTGTGGTCC TTCCAGAAAA CTGCCAGTAG AGGGCAGCCT GGGCATCCTA ATGCTTACTC	300
	TGGTTGTTAC ACAAAGAAAA TATTGGGGTC ACTGGCGAGC CCACCCACAC TCACCAGAAT	360
10	CTCCACTGTA GTCCCCCTAA CAAACAGCCC TTCACTTCCT CTCCCACTTC AGCAATTGT	420
	ATTTTGATGC CATTTGGCCTC AGATCAGAGT GTTTTAAATC ATCACGCCCT GGCTTATCCC	480
15	TGGTCGAGCC AGGACACGGG GTGCTTCAGT GGGTCTGTCA CCCTCTCTCC TTGAAGCATG	540
	TGCTTTTAT TTATTTACTT TTA CTCTCAC CCTGCTCCTG TACCAGCAGG GGCCACTTCA	600
	AAGCCAAGGT ACAGGGTGAT AACTTGTGGT CCAGCATCAG TTTTCTCCAC TTCTTTCTCC	660
20	CACTCACCCC CAGCAAGGTG CCTGGGGAGA CTTGAGCAGA TGTTTCATTT TGGCCTGGCC	720
	AGTGGCTGAA AGCAGGCCTC CAATGCACTG TGACCTCTGG CTTCCCCAGC AGCTTTCCCA	780
25	GAGAGGCAGA GGGGCCTTCC ACAGCCCGGG TTCTCCTGCT GCCTCCTGCC TGCTGCAGCT	840
	GCAGGCATTC TGAGGGGCAA CGTGGAGGAA GGGCCAGGGA TGCATGGGAT TTTAATTGTT	900
	TCATCACACC TTCCCCGTGG CAAAGAAACA GTCAGTCCTC TTCAGGTGTC TTCTGGATTT	960
30	CTGGTGATGG ACAGAGAAAT CTTTTTACAG TTTCAAATTA TGTTCACAA ATAAAAATTG	1020
	CATTTTTTAT TTTGGAAAAA AAAAAAAAAA AA	1052
35		

(2) INFORMATION FOR SEQ ID NO: 17:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 683 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

	AATTCGGCAG AGGCACATTAT CATGTACATA TAGCCTGTTT TTAGCATMG TTAGACAAAG	60
50	TAGGCATATT CCTTCCATC CAAGAACTCA TAACCTAGTA ATTGTAGTTG GCTGATAGCT	120
	CATTGCCCAT ACACAAGGAT CTAACACAAC CTCTTGAATA AACATCCCCC TTATTCAGAA	180
	ATGCCCTTTC CTATTTCCAT ATTGCAACTT TGCTTACAAA TTTCCAATCT GTCPTTCTGT	240
55	TTACAGAAGA TATACAAAAT TCCTTTTGTA TGATCTCTTT ATATCTCTTG ATTTTCTTTT	300
	GTGTTTGCTA CCAAAGGGCC TGCACATAGT GAGAAGATTG TGCATGATCT GTGAGCTCTA	360
60	CCACACCTGG AATTAGGGAT CACCAATATG AGAAAAAAA TTGGAGGTAC AAATAACATT	420

ATCATATGTW ATTGGCATAT AAATTACAGA TGTWTCATG ACTAAAAACC CTGTGGATAT 480
 WAACCMATG CAGATAAWTW TAATAAAATW TWTAAAAATW TWATCMAATA ATGATAGTGC 540
 5 TATTCAAATA CTTCAAATTT GCACAGTGAT TTATTTCTTA AAATATGTTA ACACATGTGA 600
 GCCAATACAC TGAGGTCACCT GGATAAATAA ACAGATTCTT GCAAAAAAAA AAAAAAAAAA 660
 10 ACTCGAGGGG GGCCCGTACC CTT 683

15 (2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1054 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

25 AAATCATTT AGGTGACACT ATAGAAGGTA CGCCTGCAGG TACCGGTCCG GAATCCCCGG 60
 GTCGACCCAC GMGNCCGGCG ACAAGATGGC AGCAGCGTGT CGGAGCGTGA AGGGCCTGGT 120
 30 GCGGTAATA ACCGGAGGAG CCTCGGGCCT GGGCCTGGCC ACGGCGGACG ACTTGTGGGG 180
 CAGGGAGCCT CTGCTGTGCT TCTGGACCTG CCCAACTCGG GTGGGGAGGC CCAAGCCAAG 240
 AAGTTAGGAA ACAACTGCCGTTTCGCCCCA GCCGACGTGA CCTCTGAGAA GGATGTGCAA 300
 35 ACAGCTCTGG CTCTAGCAAA AGGAAAGTTT GGCCGTGTGG ATGTAGCTGT CAACTGTGCA 360
 GGCATCGCGG TGGCTAGCAA GACGTACAAC TTAAAGAAGG GCCAGACCCA TACCTTGGA 420
 40 GACTTCCAGC GAGTTCTTGA TGTAATCTC ATGGGCACCT TCAATGTGAT CCGCCTGGTG 480
 GCTGGTGAGA TGGGCCAGAA TGAACCAGAC CAGGGAGGCC AACGTGGGGT CATCATCAAC 540
 ACTGCCAGTG TGGCTGCCTT CGAGGGTCAG GTTGGACAAG CTGCATACTC TGCTTCCAAG 600
 45 GGGGAATAG TGGGCATGAC ACTGCCCAT TCTCGGGATC TGGCTCCCAT AGGTATCCGG 660
 GTGATGACCA TTGCCCCAGG TCTGTTTGGC ACCCACTGCT TGACCAGCCT CCCAGAGAAA 720
 50 GTGTGCAACT TCTTGGCCAG CCAAGTGCCC TTCCCTAGCC GACTGGGTGA CCCTGCTGAG 780
 TATGCTCACC TCGTACAGGC CATCATCGAG AACCATTCC TCAATGGAGA GGTATCCGG 840
 CTGGATGGGG CCATTCTGAT GCAGCCTTGA AGGGAGAAGG CAGAGAAAAC ACACGCTCCT 900
 55 CTGCCCTTCC TTTCCCTGGG GTACTACTCT CCAGCTTGGG AGGAAGCCCA GTAGCCATTT 960
 TGTAAGTGCC TACCAGTCGC CCTCTGTGCC TAATAAAGTC TCTTTTCTC ACANAAAAA 1020
 60 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA 1054

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

5	GGAACAAGCT GGGATATGTG AGCGTTAAGC TACTCACATC CTTCAAAAAG GTGAAACATC	60
15	TTACACGGGA CTGGAGAACC ACAGCACATG CTTTGAAGTA TTCAGTGGTC CTGAGTTGA	120
	ATGAGGNCCA CCGGAAGGTG AGGAGGACCA CCCCCGTCCC ACTGTTCCCC AACGAGAACC	180
20	TCCCCAGCAA GATGCTCCTG GTCTATGATC TCTACTTGTY TCCTAAGCTG TGGGCTCTGG	240
	CCACCCCCCA GAAGAATGGG AAGGGTGCAA GARAAGTGA TGGAACACCT GCTCAAGCTT	300
25	TTTGGGACTT TTGGAGTCAT CTCATCAGTG CGGATCCTCA AACCTGGGAG AGAGCTGCCC	360
	CCTGACATCC GGAGGNTCCA GCAGCCGCTA CAGCTCCTCT GACCCCGAGA GCAACCCAC	420
	ATCCCTATG GCGGGCCGAC GGCACGNGKC CACCAACAAG CTCAGCCCGT CTGGCCACCA	480
30	GAATCTCTTT CTGAGTCCAA ATGCCTCCCC GTGCACAAGT CCTTGGAGCA GCCCCTTGGC	540
	CCAACGCAAA GCGGTTTCCA GAAAGTCCCC ACTGGCGGAG GAAGGTAGAC TGAAGTGCAG	600
35	CACCAGCCCT GAGATCTTCC GCAAGTGTAT GGATTATTCC TCTGACAGCA GCGTCACTCC	660
	CTCTGGCAGC CCCTGGGTCC GGAGGCGTCG CCAAGCCGAG ATGGGGACCC AGGAGAAAAG	720
	CCCCGGTACG AGTCCCCTGC TCTCCCGGAA GATGCAGACT GCAGATGGGS TACCCGTAGG	780
40	TNGCTTGAGG TTGCCCAGGG GTCCTGACAA CACCAGAGGA TTTTATGGCC ATGAGAGGAG	840
	CAGGGCCTGT GTATAAATAC CTTCTATTTT TAATACAAGC TCCACTGAAA ACCACCTTCG	900
45	TTTTCAAGGT TCTGACAAAC ACCTGGCATG ACAGAATGGA ATTCGTTCCC CTTTGAGAGA	960
	TTTTTTATTC ATGTAGACCT CTTAATTTAT CTATCTGTAA TATACATAAA TCGGTACGCC	1020
	ATGGTTTGAA GACCACCTTC TAGTTCAGGA CTCCTGTTCT TCCCAGCATG GCCACTATTT	1080
50	TGATGATGGC TGATGTGTGT GAGTGTGATG GCCCTGAAGG GCTGTAGGAC GGAGGTTCCC	1140
	TGGGGGAAGT CTGTTCTTTG GTATGGAATT TTCTCTCTT CTTTGGTATG GAATTTTTC	1200
55	CTTCAGTGAC TGAGCTGTCC TCGATAGGCC ATGCAAGGCG TTCCTGAGAG TTCAGGAAAG	1260
	TTCTCTTGTA CAACAGCAAG TAGCTAAGCC TATAGCATGG TGTCTGTAG GACCAAATCG	1320
	ATGTTACCTG TCAAGTAAAT AAATAATAAA ACACCCAAC TGGAGTGCTG AAAAAAANA	1380
60	ANNAAAAAAC TCG	1393

5 (2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1215 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

15 AGGAAAAGTT TTCCNAATTG GAAAGCGGCC AGTGAGCGCA ACGCAATTAA TGTGAGTTAG 60
NTCANTCATT AGGCACCCCA GGCTTTACAC TTTATGCTTC CGGNTCGTAT GTTGTGTGGA 120
20 ATGTGTGAGCG GATAACAATT TCACACAGGA AACAGCTATG ACCATGATTA CGCCAAGCTN 180
TAATACGACT CACTATAGGG AAAGCTGGTA CGCCTGCAGG TACCGGTCCG GAATTCCCGG 240
GTCGACCCAC GCGTCCGCC ACGCGTCCGT GAAAATCCGA AGTGCCGCGG AAAGTGGAGG 300
25 TGAGGGCCGC CCGCCCTAGA GGTGCCCGTC CGAGAGGCAG AGCTGACAAG GAAGGTTTCG 360
AGCGTTTTGC TGGCAAAGGG ATTTCTTACA ACCTCCAGGC ATGCGTCTTT CTGCCCTGCT 420
30 GGCTTTGGCA TCCAAGGTCA CTCTGCCCCC CCATTACCGC TATGGGATGA GCCCCCAGG 480
CTCTGTTGCA GACAAGAGGA AGAACCCCC ATGGATCAGG CGGCGCCAG TGGTTGTGGA 540
ACCCATCTCT GATGAAGACT GGTATCTGTT CTGTGGGGAC ACGGTGGAGA TCCTAGAAGG 600
35 CAAGGATGCC GGAAGCAGG GCAAAGTGGT TCAAGTTATC CGGCAGCGAA ACTGGGTGGT 660
CGTGGGAGGG CTGAACACAC ATTACCGCTA CATTGGCAAG ACCATGGATT ACCGGGGAAC 720
40 CATGATCCCT AGTGAAGCCC CCTTGCTCCA CCGCCAGGTC AAAGTTGTGG ATCCTATGGA 780
CAGGAAACCC ACTGAGATCG AGTGGAGATT TACTGAAGCA GGAGAGCGGG TACGAGTCTC 840
CACACGATCA GGGAGAATTA TCCCTAAACC CGAATTTCCC AGAGCTGATG GCATCGTCCC 900
45 TGAAACGTGG ATTGATGGCC CCAAAGACAC ATCAGTGGAA GATGCTTTAG AAAGAACCTA 960
TGTGCCCTGT CTAAAGACAC TGCAGGAGGA GGTGATGGAG GCCATGGGGA TCAAGGAGAC 1020
50 CCGGAAATAC AAGAAGGTCT ATTGGTATTG AGCCTGGGGC AGAGCAGCTC CTCCCCAACT 1080
TCTGTCCCAG CCTTGAAGGC TGAGGCACTT CTMTTTCAGA TGCCAATAAA GAGCACTTTA 1140
TGAGTCCTCC AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1200
55 AAAAGGGGCG GCCCG 1215

60 (2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2042 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

10	CTGCATCCAG GCGCAGAATA ACCTGGGTAT CTTGTGGTCT GAAAGAGAGA AATTGAAACT	60
	GCACAGGCTT ACCTAGAGTC ATCAGAAGCA CTATATAATC AGTATATGAA AGAGGTTGGG	120
	AGTCCTCCTC TTGATCCTAC TGAGCGTTTT CTTCTGAAGA AGAGAACTT ACTGAACAAG	180
15	AGAGATCAAA AAGATTGAA AAGGTTTATA CTCATAACCT ATATTACCTA GCTCAAGTCT	240
	ACCAGCATCT GGAAATGTTT GAGAAGGCTG CTCACTATTG CCATAGTACA CTAAAACGCC	300
20	AGCTTGAGCA CAATGCCTAC CATCCTATAG AGTGGGCTAT CAATGCTGCT ACCTTGTAC	360
	AGTTTTACAT CAATAAGCTA TGCTTTATGG AGGCCAGGCA CTGTTTATCA GCTGCTAATG	420
	TCATTTTGG TCAAAGTGA AAGATCTCAG CCACAGAAGA CACTCCTGAA GCTGAAGGAG	480
25	AAGTGCCAGA GCTTTATCAT CAAAGAAAGG GGGAAATAGC AAGGTGCTGG ATCAAATACT	540
	GTTTGACTCT CATGCAGAAT GCCCAACTCT CCATGCAGGA CAACATAGGA GAGCTTGATC	600
30	TTGATAACA GTCTGAACCT AGAGCTTTAA GGAAAAAGA ACTAGATGAG GAGGAAAGCA	660
	TTCGGAAAAA AGCTGTGCAG TTTGGAACCG GTGAACTGTG TGATGCCATC TCTGCAGTAG	720
	AAGAGAAAGT GAGCTACTTG AGACCTTTAG ATTTTGAAGA AGCCAGAGAA CTTTCTTAT	780
35	TGGGTCAGCA CTATGTCTTT GAGGCAAAAG AGTTCTTTCA GATTGATGGT TATGTCACTG	840
	ACCATATTGA AGTTGTCCAA GACCACAGTG CTCTGTTTAA GGTGCTTGCA TTCTTTGAAA	900
40	CTGACATGGA GAGACGGTGC AAGATGCATA AACGCRGAAT AGCCATGCTA GAGCCCCTAA	960
	CTGTAGACCT GAATCCACAG TATTATCTGT TGGTCAACAG ACAGATCCAG TTTGAAATG	1020
	CACATGCTTA CTATGATATG ATGGATTTGA AGGTTGCCAT TGCTGACAGG CTAAGGGATC	1080
45	CTGATTCACA CATGTAAAA AAAATAAATA ATCTTAATAA GTCAGCACTG AAGTACTACC	1140
	AGCTCTTCTT AGACTCCCTG AGAGACCCAA ATAAAGTATT CCCTGAGCAT ATAGGGGAAG	1200
50	ATGTTCTTCG CCCTGCCATG TTAGCTAAGT TFCGAGTTGC CCGTCTCTAT GGCAAAATCA	1260
	TTACTGCAGA TCCCAAGAAA GAGCTGGAAA ATTTGGCAAC ATCATTTGGA ACATTACAAA	1320
	TTTATTGTTG ATTACTGTGA AAAGCATCCT GAGGCCGCCC AGGAAATAGA AGTTGAGCTA	1380
55	GAACCTAGTA AAGAGATGGT TAGTCTTCTC CCAACAAAAA TGGAGAGATT CAGAACCAAG	1440
	ATGGCCCTGA CTTAATCCTT GTTTTAAAG AAAGGAAATG TGCAATATTG AAGTGATCTT	1500
60	TTTCCCTAGT CAGACAGGCC CAATTCCATT GTGATGTTTA CCTTTATAGC CAGGTGAGTG	1560

	CAGTTTGAAC TTGAGATACA GTCAACTGAG TGTTCGCTAG GATCCTAAGG AACATAAAGT	1620
5	TAATTAAAAA CTTACACCTA ATTATGTAAA TTGCCTTGTT AAAGACATGT GATTTGTATT	1680
	TTAGATGCTT GTTTCCTATT AAAATACAGA CATTTCTACC CTCAGTTTCT AAATGTAGAC	1740
	TATTTGTTGG CTAGTACTTG ATAGATTCCCT TGTAAGAAAA AATGCTGGGT AATGTACCTG	1800
10	GTAACAAGCC TGTTAATATA TTAAGATTGA AAAAGTAACT TCTATAGTTA CTCCTTCTAA	1860
	AATATTTGAC TTCCTACATT CCCCCACCC AAAATCTTTC CCTTTTGAAA ATACTAAAAA	1920
15	CTAAGTTATG TTATTATAAA GTGTAAAATG GTTTGTCTTA ATTATAGGAG AAAAAGGCCT	1980
	TGTTAGAAAT AAAATAAACT GACTTATTTT ACTAATGAAA AAAAAAAAAA AAAAAAAAAA	2040
	TT	2042

(2) INFORMATION FOR SEQ ID NO: 22:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1872 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

	GGGTCGACCC ACGCGTCCGA TTGGCCTAGA GCTCCTGTGA CCGAGAGCGC CACGGAAGCC	60
35	TGGGGATGAT GTCGGGCAGC TTTATTCTTT GCTTGGCTTT GGTAAGTAGG TGGTCCCCCTC	120
	AAGCATCCTC AGTTCCTCTT GCTGTTTATG AATCTAAGAC AAGGAAGTCC TATAGAAGCC	180
40	AAAGGGACAG GGACGGAAAG GACAGGTCCC AAGGGATGGG GCTGTCTTTA CTTGTGGAAA	240
	CCAGGAAATT GCTCCTCTCA GCCAACCAAG GTTGACCACA CACCACCCTT CCGGAGCAGC	300
	TCAGTCAGCC CTCGGGGACG RGAAACCACA AGCGCAGAGA CGCTGAGGCC CAGGCAGGTG	360
45	AAGAGGAAGT GGCTTTGGGT TTTTAAAGTA GGTGAGCGTG ACCTCTCTGA CTGCTTCTTC	420
	CCCCGGGGGG ACTGCAAACC GCTCAGGGTT GCGGCAGAGC CATGGACTTC CGGTCCCTGC	480
50	AACGGGTGAC CTAAGCGTGG TGCACCCATC AGTCACGCAG GAGGACTGAC TTGACAGACG	540
	AAAGACAAGC CCGGATGACA CAGGGTGAGA AGAGTCAGGG CCGCACCTCT GTCCCTGCAA	600
	ACCAACAGGT GCATGGTGAG TGTGGCAGTC CCCACAGCTC CACAATGGGC TCCCCGCCA	660
55	ACGGGGACGA CAGGGATCTT CAGGAACTTC TGACCTCACC AAGTCAAGTG GACCACTCTC	720
	CACTCCACGA GGATGTGAAA CGGTTCTTTA AAATGGGATT TTAGAGCCTC GGGAATGCAT	780
60	GTGCGTCGCA TCTTTCATAT TATGGGTCAG GATAGATTCA TTTCTTGCAA CATAGTGGA	840

AAGATATAAG CTGCAGTAAT TTGCTCTTTG AATGACCGTC ACCCCCAGTA TAGGATATGC 900
 TTGTATCCCC CCGTCACTCC TCCGCCTGTT TTTTAACTT TTCCACCACC TCGTCCAAA 960
 5 AAGAATGTTA TAGCGAGTGC TCTTAAATGT TGAACCTGGG TGTTCCTCC GGGCCAGTCT 1020
 GCGTGGCTCC ATGAAAAGCT CACTGCTGCC CCAGCCGGGC TTCTTAGAGG AGGTCAGTTG 1080
 10 TCCTATGTAT CATCATTTAC TCTGGGAATC TACTGTGAA ATCATGTCTG TATTTTCTG 1140
 GAGCAGTTCA CATAGAGTAG AATGTGGAAT TTCCCGTGAA CGTCTCCTTC CTCCCCGTA 1200
 TCTGCCGCCT GTCACTTCGC CACCGTGCTA GAATACTGTT GTGTTGTAAG ATGACTAATT 1260
 15 TTAAAAGAAC CTGCCCTGAA AAGTTCTTAG AAACGCAATG AAAGGGAGGA ACTTGTCTTT 1320
 TACCCAGTTT TTCCTTTGTA GGATGGGAAA GTATAAAAAG GCACAGAAGG TTGTCATGGG 1380
 CTGTTCTCTG GGGGTTTTTA TCCTGCTCAC CGTGGAGATA AGCCTGCGGC TTGTCTAACC 1440
 20 AGCGCAGCGM AAAGGTCTCA ATGCCTTTTG GTAACATCCG TCATTGCAGA AGAAAGTTTA 1500
 CACGACGTCA AAAAGTGACG TTCATGCTAA GTGTTMTTCC AGAAATATTG GTTTCATGTT 1560
 25 TCTTATTKGC TCTGCCTCCT GTGCTTATAT CATCCAAAAA CTTTTTAAAA AGGTCCAGAA 1620
 TTCTATTTTA ACCTGATGTT GAGCACCTTT AAAACGTTTCG TATGTGTGTT GCACTAATTC 1680
 TAACTTTGG AGGCATTTTG CTGTGTGAGG CCGATCGCCA CTGTAAAGGT CCTAGAGTTG 1740
 30 CCTGTTGTC TCTGGAGATG GAATTAAACC AAATAAGAG CTTCCACTGG AGGCTTGAT 1800
 TGACCTTGTA ACTATATGTT AATCTCGTGT TAAAATAAAA TATAACTTGT GAAAAAAAAA 1860
 35 AAAAAAAAAAC NT 1872

40 (2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

50 CATTTACCCA CCTATCAACA TGTTTGCTTT CTCCTTTGTT GGTGAGAATG AGTGGCTTCT 60
 TGCTCCTAGC TAGAGCCAGT CCTTCCATAT GTGCTTTAGA TTCTTCCTGT TTTGTTCAAG 120
 AATATTGCTC AAGCTATTCT TCCTCCTGTT TCCTGCATCA GCATTTCCCC TCTCTACTAG 180
 55 ATCATCTCTG TCAGTAAATG AACATGTTGT TGTTTCTCCT AGAAGTACTG TTTCTATATC 240
 TAGATAGTAC TCTAGCTAGA GTTAAAAAAA AAAAAAAAAA CCTNNGGGG 289

60

(2) INFORMATION FOR SEQ ID NO: 24:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3533 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TTTTATTAC TTCAAATTAA CTGTACTTTA CTCAAATAGA AAANGAATAA TTTTCACATT 60
15 ATGAAGCTAC ACAATTCCAA AATACACATG CTGAGGCTCT TTTTAAGTCC GAATTGTCTA 120
GTAATTACAA AAAAGTGAAG AGTTTACAGA TATACAAGGA AATAAAGGCG AATTATTGCA 180
20 AAGAAAACAA GTTTAATTTC ACTTTGAATG ACAACGATTT TTCTGGAAAG CAGATACTTC 240
ACTCCTTTAA GTTTCCACCC AAGCCACAAT AATTTCAAAC GGTCTTGCGG ATGACCCAGC 300
TGGTCACTCT TGTTTATGTG GGGACTGGAG GTAATGAGAG CCAAAAAAAG TGCTATAAAC 360
25 CTAATTTGGC TAGAGCAAGT TCACACGACA CGACCGTGCT TTA AAAACTT GCTCTCCATT 420
ATGTACTTCC TTCCATCAGG TTGGGGAAAA AAAATGGTG GGGATGGTGA GTAAACACAC 480
30 CAGTGGTTTC ATCAGAGGGG AACTCACTAC TCAGGAGGTG ACGGTGACGT GGTGCCGGTC 540
CCTGAAGTAC GCGCACAAGC TCCGGAGGTT GCGGGAGCTT CCGCTGCCGC CTGGAGGGAA 600
GCCGGAGCGA CGGGGGTCAC GCGGGCGGTC AGAGGGTAAA GGTCTTGCTC CCAGCAGCCT 660
35 CCGCGGTGGA TACGTCGCCA TCTTGATCC GCGGGACAAG AAAATTCATG CGAGGGAGAC 720
GTGTGGGCG GTCCTTCCTG TGACACGACC CTTGAGTGAC AGTTCTATTT GATTGCCTCC 780
GGTACTGTGA GGAAAGGACA CGACTCTATG GTGAGGACTG ATGGACATAC ATTATCTGAG 840
40 AAAAGAACT ACCAGGTGAC AAACAGCATG TTTGGTGCTT CAAGAAAGAA GTTTGTAGAG 900
GGGGTCGACA GTGACTACCA TGACGAAAAC ATGTACTACA GCCAGTCTTC TATGTTTCCA 960
45 CATCGGTCAG AAAAAGATAT GCTGGCATCA CCATCTACAT CAGGTCAGCT GTCTCAGTTT 1020
GGGCAAGTT TATACGGGCA ACAAAGTGCA CTAGGCCTTC CAATGAGGGG GATGAGCAAC 1080
AATACCCCTC AGTTAAATCG CAGCTTATCA CAAGGCACTC AGTTACCGAG CCACGTCACG 1140
50 CCAACAACAG GGTACCAAC AATGTCACCT CACACGCCTC CATCTCCAAG CAGGGGTATT 1200
TTGCTATGA ATCCTARGAA TATGATGAAC CACTCCAGG TTGGTCAGG CATTTGGAATT 1260
55 CCTAGCAGGA CAAATAGCAT GAGCAGTTCA GGGTTAGGTA GCCCCAACAG AAGCTCGCCA 1320
AGCATAATAT GTATGCCAAA GCAGCAGCCT TCTCGACAGC CTTTACTGT GAACAGTATG 1380
TCTGGATTTG GAATGAACAG GAATCAGGCA TTTGGAATGA ATAACCTCTT ATCAAGTAAC 1440
60

	ATTTTAAATG GAACAGACGG AAGTGAAAAT GTGACAGGAT TGGACCTTTC AGATTTCCCA	1500
	GCATTAGCAG ACCGAAACAG GAGGGAAGGA AGTGGTAACC CAACTCCATT AATAAACCCC	1560
5	TTGGCTGGAA GAGCTCCTTA TGTGGAATG GTAACAAAC CAGCAAATGA ACAATCCCAG	1620
	GACTTCTCAA TACACAATGA AGATTTTCCA GCATTACCAG GCTCCAGCTA TAAAGATCCA	1680
	ACATCAAGTA ATGATGACAG TAAATCTAAT TTGAATACAT CTGGCAAGAC AACTTCAAGT	1740
10	ACAGATGGAC CCAAATTCCT TGGAGATAAA AGTTCAACAA CACAAAATAA TAACCAGCAG	1800
	AAAAAAGGGA TCCAGGTGTT ACCTGATGGT CGGGTTACTA ACATTCCTCA AGGGATGGTG	1860
15	ACGGACCAAT TTGGAATGAT TGGCCTGTTA ACATTTATCA GGGCAGCAGA GACAGACCCA	1920
	GGAATGGTAC ATCTTGCAAT AGGAAGTGAC TTAACAACAT TAGGCCTCAA TCTGAACTCT	1980
	CCTGAAAATC TCTACCCCAA ATTTGCGTCA CCCTGGGCAT CTTACCTTG TCGACCTCAA	2040
20	GACATAGACT TCCATGTTCC ATCTGAGTAC TTAACGAACA TTCACATTAG GGATAAGCTG	2100
	GCTGCAATAA AACTTGGCCG ATATGGTGAA GACCTTCTCT TCTATCTCTA TTACATGAAT	2160
25	GGAGGAGACG TATTACAAC TTTAGCTGCA GTGGAGCTTT TTAACCGTGA TTGGAGATAC	2220
	CACAAAGAAG AACGAGTATG GATTACCAGG GCACCAGGCA TGGAGCCAAC AATGAAAACC	2280
	AATACCTATG AGAGGGGAAC ATATTACTTC TTTGACTGTC TTAACGGAG GAAAGTAGCT	2340
30	AAGGAGTTCC ATCTGGAATA TGACAAATTA GAAGAACGGC CTCACCTGCC ATCCACCTTC	2400
	AACTACAACC CTGCTCAGCA AGCCTTCTAA AAAAAAAAAA AAAAAAAAAA AAAAAGACTT	2460
35	CCCTTTTCTT GGGGTATGGC TGTCTCAGCA CAATACTCAA CATAACTGCA GAACTGATGT	2520
	GGCTCAGGCA CCCTGGTTT AATTCCTTGA GGATCTGGCA ATTGGCTTAC GCAAAAGGTC	2580
	ACCATTTGAG GTCCTGCCTT ACTAATTATG TGCTGCCCAA CAACTAAATT TGTAATTTGT	2640
40	TTTTCTCTAG TTTGAGCAGG GTCTGAATTT TTTCAATAT TCCCTTTTTT GCCAGCAGAC	2700
	AGACTTGAGT CTGTAAAGAC AAGCAAATAC ACTGACAGAA GTTTACCATA GTTTCTAAAA	2760
45	TGTAAGAAAG AAAACCCCCA AAAGACTCAA GAAATTAGA CCACAAATTT TGCATTGTTC	2820
	ATTGTAGCAC TATTGGTAAT AAAATAACAA ATGTTTGTGC ATTTTATGT GAAGATCCTT	2880
	CTCGTATTTT ATTTGGAAAG ATGAGCAAGA GGTCTGCTTC CTTCAATTTA CTCCCTTC	2940
50	TGTTTTTGAA AGGCAGTTTC GCCAAGCTTA ATGCAAGAAT ATCTGACTGT TTAGAAGAAA	3000
	GATATTGCCA CAATCTCTGG ATGGTTTTC AGGGTTGTGT TATTACTGAG CTTTATCTTT	3060
55	CCAGAATGAG CAAAACACTG TCCAGTCTTT GTTACGATTT TGTAATAAAT GTGTACATTT	3120
	TTTTTAAATT TTTGGACATC ACATGAATAA AGGTATGTAT GTACGAATGT GTATATATTA	3180
60	TATATATGAC ATCTATTTTG GAAAATGTTT GCCCTGCTGT ACCTCATTTT TAGGAGGTGT	3240

GCATGGATGC AATATATGAA AATGGGACAT TCTGGAAC TGCTGGTCAGGG GACTTTGTGCG 3300
 CCCTGTGCAC TAAAAGGGCC AGATTTTCAG CAGCCAAGGA CATCCATACC CAAGTGAATG 3360
 5 TGATGGGACT TAAAAGAAGT GAACTGAGAC AATTCAC TCT GGCTGT TTTGA ACAGCAGCGT 3420
 TTCATAGGAA GAGAAAAAAA GATCAATCTT GTATTTTCTG ACCACATAAA GGCTTCTTCT 3480
 10 CTTTGTAATA AAGTAGAAAA GCTCTCCTCA AAAAAAAAAA AAAAAAACTC GAG 3533

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1148 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ACCCACGCGT CCGCAAATTA TACTTCCTCA TTCATATTAT GTTGATACAA AAGACCTTGG 60
 25 CAGCCATTTC TCCCAGCAGT TTAAAGGAT GAACATTGGA TTTCATGCCA TCCCATAGAA 120
 AACCTGTTTT AAAATTTTAG GGATCTTTAC TTGGTCATAC ATGAAAAGTA CACTGCTTAG 180
 30 AAATTATAGA CTATTATGAT CTGTCCACAG TGCCCATTTGT CACTTCTTTG TCTCATTTCT 240
 TCCCTTTGTT CCTTAGTCAT CCAAATAAGC CTGAAAACCA TAAGAGATAT TACTTTATTG 300
 AATATGGTTG GCATTAAATT TAGCATTTCA TTATCTAACA AAATTAATAT AAATTCCAGG 360
 35 ACATGGTAAA ATGTGTTTTA ATAACCCCA GACCCAAATG AAAATTTCAA AGTCAATACC 420
 AGCAGATTCA TGAAAGTAAA TTAGTCCTA TAATTTTCAG CTTAATTATA AACAAAGGAA 480
 40 CAAATAAGTG GAAGGCAGC TATTACCATT CGCTTAGTCA AAACATTCGG TTAGTCCCCT 540
 TTAATACACT CCTATCATCA GCACTTCCAC CATGTATTAC AAGTCTTGAC CCATCCCTGT 600
 CGTAACTCCA GTAAAAGTTA CTGTTACTAG AAAATTTTTA TCAATTAACT GACAAATAGT 660
 45 TTCTTTTTAA AGTAGTTTCT TCCATCTTTA TTCTGACTAG CTTCCTAAAT GTGTTCCCTT 720
 TTGAATCGA GGTFTTTTGT TTTTGT TTTG TTTTCTGAAA AAATCATACA ACTTTGTGCT 780
 50 TCTATTGCTT TTTTGTGTTT TGTTAAGCAT GTCCCTTGGC CCAAATGGAA GAGGAAATGT 840
 TTAATTAATG CTTTTTAGTT TAAATAAATT GAATCATTTA TAATAATCAG TGTTAACAAT 900
 TTAGTGACCC TTGGTAGGTT AAAGGTGCA TTATTTATAC TTGAGATTTT TTTCCCTTAA 960
 55 CTATTCTGTT TTTTGTACTT TAAAACTATG GGGGAAATAT CACTGGTCTG TCAAGAAACA 1020
 GCAGTAATTA TTAGTGAGTT AAATTGAAAA GTCCAGTGGA CCAGGCATTT CTTATATAAA 1080
 60 TAAAATTGGT GGTACTAATG TGAAAAAAA AAAAAAAAAA AACTCGAGGG GGGCCCGGTA 1140

CCCTATTA

1148

5

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 717 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GGCACGAGCT AGCTGCCGCC ACCCGAACAG CCTGTCTGCG TGCCCCGGCT CCCTGCCCCG 60
CGCCCAGTCA TGACCCTGCG CCCCTCACTC CTCCCGCTCC ATCTGCTGCT GCTGCTGCTG 120
20 CTCAGTGCGG CGGTGTGCCG GGCTGAGGCT GGGCTCGAAA CCGAAAGTCC CGTCCGGACC 180
CTCCAAGTGG AGACCCTGGT GGAGCCCCCA GAACCATGTG CCGAGCCCCG TGCTTTTGA 240
25 GACACGCTTC ACATACACTA CACGGAAGC TTGGTAGATG GACGTATTAT TGACACCTCC 300
CTGACCAGAG ACCCTCTGGT TATAGAACTT GGCCAAAAGC AGGTGATTCC AGGTCTGGAG 360
CAGAGTCTTC TCGACATGTG TGTGGGAGAG AAGCGAAGGG CAATCATTCC TTCTCACTTG 420
30 GCCTATGGAA AACGGGGATT TCCACCATCT GTCCAGCGG ATGCAGTGCT GCAGTATGAC 480
GTGGAGCTGA TTGACTAAT CCGAGCCAAC TACTGGCTAA AGCTGGTGAA GGGCATTTTG 540
35 CCTCTGGTAG GGATGGCCAT GGTGCCAGCC CTCCTGGGCC TCATTGGGTA TCACCTATAC 600
AGAAAGGCCA ATAGACCCAA AGTCTCCAAA AAGAAGCTCA AGGAAGAGAA ACGAAACAAG 660
AGCAAAAAGA AATAATAAAT AATAAATTTT AAAAAAAAAA AAAAAAAAAA AAAAAAA 717
40

(2) INFORMATION FOR SEQ ID NO: 27:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GGCACGAGCC GATGTGGACA TCATCCTGTC TATCCCCATG TTCCTGCGCC TGTACCTGAT 60
55 CGCCCCGAGTC ATGCTGCTGC ACAGCAAGCT CTTACCGAT GCCTCGTCCC GCAGCATCGG 120
GGCCCTCAAC AAGATCAACT TCAACACCCG CTTTGTGTCATG AAGACGCTCA TGACCATCTG 180
60 CCCTGGCACT GTGCTGCTCG TGTTCAGCAT CTCTCTGTGG ATCATTGCTG CCTGGACCGT 240

	COGTGTCTGT GAAAGTCCTG AATCACCAGC CCAGCCTTCT GGCTCATCAC TTCCTGCTTG	300
5	GTACCATGAC CAGCAGGACG TAACTAGTAA CTTTCTGGGT GCCATGTGGC TCATCTCCAT	360
	CACATTCCTT TCCATTGGTT ATGGGGACAT GGTGCCCCAC ACATACTGTG GGAAAGGTGT	420
	CTGTCTCCTC ACTGGCATCA TGGGTGCAGG CTGCACTGCC CTGTGGTGG CCGTGGTGGC	480
10	CCGAAAGCTG GAACTACCA AAGCGGAGAA GCACGTCAT AACTTCATGA TGGACACTCA	540
	GCTCACCAAG CGGATCAAGA ATGCTGCAGC CAATGTCTT CGGGAAACAT GGTTAATCTA	600
15	TAAACACACA AAGCTGCTAA AGAAGATTGA CCATGCCAAA GTGAGGAAAC ACCAGAGGAA	660
	GTTCTCTCCA AGCTATCCAC CAGTTTGAGG AGCGTCCCAG ATGGAACAGA GGAAAGCTGA	720
	GTGACCAAGC CAACACTCTG GTGGACCTTT CCAAGATGCA GAATGTCATG TATGACTTAA	780
20	TCACAGAACT CAATGACCGG AGCGAAGACC TGGAGAAGCA GATTGGCAGC CTGGAGTCGA	840
	AGCTGGAGCA TCTCACC GCC AGCTTCAACT CCCTGCCGCT GCTCATCGCC GACACCTGC	900
25	GCCAGCAGCA GCAGCAGCTC CTGTCTGCCA TCATCGAGGC CCGGGGTGTC AGCGTGGCAG	960
	TGGGCACCAC CCACACCCCA ATCTCCGATA GCCCCATTGG GGTGAGCTCC ACCTCCTTCC	1020
	CGACCCCGTN CACAAGTTCA AGCAGTTGCT AAATAAATCT CCCCCTCCA GAAGCATTAA	1080
30	AAAAAAAAA AAAAAAAAAA	1099

35 (2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 941 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

45	AATTCGGCAG AGAGCCAACC GAGGGCGTTC CTGTCGGGGC TGCAGCGGCG GGAGGGAGCC	60
	CAGTGGAGGC GCCCTCCCGA AGCGCCACTG CCCATGCTGA CCACCCAGCC CTCCGGCTGC	120
50	TGATGTCATG AGTAACACCA CTGTGCCCAA TGCCCCCAG GCCAACAGCG ACTCCATGGT	180
	GGGCTATGTG TTGGGGCCCT TCTTCCTCAT CACCCTGGTC GGGGTGGTGG TGGCTGTGGT	240
	AATGTATGTA CAGAAGAAAA AGCGGGTGA CCGGCTGCGC CATCACCTGC TCCCCATGTA	300
55	CAGCTATGAC CCAGCTGAGG AACTGCATGA GGCTGAGCAG GAGCTGCTCT CTGACATGGG	360
	AGACCCCAAG GTGGTACATG GCTGGCAGAG TGGCTACCAG CACAAGCGGA TGCCACTGCT	420
60	GGATGTCAAG ACGTGACCTG ACCCCCTTGC CCCACCCTTC AGAGCCTGGG GTYCTGGACT	480

GCCTGGGGCC CTGCCATCTG CTTCCCCTGC TGTACCTGG STCCCCCTGC TGGGTGCTGG 540
GTCTCCATTT CTCCCTCCAC CCACCCTCAG CAGCATCTGC TTCCCATGCC CTCACCATCA 600
5 CCTCACTGCC CCCAGGCTTT CTTGCCCTTTG TGGGTGTTGA GCTCACCGCC CACCCACAGG 660
CACTCATGGG AAGAGGCTTT CTTCTGTTGA TGGCGCGGC TGGTAGACAC CTTTGCTTTTC 720
TCTAGCCCTC CTGGGCTGGG CTTGGGCACA AATCCCCAGG CAGGCTTTGG AGTTGTTTCC 780
10 ATGGTGATGG GGCCAGATGT ATAGTATTCA GTATATATTT TGTAAATAAA ATGTTTGTG 840
GCTAAAAAA AAAAAAAAAA ATCNAAGGGG GGGCCGTAC CCAAATTCCC CCTATANTGA 900
15 ATTCGTATTA ACAATTCAT TGGGCGCTC CTTTAAANAA C 941

20 (2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 756 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

30 GGCACGAGGA AGCTGGAGCG GGCCGGCGGT GCAGTCACGG GGGAGCGAGG CCTGCTGGGC 60
TTGGCAACGA GGGACTCGGC CTCGGAGCGC ACCCAGACCA CACAGACACT GGGTCAAGGA 120
GTAAGCAGAG GATAAACAAC TGGAAGGAGA GCAAGCACAA AGTCATCATG GCTTCAGCGT 180
35 CTGCTCGTGG AAACCAAGAT AAAGATGCCC ATTTTCCACC ACCAAGCAAG CAGAGCCTGT 240
TGTTTTGTCC AAAATCAAAA CTGCACATCC ACAGAGCAGA GATCTCAAAG ATTATGCGAG 300
40 AATGTCAGGA AGAAAGTTTC TGGAAGAGAG CTCTGCCTTT TTCTCTTGTA AGCATGCTTG 360
TCACCCAGGG ACTAGTCTAC CAAGGTATT TGGCAGCTAA TTCTAGATTT GGATCATTGC 420
CCTAAGTTGC ACTTGCTGGT CTCTTGGGAT TTGGCCTTGG AAAGGTATCA TACATAGGAG 480
45 TATGCCAGAG TAAATTCCAT TTTTGAAG ATCAGCTCCG TGGGCTGGT TTTGGTCCAC 540
AGCATAACAG GCACTGCCTC CTTACCTGTG AGGAATGCAA AATAAAGCAT GGATTAAGTG 600
50 AGAAGGGAGA CTCTCAGCCT TCAGCTTCCT AAATTCGTGT TCTGTGACTT TCGAAGTTTT 660
TTAAACCTCT GAATTTGTAC ACATTTAAAA TTTCAAGTGT ACTTTAAAAT AAAATACTTC 720
TAATGGAAAA AAAAAAAAAA AAAAAAAAAA ACTCGA 756
55

60 (2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

10 NCCAGAGGCA GAAAGTCCTG CTTCTGGGGC GTAACCTACA GGATATCCTT GGAACAGAAG 60
 ATCTTATTGT GGAAGTRACT TCCAATGATG CTGTGAGATT TTATCCCTGG ACCATTGATA 120
 ATAAATACTA TTCAGCAGAC ATCAATCTAT GTGTGGTGCC AAACAAATTT CTTGTTACTG 180
 15 CAGAGATTGC AGAATCTGTC CAAGCATTTG TGGTTTACTT TGACAGCACA CAAAAATCGG 240
 GCCTTGATAG TGTCTCCTCA TGGCTTCCAC TGGCAAAAGC ATGGTTACCY GAGGTGATGA 300
 20 TCTTGGTCTG CGATAGAGTG TCTGAAGATG GTATAAACCG AAAAAAGCT CAAGAATGGT 360
 GCATCCAAAC ATGGCTTTGA ATTGGTAGAA CTTAGTCCAG AGGAGTTGCC TGAGGAGGAT 420
 GATGACTTCC CAGAATCTAC AGGAGTAAAG CGAATTGTCC AAGCCCTGAA TGCCAATGTG 480
 25 TGGTCCAATG TAGTGATGAA GAATGATAGG AACCAAGGCT TTAGCTTGCT GCAACTCATT 540
 GACTGGAACA AACCATAGCA TTGGGTCAGC AGATCCCTGT CACCCAGAGC AACCCCATTT 600
 30 GCCAGCAGCA GATAGTACTG AATCCCTCTC TGATCATCGG GGTGGTGCAT CTAACACAAC 660
 AGATGCCCAG GTTGATAGCA TTGTGGATCC CATGTTAGAT CTGGATATTC AAGAATTAGC 720
 CAGTCTTACC ACTGGAGGAG GAGATGTGGA GAATTTTGAA AGACTCTTTT CAAAGTTAAA 780
 35 GCAAATGAAA GACAAGGCTG CGACGCTTCC TCATGAGCAA AGAAAAGTGC ATGCAGAAAA 840
 GGTGGCCAAA GCATTCTGGA TGGCAATCGG GGGAGACAGA GATGAAATTG AAGGCCTTTC 900
 40 ATCTGATGAA GAGCACTGAA TTATTCATAC TAGGGTTTGA CCAACAAAGA TGCTAGCTGT 960
 CTCTGAGATA CCTCTCTACT CAGCCCAGTC ATATTTTGCC AAAATTGCC TTATCATGTT 1020
 GGCTGCCTGA CTTGTTTATA GGGTCCCTT AATTTTAGTT TTTAGTAGGA GGTAAAGGAG 1080
 45 AAATCTTTTT TTTCCTCAGT ATATTGTAAG AGAGTGAGGA ATACAGTGAT AGTAATGAGT 1140
 GAGGATTTCT TAAATRTACT TTTTTTTTGT TCTAGGAATG AGGGTAGGAT AAATCTCAGA 1200
 50 GGTCTGTGTG ATTTACTCAA GTTGAAGACA ACCTCCAGGC CATTCCTGGT CAACCTTTTA 1260
 AGTAGCATTT CCAGCATTCA CACTTGATAC TGCACATCAG GAGTTGTGTC ACCTTTCTCTG 1320
 GGTGATTTGG GTTTTCTCCA TTCAAGGAGC TTGTAGCTCT GAAGCTATGA TGCTTTTATT 1380
 55 GGGAGGAAAG GAGGCAGCTG CAGAATGAT GTGAGCTATG TGGGGCCGAA GTCTCAGCCC 1440
 GCAGCTAAGT CTCTACCTAA GAAATGCCT CTGGGCATTC TTTTGAAGTA TAGTGTCTGA 1500
 60 GCTCATGCTA GAAAGAATCA AAAAGCCAGT GTGGATTTTT AGACTGTAAT AAATGAGGCA 1560

AAGGATTTCT ATTCCAGTGG GAAGRAAACC TCTCTACTGA GTTGTGGGGG ATATGTTGTA 1620
 TGTTAGAGAG AACCTTAAGG AGTCCTTGTA TGGGCCATGG AGACAGTATG TGATAACATA 1680
 5 CCGTGATTTT CATGAAGAAA TTCTTCTGTC TTAGAGTTCT CCCCTGCTGC TTGAGATGCC 1740
 AGAGCTGTGT TGTGTCACAC CTGCAAAACA AGGCACATTT CCCCTTTTCT CTTTAAAGCC 1800
 AAAGAGAGAT CACTGCCAAA GTGGGAGCAC TAAGGGGTGG GTGGGGAAGT GAAATGTTAG 1860
 10 GCGATGAATT CCTGAGCACC TTGTTTTTCT TCCAAGGTTT GTAGCTCCTC TCTGCCCTTC 1920
 CAAGCCTGTA ACCTCGGAGG ACTATCTTTT GTTCTTTATC CTTTGTCTTG TTTGAGTGGG 1980
 15 TCAGCCCCAG AGGAACTGAT AAGCAAATGG CAAGTTTSTA AAGGAAGAGT GGAAAGTACT 2040
 GCAAATAAAA ATCCTTATTT GTTTTGTAG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAAG 2100

20

(2) INFORMATION FOR SEQ ID NO: 31:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1448 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AAAAAAAAAA AAAGCCCACC TGAAAGCCTG TCTCTTTCCA CTTTGTGTC CCTTCCAGTG 60
 GGATTATCGA GCATGTTGTT TTTTCATAGT GCCTTTTTC TATTTCAAG GGTGCTTCT 120
 35 GAGTGGTGT TTTTMTTTT TTAATTTGTT TTGTTTAAA ATAAGTTAAA GACAGTCCAG 180
 AGCTTTTCAG CCAATTTGTC TCCTACTCTG TGTAATATT TTTCCCTCCG GGCAGGGGAG 240
 40 CCAGGCTAGA GCAAAGGAGA CAAGCAGGAG TGGAAGGTGA GCGTTCTCC TGCTGTACT 300
 AAGCCAGGAG STTTAAGCTC CAGCTTTAAG GGTGTGAGC CCCTTGGGGT TCAGGGAAGT 360
 GCTTGCCCAG GGTGCACTGT GAGTGTGATG GGCCACCGGG GCAAGAGGA AGGTGACCGC 420
 45 CCAGCTCTCC CACATCCCAC TGGATCTGGC TTACAGGGGG GTCGGAAGCC TGTCTCACC 480
 GTCTCGGGG TTGTGGCCCC CGCCCCCTCC CTATATGCAC CCCTGGAACC AGCAAGTCCC 540
 50 AGACAAGGAG AGCGGAGGAG GAAGTCATGG GAACGCAGCC TCCAGTTGTA GCAGTTTCA 600
 CTATTCTAT GCTGGGTAC ACAGTGAGAG TACTCACTTT TCACTTGTCT TGCTCTTAGA 660
 TTGGGCCATG GCTTTCATCC TGTGTCCCCT GACCTGTCCA GGTGAGTGTG AGGCAGCAC 720
 55 TGGAAGCTG GAGTGTGCT TGTGCTCCC TCCCAGTGG GCTGTGTTGA CTGCTGCTCC 780
 CCACCCCTAC CGATGGTCCC AGGAAGCAGG GAGAGTTGGG GAAGCAAGA TTGGAAGAC 840
 60 AGGAAGACCA AGGCCTCGGC AGAACTCTCT GTCTTCTCT CACTTCTGGT CCCCTGTGGT 900

5 GATGTGCCTG TAATCTTTTT CTCCACCCAA ACCCCTTCCC ACGACAAAA CAAGACTGCC 960
 TCCCTCTCTT CCGGGAGCTG GTGACAGCCT TGGGCCTTTC AGTCCCAAAG CGGCCGATGG 1020
 GAGTCTCCCT CCGACTCCAG ATATGAACAG GGCCAGGCC TGGAGCGTIT GCTGTGCCAG 1080
 GAGGCGGCAG CTCTTCTGGG CAGAGCCTGT CCCC GCCTTC CCTCACTCTT CCTCATCCTG 1140
 10 CTCTCTTTTT CCTCGCAGAT GATAAAAGGA ATCTGGCATT CTACACCTGG ACCATTGAT 1200
 TGTTTTATTT TGAATTGGT GTATATCATG AAGCCTTGCT GAACTAAGTT TTGTGTGTAT 1260
 ATATTTAAAA AAAAAATCAG TGTTTAAATA AAGACCTATG TACTTAATCC TTTAACTCTG 1320
 15 CGGATAGCAT TTGGTAGGTA GTGATTAACT GTGAATAATA AATACACAAT GAATTCTTMA 1380
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAACCCCGGG GGGGGCCCCG GGCCCCAATT 1440
 20 CCCCCCAA 1448

25 (2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 456 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

35 GGCACAGCAA ACTTGACGCC ATGAAGATCC CGGTCTTCC TGCCGTGGTG CTCCTCTCCC 60
 TCCTGGTGCT CCACTCTGCC CAGGGAGCCA CCCTGGGTGG TCCTGAGGAA GAAAGCACCA 120
 40 TTGAGAATTA TGCCTCACGA CCCGAGGCCT TTAACACCCC GTTCCTGAAC ATCGACAAAT 180
 TCGATCTGC GTTTAAGGCT GATGAGTTC TGAAGTGGCA CGCCCTCTTT GAGTCTATCA 240
 AAAGGAACT TCCTTTCCTC AACTGGGATG CCTTTCCTAA GCTGAAAGGA CTGAGGAGCG 300
 45 CAACTCCTGA TGCCAGTGA CCATGACCTC CACTGGAAGA GGGGGCTAGC GTGAGCGCTG 360
 ATTCTCAACC TACCATAACT CTTTCTGCC TCAGGAATC CAATAAACA TTTTCCATCC 420
 50 AAAAAAAAAA AAAAAAAC CCCNGGGGG GCGCGG 456

55 (2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1326 base pairs
 (B) TYPE: nucleic acid
 60 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

5 GGCACGAGTG CAGGCCCAGA GAGGACTCAT TGAAAGGACT GAAAGGGGAG GTGGCGTTTT 60
 CTTCTTACCC AAACCTTACCC CTGTGAGCTG GACAGCTTGG TAGCACCTGC CTGGACTTAG 120
 ATGGTGGTAG CCAAGAAGAC TGACATTTTA GGGAACAGGA CGGGGAGGAG AAGGCTCTGG 180
 10 CACACACACA TGTGTCCATA TGTCTGCAA TGGTCTGGGG ACTATTGCTA GGCTAGGAGC 240
 CCTAAGTGTC TTCTTCTCA TGTCTMTTCT CCCCTGTSTC ATGGGCCCTA AGRTCTCTTT 300
 CACTGGGCCT GCCTCAATGA ACGTGCTGCC CAGCTACCCC GAAACACGGC ANCTGCCGGC 360
 15 TATCAATGCC CCAGCTGCAA TGGCCCATCT TCCCCAACCC AACCTGGCTG GGCCCGTGGG 420
 CTCCGCACTG AGARARAAAS TTGGCACART CAACTGGGCC CGGGCAGGAC TGGGCCYCCC 480
 20 TCTGATCGAT GAAGKTGGTG ARCCCAGAGC CCGAGCCCCCT CAACACGTCT GACTTCTCTG 540
 ACTGGTCTAG TTTTAATGCC AGCAGTACCC CTGGACCAGA GGAGGTAGAC AGCGCCTCTG 600
 CTGCCCCAGC CTTCTACAGC CGAGCCCCCC GGCCCCAGC TTCCCCAGGC CGGCCCCAGC 660
 25 AGCACACAGT GATCCACATG GGCAATCCTG AGCCCTTGAC TCACGCCCCCT AGGAAGGTGT 720
 ATGATACGCG GGATGATGAC CGGACACCAG GCCTCCATGG AGACTGTGAC GATGACAAGT 780
 30 ACCGACGTCG GCCGGCCTTG GGTGGCTGG CCCGGCTGCT AAGGAGCCGG GCTGGGTCTC 840
 GGAAGCGRCC GCTGACCCTG CTCCAGCGGG CGGGGCTGCT GCTACTCTTG GGACTGCTGG 900
 GCTTCTGGC CCTCCTTGGC CTCATGTCTC GCCTAGGCCG GGCCGCAGCT GACAGCGATC 960
 35 CCAACCTGGA CCCACTCATG AACCCTCACA TCCGCGTGGG CCCCTCCTGA GCCCCCTTGC 1020
 TTGTGGCTAG GCCAGCCTAG GATGTGGGTT CTGTGAGGA GAGGCGGGGT AATGGGGAGG 1080
 40 CTGAGGGCAC CTCTTCACTG CCCCTCTCCC TCAAGCCTAA GACACTAAGA CCCCAGACCC 1140
 AAAGCCAAGT CCACCAGAGT GGCTGCAGGC CAGGCCTGGA GTCCCCGTGG GTCAAGCATT 1200
 TGTCTTGACT TGCTTTCCTC CCGGGTYTCC AGCCTCCGAC CCCTCGCCCC ATGAAGGAGC 1260
 45 TGGCAGGTGG AAATAAACAA CAACTTTATT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1320
 AAANAA 1326
 50

(2) INFORMATION FOR SEQ ID NO: 34:

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 710 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

	GCGAAAGAGA AAAAGGCTGG AGCTCCCGCC CCCGGGGCTG TCAGATGGCT TGGGTTTCTG	60
5	CGACGCGATT GGCTCGCGGA GGGCAGAAAT TACTCAGCAA ACATGACTAT TATTAGCTGC	120
	TTAGCAACAG CTCACCAAAG TAGAGAGACC ACCCAGGTAG GCAACCCAGT GTGTGCATCC	180
10	TCGGCTTCGG GGCAGCCTCT GAGAGCGCCA ACCTTCTCGC ATGCAATACT TCCATTAAGG	240
	AATGCTCCCC CTCCTTTCTC TCTTATTCCT TTTCTTTTCA ACAGTGTCTT CTTTTTGTGG	300
	GATGCCTTTG CGCGCACACA CGCGCGCGCA GGCACACACA CGAACATTTG CCTCGCGGTA	360
15	GACACGGGGG GAAATGTWAT ATTTTMTTAA GCGCTTAAAC AATTTCTGAA ATTCTCATAA	420
	GAAAAGCCTT TCAGARGCAC CTTGGCCTCA AGCTGCAACA AATACTGGGA RGTCCGGCTC	480
20	GCATTCCCAG GCCTGCACCA ATAATGACAG CGTGCTGGAT ARTGCGCCAG TGTGTGCCAG	540
	ATTTTMTTMTT CCTCTTCTCT TTTCTTTTAT AACTAAAGGG AAGACTTAGG CTCTTGCAAG	600
	GAACAACGCC TCGCATTAAAG ATAAACAGAA TGGAAAGTTA AAGAGGAAAG CAAGGACGTT	660
25	GGGAAAAGCC ATCTTTCTTA AAATCCGTCT GCCCCCAGC CGCTTTCTCC	710

30 (2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 1188 base pairs
35	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

40	GATGGCTTTT ATATCTATTA TCGACCCACA GACAGTGACA ATGATAGTGA CTACAAGAAG	60
	GATATGGTGG AAGGGGACAA GTACTGGCAC TCCATCAGCC ACCTGCAGCC AGAGACCTCC	120
45	TACGACATTA AGATGCAGTG CTTCAATGAA GGAGGGGAGA GCGAGTTCAG CAACGTGATG	180
	ATCTGTGAGA CCAAAGCTCG GAAGTCTTCT GGCCAGCCTG GTCGACTGCC ACCCCCAACT	240
	CTGGCCCCAC CACAGCCGCC CTTTCTTGAA ACCATAGAGC GGCCGGTGGG CACTGGGGCC	300
50	ATGGTGGCTC GCTCCAGCGA CCTGCCCTAT CTGATTGTCT GGGTCGTCTT GGGCTCCATC	360
	GTTCTCATCA TCGTCACCTT CATCCCCTTC TGCTTGTGGA GGGCCTGGTC TAAGCAAAAA	420
55	CATACAACAG ACCTGGGTTT TCCTCGAAGT GCCCTTCCAC CCTCTGCCC GTATACTATG	480
	GTGCCATTGG GAGGACTCCC AGGCCACCAG GCAGTGGACA GCCCTACCTC AGTGGCATCA	540
	GTGGACGGGC CTGTGCTAAT GGGATCCACA TGAATAGGGG CTGCCCCTCG GCTGCAGTGG	600
60	GCTACCCGGG CATGAAGCCC CAGCAGCACT GCCCAGGCGA GCTTCAGCAG CAGAGTGACA	660

5 CCAGCAGCCT GCTGAGGCAG ACCCATCTTG GCAATGGATA TGACCCCCAA AGTCACCAGA 720
 TCACGAGGGG TCCCAAGTCT AGCCCGGACG AGGGCTCTTT CTTATACACA CTGCCCAGC 780
 ACTCCACTCA CCAGCTGCTG CAGCCCCATC ACGACTGCTG CCAACGCCAG GAGCAGCCTG 840
 CTGSTGTGGG CCAGTCAGGG GTGAGGAGAG CCCCCGACAG TCCTGTCTCTG GAAGCAGTGT 900
 10 GGGACCCTCC ATTTCACTCA GGGCCCCCAT GCTGCTTGGG CCTTGTGCCA GTTGAAGAGG 960
 TGGACAGTCC TGACTCCTGC CAAGTGAGTG GAGGAGACTG GTGTCCCCAG CACCCCCTAG 1020
 GGGCCTACGT AGGACAGGAA CCTGGAATGC AGCTCTCCCC GGGGCCACTG GTGCGTGTGT 1080
 15 CTTTGTAAAC ACCACCTCTC ACAATTTAGG CAGAAGCTGA TATCCAGAA AGACTATATA 1140
 TTGTTTMTT TTTAAAAAA AAAAAAAAAA AWCYCGGGG GGGGCCCC 1188

20

(2) INFORMATION FOR SEQ ID NO: 36:

25

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 956 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GGCAGAGCAG TGAAAATGCA TCCTAAAAAT TCAATGTTTA TACCAGGCTC ATGACACTAA 60
 35 GATGTGACAT CTGGACACGA GGGGTGAGCC ACGTGGATAC ATCCCTCCCA GATTGCATCT 120
 CCAGGAATCA CTCTGCTAGC AGAATGGGCG CCCCATCCCT TACTATGCTG CTCCTCCTCA 180
 AAGTGCAGCC CAGAAGGACC CAGGCCTTTG ATGCACATTG GGTGGGTCTC CCACTACTTT 240
 40 AGTTGAAATG GGAGCATGCT GGAGTCGGCG TTCTGTTGCT TCTGGTGAGA AGGACATCCC 300
 ATTGACCCCT GGCCACCAGG TCCAGTATTC CATCCTTCCT TCTGTCCCAG CCTATCGCCC 360
 45 TCCCCACYAG GCCCAGCCCC ACAACTTCTC CTCAAGGGAG GTTNTCCCGC AGCTGGAGGG 420
 CTTGCACAGA CCAGCAGTCA CAGAAATCAT TCTTCCTGCT GTACTGGGCC TTAAGTGCCT 480
 GCAAATGTCC GAGCACTACT GCATAGGATG CCAGAGCCAC CGAAGATAAA CACAGCCAAG 540
 50 TTTAATAATA ATAAAAGGAA AAATCTCAGC CTGCAGAACT CTGGTMTTGA CCCACCATCG 600
 GCCAGATGCA CATCTTCAGG GCCTGTTGAG CACCTTCTGA AAAGCAGGGC TCGTAATAGA 660
 55 CTCCAGCACA TTCCATCAGA GTCAGGAAAA CTGCGGTGAG TCCCAGAGAA TCTAGGGTGC 720
 AGGGCAGGGA GCAGGAGTCA TAAGGAGTGA TAACCTAAAC TGTGTGTAGT CAGCGGGGAG 780
 GGTCTTATGT TATCAGGTGA AATGAGAGCC AGTAAGTTAG TTGATCCTGT CACAGATATA 840
 60

ACCCTGATAA CACCCCATAG ATACGCGACA CGTGTGTCCT GCCCCTGCTT TCCCCATCCA 900
 ACATGGTTCT TCTGTTCCAC AGACATTAAA GGGGCTTTCT GCAATTACTT AAAAAA 956

5

(2) INFORMATION FOR SEQ ID NO: 37:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1603 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

TCGACCCACG CGTCCGCTCT GCCAGGAATC TGGTCTTTCT GTAGACCCAA GTCAGAAAGA 60
 20 ACCATTTGTG GAGTTAAATC GAATATTAGA RGCATTAAAR GTCAGAGTTC TGAGACCTGC 120
 TCTGGAATGG GCAGTTTCAA ACCGAGAGAT GCTTATAGCC CAAAACAGCT CCTTGGAATT 180
 25 TAAACTACAC AGACTGTATT TTATTAGCTT RTTAATGGGT GGAACACAAA TCAGCGAGAR 240
 GCATTACAAT ATGCTAAAAA TTTTCAGCCA TTTGCCCTAA ATCATCAAAA AGACATTCAG 300
 GTTTTGATGG GAAGCCTTGT GTACCTGAGA CAAGGGATTG AGAACTCACC ATATGTTTAC 360
 30 CTACTTGATG CAAACCAAGT GGCTGATATC TGTGACATCT TTACACGGGA TGCTTGTTGCC 420
 CTCCTGGGGC TCTCCGTGGA GTCCCCTCTC AGTGTCACTT TCTCAGCAGG TTGTGTGGCG 480
 CTGCCAGCTT TAATTAACAT CAAAGCCGTG ATTGAACAGA GGCAGTGTAC TGGAGTTTGG 540
 35 AACCAGAAAG ATGAATTACC TATTGAAGTG GACCTTGGTA AAAAGTGCTG GTATCACTCT 600
 ATATTTGCCT GCCCATTTCT TCGTCAGCAA ACAACAGATA ACAATCCACC CATGAAATTG 660
 40 GTCTGTGGTC ATATTATATC AAGAGATGCC CTGAATAAAA TGTTTAATGG TAGCAAATTA 720
 AAATGTCCCT ACTGTCCAAT GGAACAAAGT CCAGGAGATG CCAAACAGAT ATTTTCTGA 780
 45 AGAGATAACT TTAGTTTGCA ATTTGTAAGT GAAACTGAAT CGTGGGTGCA TTTCAGAAGA 840
 GAACGTTCCA TATAATGCAG CTAACCAAGG ACTCCTGTGT TTCTATAAGC TAATGCTCCA 900
 GAAACTTTGC CAACCTGTTA GTGTACACAC ACTGAGGGGA GTGCTCCCGG TGAATATTAT 960
 50 CATAGGGCTT TATTATATTC TTGGTCTTCA TTTCTGATCA AGTAAATACA CCAGCAGTTG 1020
 TCATTCAATG CAGGTTTTTG TACTTAATTA TATGGTGATT TTTTACTTTT TTAAGAGCAG 1080
 55 AAACGGAAAT TGACCTCCCC GCCATGTGTT TAATATTCCT CCTGCTTTTA CTTTGTGCAT 1140
 TTTCTTGATA ATCGTAAGCC TTGAGAGTGT TTGTGAAAAA GTTTTATTTT CTGTTATGTA 1200
 TACATAATTA AATGAAAATT CTTCAGAAAA AGTTTGATAA ATTGAATTGT GGTATGAAA 1260
 60 CTAATTTGCA TTTTATTTTG CTTAAGAAAG AAAGCTGTGA TAGATTCCAG ATATGCTTTT 1320

5 TGATGTTTTTCTCTGCTCCA GCTCCAAGAA GTCAGCACAC CTGCATTTTA GCTCTGCATG 1380
 CAGCCCCAGC AGGCTGCGTG TTAAAGAATT TCATTGTTTA ACTGGCTGGT GTGAGAAGTC 1440
 TTCCGTTAGC ATAGAGTGGA AGGAGTACTA TTGTTTGGTT GGGTTTMTGT TTGTTTGTMT 1500
 TTTGTTTMTG CTTTTATTGC CAAGAGGTGC TTGTTTAA AGTATGTTTA ATAAATGAA 1560
 10 ATTCTAAAGT TAARAAGTGT TCTTAAAGTT GATATTTAAC TCT 1603

15 (2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1089 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

25 GGCACGAGCT ACCTTTCTGC CTGCTTTGCT GGCTGCAACA GCACGAATCT CACGGGCTGT 60
 GCGTGCCTCA CCACCGTCCC TGCTGAGAAC GCAACCGTGG TTCCTGGAAA ATGCCCCAGT 120
 CCTGGGTGCC AAGAGGCCTT CCTCACTTTC CTCTGTGTGA TGTGTATCTG CAGCCTGATC 180
 30 GGTGCCATGG CAAGACACCC TCAGTCATCA TCCTCATCAG GACAGTCAGC CCTGAACTCA 240
 AGTCTTACGC TTTGGGAGTT CTTTTTCTCC TCCTTCGTTT GTTGGGCTTC ATCCCTCCAC 300
 35 CCCTCATCTT CGGGGCTGGC ATCGACTCCA CCTGCCTGTT CTGGAGCAGG TTCTGTGGGG 360
 AGCAAGGCGC CTGCGTCTTC TACGACAATG TGGTCTACCG ATACCTGTAT GTCAGCATCG 420
 CCATCGCGCT CAAATCCTTC GCCTTCATCC TGTACACCAC CACGTGGCAG TGCTGAGGAA 480
 40 AAATATAAAA CGCTACATCA AAAACCACGA GGGCGGGCTG AGCACCAGTG AGTTCTTTGC 540
 CTCTACTCTG ACCCTAGACA ACCTGGGGAG GGACCCTGTG CCCGCAAACC AGACACATAG 600
 45 GACAAAGTTT ATCTATAACC TGGAAGACCA TGAGTGGTGT GAAAACATGG AGTCCGTTTT 660
 ATAGTGACTA AAGGAGGGCT GAACTCTGTA TTAGTAATCC AAGGGTCATT TTTTCTTAA 720
 AAAAAGAAAA AAAGGTTCCTA AAAAAACCA AAACCTAGTA CACACACACA GGCACAGATG 780
 50 CACACACACG CAGACAGACA CACCGACTTT GTCCTTTTTC TCAGCATCAG AGCCAGACAG 840
 GATTGAGAAT AAGGAGAGAA TGACATCGTG CGGCAGGCTC CTGGAGGCCA CTCGCGGGC 900
 55 TGGGCCACAG AGTCTACTTT GAAGGCACCT CATGGTTTTC AGGATGCTGA CAGCTGCAAG 960
 CAACAGGCAC TGCCAAATTC AGGGAACAGT GGTGGCCAGC TTGGAGGATG GACATTTCTG 1020
 GATACACATA CACATACAAA ACAGAAAACA TTTTAAATAA GAAGTTTCCT AAAATAAAAA 1080
 60

AAAAAAAA

1089

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(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 629 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

AGCTCAGTTC CCTAGAAAT GAAATTTTAA ATGACACTAC CAGGTAAGCC ACTGAGACCA 60
GTGGAGGTGA TAGCTAAGAA CATAAGGAAT TAAGAATTTT TAATGGAGAA AGGAGGTAAT 120
20 GAATACCACT TACATCCTAA GACTCACTGT AGTGGTGAGT GTTGTAAATTT ATCTCGCTAT 180
CCATCCTCTT TTAAGTTTTT CCTTAGAAAG TCCTCTATTG GTACCTTGGA GGGACTGCTG 240
TCAAAATATA TGGAAAAGTG GGTCTGTGTG GTACAAGAGG TGGACTTTGC CACACATGGA 300
25 AGTTTGCTGC CAAGATCTTC ACTAATGAAA GAAATCACCA GTGAGCTGCA CAGATTAGCC 360
AAATACTGAG CTCATTAGAA CTACTAAGGC CTGGACATTT CTGCCTAATC CAGGACTCCT 420
30 GTAATPATCA GTCTTTGCTT TGGAGCTTCC CATTTGTGTAG CTGARAATTT GTCATATCTG 480
CATTATAATC TAAGGCTCCA CATACTTAAT CCTGCTTCTC CCCCTTTTTC TTTCCCTTTC 540
CCAGCGGTCA GCTCTGCTGC ATAGTCTGAA GACTTTCCCT GCCCAATCCT GATAAAATTC 600
35 TTGCACTCGT AACCCCATCT CAGTGTCTG 629

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(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 1964 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

AAGAAGACAT GGAAATGCTT GAAGGATGTT TCAGGCATAT TAAGAAAATC TTTACGCAGC 60
TTGAGGAATT CAGAGCCTCT GAATTGCTTC GAAGTGGACT GGACAGATCT AAATACCTTT 120
55 TAGTGAAAGA AGCCAAAATT ATTGCTATGA CCTGTACTCA TGCTGCCTTA AAACGACATG 180
ACTTGGTCAA GCTAGGTTTC AAGTATGACA ACATTTTGAT GGAAGAGGCT GCTCAGATTC 240
TGGAGATAGA AACTTTTATC CCTCTTCTTC TACAGAATCC TCAGGATGGA TTTAGCCGAC 300

60

	TAAAACGATG GATTATGATT GGCGATCATC ACCAGTTACC TCCAGTTATT AANGAACATG	360
	GCCTTTCAAA AGTACTCAAA CATGGAGCAG TCTCTCTTCA CTCGCTTTGT TCGCGTTGGA	420
5	GTTCCGACTG TTGACCTTGA TGCTCAAGGG AGAGCCAGAG CAAGCTTGTG CAMCTNCTAC	480
	AACTGGCGAT ACAAGAATCT AGGAAACTTA CCCCATGTGC AGCTCTTGCC AGAGTTTAGT	540
10	ACAGCAAATG CTGGCTTACT GTATGACTTC CAGCTCATTA ATGTTGAAGA TTTTCAAGGA	600
	GTGGGAGAAT CTGAACCTAA TCCTTACTTC TATCAGAATC TTGGAGAGGC AGAATATGTA	660
	GTAGCACTTT TTATGTACAT GTGTTTACTT GGTTACCCCTG CTGACAAAAT CAGTATTCTA	720
15	ACAACATATA ATGGCCAAAA GCATCTTATT CGCGACATCA TCAATAGACG ATGTGGAAAC	780
	AATCCATTGA TTGGAAGACC AAACAAGGTG ACAACTGTTG ATAGATTTC AAGTCAACAG	840
20	AATGACTATA TTCTTCTTTC TCTGGTACGA ACCAGGGCAG TGGGCCATCT GAGGGATGTC	900
	CGTCGCTTGG TAGTGGCCAT GTCTAGAGCC AGACTTGGAC TTTATATCTT CGCCAGAGTA	960
	TCCCTCTTCC AAAACTGTTT TGAACGACT CCAGCTTTCA GTCAGCTCAC AGCTCGCCCC	1020
25	CTTCATTTC ATATAATTCC AACAGAACCT TTCCCAACTA CTAGAAAGAA TGGAGAGAGA	1080
	CCATCTCATG AAGTACAAAT AATAAAAAAT ATGCCCCAGA TGGCAAAC TT TGTATACAAC	1140
30	ATGTACATGC ATTTGATACA GACTACACAT CATATCATC AGACTTTATT ACAACTACCA	1200
	CCTGCTATGG TAGAAGAGGG TGAGGAACTT CAAAATCAAG AAACAGAATT GGAAACAGAA	1260
	GAAGAGGCCA TGA CTGTTCA AGCTGACATC ATACCCAGTC CAACAGACAC CAGCTGCCGT	1320
35	CAAGAACTC CAGCCTTTCA AACTGACACC ACCCCAGTG AGACAGGAGC CACTTCCACT	1380
	CCAGAAGCCA TCCCTGCTTT ATCTGAGACC ACCCCTACTG TGGTAGGAGC TGTATCTGCA	1440
40	CCGGCAGAAG CTAACACACC TCAGGATGCC ACATCTGCCC CAGAAGAGAC CAAGTAGCCA	1500
	AACTGTAGTC CTTCTAAAGG AGGACATGGC AGTCAAAAAG TCTGAGTAAA GCTGTTTTTT	1560
	GTATTTTATA TTTGCTTCTG CCATTTTACT GTCAC TAATT AATGTTTAGT TCTTATATTT	1620
45	GTAACTGAT TTCGGTGTCT TGAATATATT TTTTAAATT ATGTGTATGA ACAATTCTAG	1680
	TTTCATTGT TCAATCAGAA GAGCAAATAA CCATTCCCTT CATGTTTGA TCACTGAGTG	1740
50	TGTCTGTAAT CATACCTACA TTAAATCAT TTTCTATGAA TATATAATAT ATACTTCACA	1800
	TTTTTAGTGA ACTTCTCTAA AGAAGAGGAC AGAATATACT GGACTTAACC ACGAATACCC	1860
	TTGAGTGTC AAATTGGGAA GGAACKGTT TCTTCYGT A TACTAYCAA TGCTTAAATT	1920
55	CKGTTTCCTT TTTTCTTACC TTTGTTTGCT GTCTTTATGT AAAG	1964

60 (2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1522 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

10	CGTGTCCGCG CGCCTGGGAG ACGCTGCCTC GGCCCGGACG CGCCCGCGCC CCCGCGGCTG	60
	GAGG3TGGTC GCCACTGGGA CACTGTGAAC CAGGAGTRAG TCGGAGCTGC CGCGCTGCCC	120
15	AGGCCATGGA CTGTGAGGTC AACAAACGGTT CCAGCCTCAG GGATGAGTGC ATCACAAACC	180
	TACTGGTGTGTT TGGCTTCCTC CAAAGCTGTT CTGACAACAG CTTCCGCAGA GAGCTGGACG	240
	CACTGGGCCA CGAGCTGCCA GTGCTGGCTC CCCAGTGGGA GGGCTACGAT GAGCTGCAGA	300
20	CTGATGGCAA CCGCAGCAGC CACTCCCCTG TGGGAAGAAT AGAGGCAGAT TCTGAAAGTC	360
	AAGAAGACAT CATCCGAAT ATTGCCAGGC ACCTCGCCCA GGTGCGGGAC AGCATGGACC	420
25	GTAGCATCCC TCCGGGCCTG GTGAACGGCC TGGCCCTGCA GCTCAGGAAC ACCAGCCGGT	480
	CGGAGGAGGA CCGGAACAGG GACCTGGCCA CTGCCCTGGA GCAGCTGCTG CAGGCCTACC	540
	CTAGAGACAT GGAGAAGGAG AAGACCATGC TGGTGTGGC CCTGCTGCTG GCCAAGAAGG	600
30	TGGCCAGTCA CACGCCGTCC TTGCTCCGTG ATGTCTTTCA CACAACAGTG AATTTTATTA	660
	ACCAGAACCT ACGCACCTAC GTGAGGAGCT TAGCCAGAAA TGGGATGGAC TGAACGGACA	720
35	GTTCAGAAAG TGTGACTGGC TAAAGCTCGA TGTGGTCACA GCTGTATAGC TGCTTCCAGT	780
	GTAGACGGAG CCCTGGCATG TCAACAGCGT TCCTAGAGAA GACAGGCTGG AAGATAGCTG	840
	TGACTTCTAT TTTAAAGACA ATGTTAAACT TATAACCCAC TTTAAATAT CTACATTAAT	900
40	ATACTTGAAT GAAAAATGTC ATTTACACGT ATTTGAATGG CCTTCATATC ATCCACACAT	960
	GAATCTGCAC ATCTGTAAAT CTACACACGG TGCCTTTATTT TCCACTGTGC AGGTTCACCAC	1020
45	TTAAAAATTA AATTGGAAAG CAGGTTTCAA GGAAGTAGAA ACAAATACA ATTTTTTTGG	1080
	TAAAAAATAA TTAAGTTTAA TTAAGTACA ACCATAGAGG ATGGTCTTAC AGCAGGCAGT	1140
	ATCCTGTTTG AGGAAAGCAA GAATCAGAGA AGGAACATAC CCCTTACAAA TGAAAAATTC	1200
50	CACTCAAAAT AGGGACTATC YATCTTAATA CTAAGGAACC AACAATCTTC CTGTTTAAAA	1260
	AACCACATGG CACAGAGATT CNGAACTAAA GTGCTGCACT CAAATGATGG GAAGTCCCGG	1320
55	CCCCAGTACA CCAGGGGCTT TGGACTTTTT TCAACTTCGT TTCCTTTTGT TTGGANTCCA	1380
	AAAGAACCAC TTTGTGGTTC TTTAAAGGGT GTGAAGGTGA TTTAAGGGGC CCAGGTCAGC	1440
	CACTGGTTGG TTTACAAAAT CNGGGTAACT AACTGCATAC AACTTTTTCC CNTTTCCATG	1500
60	NCATCAGGAC TTTGCTAAAG AC	1522

5 (2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 875 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

15 TGGGATTTCCT CTTTATCATG GAGGCCTTGT CCCACTTCCT CTATGTCCCT TTCCTTGGTG 60
TCTGTGTCTG TGGGGCCATC TACACTGGCC TGTTCCCTCC TGAGACCAA GGCAAGACCT 120
TCCAAGAGAT CTCCGAGGAA TTACACAGAC TCAACTTCCC CAGGCGGGCC CAGGGCCCCA 180
20 CGTGAGGAG CCTGGAGGTT ATCCAGTCAA CAGAACTCTA GTCCCAAAGG GGTGGCCGTA 240
GCCAAAGCCA GCTACCGTCC TGTCTCTGTC TTCTGCCAG GGCCCTGGTC CTCAMTYCCT 300
25 YCTGCATTCC TCATTTAAGG AGTGTTTATT GAGCACCTT TGTGTGCAGA CATGGCTCCA 360
GGTGCTTAGC AATCAWGGT GAGCGTGGTA TCCAGGCTAA AGGTAATTAA CTGACAGRAA 420
ATCAGTAACA ACATAATTAC AGGYTGGTGTG TGGCAGYTCA TGA CTGTAAT CCCAGCACTT 480
30 TTGGGAGCCA AGGTGGGARG ATCAATTGAG GCCAGAGTTT GAAAMCAGCT AGGTAACATA 540
GTGAGACCCC CTATCTCTAC AAAAAATT TT AACATTAGC TGGGCATGGT GGTATGTGCT 600
35 AACAGCTCTA GCTACTCAGG AGGCTGAGGC AGCAGGATCA CTTGAGTCCA AGAGTTCAAG 660
GTAGCAGTAA GCTACAATCA CACCACTGCA TGCCAGACTG GGTGACAGAG GGAGACTTCA 720
TCTCTTTAAA ACATAATAAT AATAATTACA GACTCAGGAA ATGCAGTGAA AGAAAAATAC 780
40 AGGTTGGCCA GGTGAGGTGG CTGATGCCTG TAATCCCAGC ACTTTGGGAG GCCAAGATGG 840
GAAGATTGCT TTGAGACCAG AAGTTTGAGA CCAGC 875

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(2) INFORMATION FOR SEQ ID NO: 43:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CCCACGCGGT CCGNATCGTC CTTCCCTCAC TTCAGAGGGT GGCCAGAGCT GAATACCCAG 60
60 AGAGGGACAA GTAAGGTGCC AGTTCCAAAA CATCATGAGG ATGTATCATC CCACGTGTCT 120

CACCTGACAG TTACAGAGGA AACCCGCACC CAGAATGCAC GTGCTGTCTT ATGGGAACAC 180
 TCAGCGCAGA GTGCTCAGGT CCGGCCACAC TCGGGCTGTG CTTGGTCGTG CCATGGAATT 240
 5 CCTCAGGACT TTCTCAGCCT CCCTAATGGC AGAAGCCCCT TTACAGCAAG ACATTTACCG 300
 TTTGTCTGAA AATAGCCGAA CTGAGCTTTT CTTCAGGCTA TATGAGAAGT CTCTAGACAG 360
 10 TGGGCACCGT CAGAAAGCCC AGAGCCTTGT GATAGCTCCC ACCCTGCCTG GCTCAGATCT 420
 TCCCATTFTT TTTCTCTGG CACTAACCTC ACCTTTTGT TTTTGTGTT TGTGTTTGT 480
 15 TTTGTTTTTG CAGAGTTGGA TTACAGAAAC TCCTATGAAA TTGAATATAT GGAGAAAATT 540
 GGCTCCTCCT TACCTGTAAG TTCGTCTGCC TCGGGCCACT TAGGGGACTC GCTTTCCTGC 600
 CTTCAGGGGC CTCCTCCCCT GTGCAGAGTG TCTCTGGGAG CTCAGACCCC AAATCGAGTG 660
 20 TTTTCTGTGT ACACAGCTTC CCGGGTGCAC AGCAATGATG GACTGGGGCT GGGGGTTGA 720
 GGTTTGTACT CAATCCACTT CGTTTGACAT TTTCAGGGAG AAAATGATAG AATACAATTA 780
 25 GACGTCCTGC AGAATTACTT TCCTAGACTG AGAAAGAGCT AGAGATTCTT TTAATAAAAA 840
 AAA 843

30

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 489 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

40

CTCTTAGGCT TTGAAGCATT TTTGTCTGTG CTCCCTGATC TTCAGGTCAC CACCATGAAG 60
 TTCTTAGCAG TCCTGGTACT CTTGGGAGTT TCCATCTTTC TGGTCTCTGC CCAGAATCCG 120
 45 ACAACAGCTG CTCCAGCTGA CACGTATCCA GCTACTGGTC CTGCTGATGA TGAAGCCCCT 180
 GATGCTGAAA CCACTGCTGC TGCAACCACT GCGACCACTG CTGCTCCTAC CACTGCAACC 240
 ACCGCTGCTT CTACCACTGC TCGTAAAGAC ATTCCAGTTT TACCCAAATG GGTGCGGGAT 300
 50 CTCCCGAATG GTAGAGTGTG TCCCTGAGAT GGAATCAGCT TGAGTCTTCT GCAATTGGTC 360
 ACAACTATTC ATGCTTCCTG TGATTTTCATC CAACTACTTA CCTTGCCTAC GATATCCCCT 420
 55 TTATCTCTAA TCAGTTTATT TTCTTTCAAA TAAAAAATAA CTATGAGCAA CAAAAAATAA 480
 AAAAAATAA 489

60

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 534 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GAAGCAGTGT GTATCTATGA TTATATCTCT GTTCATCTAT ATATTTTGA CATGTAGCAA 60
CACCTCTCCA TCTTATCAAG GAACTCAACT CGGTCTGGGT CTCCCCAGTG CCCAGTGGTG 120
15 GCCTTTGACA GGTAGGAGGA TGCAGTGCTG CAGGCTATTT TGT'TTTTGT TACAAAAC TG 180
TCTTTTCCCT TTTCCCTCC ACCTGATTCA GCATGATCCC TGTGAGCTGG TTCTCACAAT 240
20 CTCTGGGAC TGGGCTGAGG CAGGGGCTTC GCTCTATTCT CCCTAACCAT ACTGTCTTCC 300
TTCCCTTG CCACTTAGCA GTTATCCCC CAGCTATGCC TTCTCCCTCC CTCCCTTGCC 360
CTGGCATATA TTGTGCCTTA TTTATGCTGC AAATATAACA TTAAACTATC AAGTGAAAAA 420
25 AAAAAAAAAA AAAACTCAA GGGGGGGCCG GTACCAATT CCCCTATAN TGAGTCNTAT 480
TACAATTAC TGGGCCGTCG TTTTACAACG TCGTGAATGG GAAACCTGG GCGT 534

30

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GGCACGAGTC CGGATGAGC TCAGCCGCGG CCGACCACTG GCGTG GTTG CTGGTGCTCA 60
45 GCTTCGTGTT TGGATGCAAT GTTCTTAGGA TCCTCCTCCC GTCCTTCTCA TCCTTCATGT 120
CCAGGGTGCT GCAGAAGGAC GCGGAGCAGG AGTCACAGAT GAGAGCGGAG ATCCAGGACA 180
TGAAGCAGGA GCTCTCCACA GTCAACATGA TGGACGAGTT TGCCAGATAT GCCAGGCTGG 240
50 AAAGAAAGAT CAACAAGATG ACGGATAAGC TCAAAACCCA TGTGAAAGCT CGGACAGCTC 300
AATTAGCCAA GATAAAATGG GTGATAAGTG TCGCTTCTTA CGTATTGCAG GCTGCCCTGA 360
55 TGATCTCACT CATTTGGAAG TATTATTCTG TCCCTGTGGC TGTCGTGCCG AGTAAATGGA 420
TAACCCCTCT AGACCGCCTG GTAGCCTTTC CTA CTAGAGT AGCAGGTGGT GTTGAATTA 480
CCTGTTGGAT TTAGTCTGT AACAAAGTTG TCGCTATTGT GCTTCATCCG TTCAGCTGAA 540

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	CAGGAGGATG GATACAGCCG CGAGGCTAAA AAACGGATT TCTCTTCCTA GCTTAAAATC	600
	TGATTTACAC TGTMTTGT TTTAAGAAAC AAAAGTGCAT AGTTTAGATT TTTTTTTTG	660
5	TTGAATATGT TTGTCTTGG ACTTTATGAG AGAGTCTTAT AAGAATCACG ATTTTCTACA	720
	CCTGTCTATG AGCCAAGAAA GTCCAGTTTA TGACACGTAT GTACTAGTGA ACACCGTCTT	780
10	CGATCTGTAC GAAATGTGAA ATGTTTAGGG ACATCTCCAT GCTGTCAC TT GTGATTTGCC	840
	CTCTTATGTA TTTTGGTCAT ATTGCCAACT GGAAAGTCAA AATTTTCTAA CAACTTTAAG	900
	TAAGTTCTTT GAAGACTTAG TGCTGTTTTT AATCCAGTTT AGAAAGTAAC TTAATTTTAA	960
15	TACCACTACT AAAAATTCGA AAATTTCTTC TTTAATCACA TTCAATATGG TTAAAAGAAC	1020
	AACACTAATT GACATTGCGT GGGCTTTTTT TCCCTTTGTT TAAAATGTCA TTTGTGAGC	1080
20	AAGAGTTGTA TAGTATTATC TACTTACTTG AGGCTGTTAA TTTTTCATTA CAGTGTTTTG	1140
	TAAATGTATC CACGAGACCA TGATGCATTG TTTTGTGCTC AACTGTGTT TTGTATTTAA	1200
	AGCATTTTGA ATGAAGTGTA TTTTATAAGC ATTTAATATT TATGCTCTTT AGAATGGAAC	1260
25	ACAGAAAACA AACCTTATAA GTCCTGATTA ATCTGAACCA ATAACCTGTG TGGCCTACAA	1320
	AGTATAATTC TATTAAATGT TCCTTAAAC AAAAAAAAAA AAAAAAAAAA AAAA	1374

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(2) INFORMATION FOR SEQ ID NO: 47:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 596 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

	GAATTCGNCA CGAGATTACT TGGACATGAA AGAACTCAGG TTCAAGTTTA TTCATTTACT	60
	AAGTTAGTTA AATCATGTGC CTTCCATGAG CCTTCATTTG GTAAGTTGGA AAATGGAAAT	120
45	AATAACACTA GTCATATATA TTCTACACTG CTACCATATG GACCAAAGGG ATTATAGATT	180
	ACAATCACCA TCATTCCCTGC TGACAGGTAT ATAGAAAACA ATTTCAATTGA AGAAAAGTCC	240
50	TTACATTTAT CCTTTTCCTA ATATCTGCAT GGGTAACTA ATAAATATAG TCATTAGAAA	300
	ACCCTTATTA TTATTATTAG TTCAATGTGA GAACTGCTGC AGAAAAATA TGCTTTATAA	360
	TATTTTCTTG AATATACATA ATATTCATAA ATTTTCAAAT CATTGAAAAT TACCTTAAAA	420
55	TTGGAAAAAA TGTGCAATTC TACTCATATA ACAGTATAAA ATTCCTATGT CAATCTCTTT	480
	TTTTTTTTTT TGTMTTGAGT TGGAGTCTCG CTCTGTGCCC CAGGCTGGGC AACAGAGCAG	540
60	GACCCTGTCT TAATTAATAA AAAAAAAAAA AAACTCGAGG GGGGCCCGGT ACCCTA	596

5 (2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 851 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

15 CACATGAAGA CACACAGTGG TGAGAAGCCC TTCCGCTGCG CCCGCTGTCC TTATGCCTCT 60
CCTCATCTGG ATAACCTGAA ACGGCACCAG CGCGTCCATA CAGGAGAGAA GCCCTACAAG 120
TGCCCCCTCT GCCCTTATGC CTGTGGCAAT CTGGCCAACC TCAAGCGTCA TGGTCGCATC 180
20 CACTCTGGTG ACAAACCTTT TCGGTGTAGC CTTTGCAACT ACAGCTGCAA CCAGAGCATG 240
AACCTCAAAC GTCACATGCT GCGGCACACA GCGGAGAAGC CTTCCGCTGT GCCACCTGCG 300
25 CCTATACCAC GGGCCACTGG GACAACTACA AGCGCCACCA GAAGGTGCAT GGCCACGGTG 360
GGGCAGGAGG GCCTGGTCTC TCTGCCTCTG AGGGCTGGGC CCCACCTCAT AGCCACCCCT 420
CTGTTTTGAG CTCTCGGGGC CCACCAGCCC TGGGGACTGC TGGCAGCCGG GCTGTCCACA 480
30 CAGACTCATC CTGAACTAGG TCCTTCTTCC CCATGTTTTA TACAGACGGA CCAGAAGCCA 540
CCTTTTCTC CCCCCTGGC CAGGGGCTCC ACACAGACTA ACGTAGGCAC TATAAGGACC 600
35 AGCCCAACCC CATGGGCGGG GGGGCCATA TGGACCAGG GACCTTGCTT TGAAGGAGC 660
ACTTCACGAG CTCAGTGAGA AGGGCCCTGT ATTCACCTCC ACTGCCCCCA GGGGCTGTGG 720
ACAAACCGGC TGGGGGACTG CCCAGCCTCC CACCTGTTTA TTAACTTAT TTCAGTGCTT 780
40 TATAATAAAG GAAACACTAA CAAAGCCATG TCTATGCTGA ATTGGCAATG GCAGGCAATT 840
TGGCCTTACC C 851

45

(2) INFORMATION FOR SEQ ID NO: 49:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2020 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GTGAAATGAA AACAGTCITT TTATAGCCTT TAGCTTGTGA GTTTGGAAGT TTGGGGGGTC 60
60 TTATGTTTGT TTGCCTCTT CTGTTTCTTG GAGGAGAGTT GAGGCTTTTC TTAGGTGCAT 120

	ACACAGACCC AGGTGAACAC GCTGACTGTG AACCTGCCCT GTATCCGGAG CTGTGCTGGG	180
5	CACTGAGGGG ATGCAACAAA ATTAGGAGAG GWTCCCTTGCT CCCAACGTCT ACTTCTCCTA	240
	CCTCAACAGG GGTCCAGGGT GCAGTGAAC T CAGTTCTTGG CCCTTGGGTG AGGATTCATG	300
	GATGAATGAA AGCTAGACCT GATGGGGAGG CATTATGACT AAATAGGCCC AGCCTCCTTC	360
10	CCTTCCAGCT CTGTCCTAGG AGCATAGGCG GGAAATCTGA GTAGAGTCTG ACTGCAGTTT	420
	TTGCTTATGA TTTGTAAAAG CCGTCATGGG GTCAATAAGA AAATAGGGGT GATGGAGGGG	480
15	GAGAAGCCCA GGA CTGGGAG AATCGCACGT GCGCCAGGGG TTTTCACCAA GGATTTTCAA	540
	GACAACTGG AGTAAGAATT AAAGCCCCAG AGGATTTAAT TATCCTGGTT TGCAAAAGAG	600
	CCTCCCATGC CAGTACCGCC CAGCCTTGGA GGCCGGAATG CTCATGGCCC CTGTGGTCTG	660
20	CTTGTCTCTC AGCCCATGCC CAGCAGATAC CTCTCTGACT GGAGACGGGC TCAAAGCTGG	720
	ATTAGAAAGG GGAGMGGCAC TTGTGACTTT GTTTGACTCT GTGACTCACT TCCTCGCTCA	780
25	CACCTTGT TT GA ACTACTGG ACTTTCAACT GGCTTTCCTT AGGTCAGGCA AGCAGACAGC	840
	TCCCCACTGA AGAGGTCTGT ACAGTGACAA CCCGGGCCGG CAGCAAGGAC ACAGATGCAG	900
	CCACAGTAAG GCTCCATCAG GACTGGGTCA GTGATGGCAA CAGGATGGCC AAGGATGGCT	960
30	CTAGAACAYT CTGTCCATGC GTCACTCCCC CCAGTTTTRT TTTTAGCTTT GGCTTCAGGG	1020
	AGTGACAGCC ATCACAAATA GCCACATTCT GCTCTACTCT CCAACATACC AGATTSTACA	1080
35	CTGTTGTTAT TTCATGAGAC GTGAATGTTG CAGAGAGTGG GGGGATTCTG GTTGTAAAGG	1140
	AACTTACACT GGGGAGCTTT ACTCTCCGT GTCAACAATG TGA CTACATG TTCTCCAGAT	1200
	TAGCCACACA TGCAACATC AGTGTCTTTC TAGCTTTTANC CGAGAAAGAA ACCAGTCCCA	1260
40	GGGAATGAAT GGTGGTCTCC CCACTCCCGG CAGCACTTTA GGCAGCCCAT AAGCTATGCG	1320
	AGAATGTGAA CGCTCACCTT GCTCCGTCAC GGTTC TGACC TACCACATAA ACAGGAAGAA	1380
45	GCCAGTGACC GGAACAGCTC TAGGAATAAC AAGTCAGAAT AGAAGTGTCC TTTATATTAC	1440
	CAGAAAATAT GGGCTTGCC TAAGTCGCTG TCTCTAACC TGCCGGGGTC ATTCCCCACC	1500
	AAACACCCCA TACTAAGGAG CCATGAGCCA CCTGGACATT CACCTTTTCT TTGACCATCT	1560
50	GGAGTCTGGG GCAACTTAAG GAAGGCNCCA CACAGTGCTG CAGGCACATT TCCAAGCGTA	1620
	GGTGTCCCTG GCTTTTGTGG CCAAAGCTAG TGTTATGGTC AACAAACAGGC CAGGGTCTGT	1680
55	GGGGCACTGA CCTTGAAAGT GGCAAAATGG AGGTTTCACA GGCTGTGCGG GAGCAGGACG	1740
	GCTTGCTTCA TCTAACAATC TCAGTTTCCT TAAAAAAAAG AAAGAAAGGA AAAGATTTCA	1800
	TAAGCAGGTG TCAGTGGACA GTTTAAGYAC TTAACCATTT CTCTTCTTTC TTATGGATGT	1860
60	GAAGTGTGCT GTGGATAAAT CATTTGTATT TCTTGAATGT TCTCTATGAC TAACAGTTAT	1920

	TAAGTCGGTT GTGTATATGT GTAACATAATG TAACTGCCTT TTAAAATTTC ATTACAATAA	1980
5	AAATGACTTT GCTCTGAAMA AAAAAAAAAA AAAAAGTCGA	2020
10	(2) INFORMATION FOR SEQ ID NO: 50:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 2432 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:	
20	ATGAAGGGTC GTTGGTGGGA AAGATGGCGG CGACTCTGGG ACCCCTTGGG TCGTGGCAGC	60
	AGTGGCGGCG ATGTTTGTGCG GCTCGGGATG GGTCCAGGAT GTTACTCCTT CTTCTTTTGT	120
	TGGGTCTGCG GCAGGGGCCA CAGCAAGTCG GGGCGGTCA AACGTTGAG TACTTGAAAC	180
25	GGGAGCACTC GCTGTGGAAG CCCTACCAGG GTGTGGGCAC AGGCAGTTCC TCACTGTGGA	240
	ATCTGATGGG CAATGCCATG GTGATGACCC AGTATATCCG CCTTACCCCA GATATGCAAA	300
30	GTAAACAGGG TGCCTTGTGG AACCGGTGTC CATGTTTCCT GAGAGACTGG GAGTTCAGG	360
	TGCACTTCAA AATCCATGGA CAAGGAAAGA AGAATCTGCA TGGGGATGGC TTGGCAATCT	420
	GGTACACAAG GAATCGGATG CAGCCAGGGC CTGTGTTTGG AAACATGGAC AAATTTGTGG	480
35	GGCTGGGAGT ATTTGTAGAC ACCTACCCCA ATGAGGAGAA GCAGCAAGAG CGGGTATTCC	540
	CCTACATCTC AGCCATGGTG AACACGGCT CCCTCAGCTA TGATCATGAG CGGGATGGGC	600
40	GGCCTACAGA GCTGGGAGGC TGCACAGCCA TTGTCCGCAA TCTTCATTAC GACACCTTCC	660
	TGGTGATTCG CTACGTCAAG AGGCATTTGA CGATAATGAT GGATATTGAT GGCAAGCATG	720
	AGTGGAGGGA CTGCATTGAA GTGCCCGGAG TCCGCCTGCC CCGCGGCTAC TACTTCGGCA	780
45	CCTCCTCCAT CACTGGGGAT CTCTCAGATA ATCATGATGT CATTTCTTGG AAGTTGTTTG	840
	AACTGACAGT GGAGAGAACC CCAGAAGAGG AAAAGCTCCA TCGAGATGTG TTCTTGCCCT	900
50	CAGTGGACAA TATGAAGCTG CCTGAGATGA CAGCTCCACT GCCGCCCTG AGTGGCCTGG	960
	CCCTCTTCTT CATCGTCTTT TTCTCCCTGG TGTMTTCTGT ATTTGCCATA GTCATTGGTA	1020
	TCATACTCTA CAACAAATGG CAGGAACAGA GCCGAAAGCG CTTCTACTGA GCCCTCCTGC	1080
55	TGCCACCACT TTTGTGACTG TCACCCATGA GGTATGGAAG GAGCAGGCAC TGGCCTGAGC	1140
	ATGCAGCCTG GAGAGTGTTC TTGTCTCTAG CAGCTGGTTG GGGACTATAT TCTGTCACTG	1200
60	GAGTTTGTAA TGCAGGGACC CCGCATTTCC ATGGTTGTGC ATGGGGACAT CTAAGTCTGG	1260

	TCTGGGAAGC CACCCACCCC AGGGCAATGC TGCTGTGATG TGCCTTTCCC TGCAGTCCTT	1320
	CCATGTGGGA GCAGAGGTGT GAAGAGAATT TACGTGGTTG TGATGCCAAA ATCACAGAAC	1380
5	AGAATTTTCAT AGCCCAGGCT GCCGTGTGTG TTGACTCAGA AGGCCCTTCT ACTTCAGTTT	1440
	TGAATCCACA AAGAATTAAA AACTGGTAAC ACCACAGGCT TTCTGACCAT CCATTCTGTG	1500
10	GGTTTTGCAT TTGACCCAAC CCTCTGCCTA CCTGAGGAGC TTTCTTTTGA AACCAGGATG	1560
	GAAACTTCTT CCCTGCCTTA CCTTCCTTTC ACTCCATTCA TTGTCCTCTC TGTGTGCAAC	1620
	CTGAGCTGGG AAAGGCATTT GGATGCCTCT CTGTTGGGGC CTGGGGCTGC AGAACACACC	1680
15	TGCGTTTCAC TGGCCTTCAT TAGGTGGCCC TAGGGAGATG GCTTTCTGCT TTGGATCACT	1740
	GTTCCCTAGC ATGGGTCTTG GGTCTATTGG CATGTCCATG GCCTTCCCAA TCAAGTCTCT	1800
20	TCAGGCCCTC AGTGAAGTTT GGCTAAAGGT TGGTGTAATA ATCAAGAGAA GCCTGGAAGA	1860
	CATCATGGAT GCCATGGATT AGCTGTGCAA CTGACCAGCT CCAGGTTTGA TCAAACCAAA	1920
	AGCAACATTT GTCATGTGGT CTGACCATGT GGAGATGTTT CTGGACTTGC TAGAGCCTGC	1980
25	TTAGCTGCAT GTTTTGTAGT TACGATTTTT GGAATCCAC TTTGAGTGCT GAAAGTGTA	2040
	GGAAGCTTTC TTCTTACACC TTGGGCTTGG ATATTGCCCA GAGAAGAAAT TTGGCTTTTT	2100
30	TTTTCTTAAT GGACAAGAGA CAGTTGCTGT TCTCATGTTT CAAGTCTGAG AGCAACAGAC	2160
	CCTCATCATC TGTGCCTGGA AGAGTTCACT GTCATTGAGC AGCACAGCCT GAGTGCTGGC	2220
	CTCTGTCAAC CCTTATTCCA CTGCCTTATT TGACAAGGGG TTACATGCTG CTCACCTTAC	2280
35	TGCCCTGGGA TTAAATCAGT TACAGGCCAG AGTCTCCTTG GAGGGCCTGG AACTCTGAGT	2340
	CCTCCTATGA ACCTCTGTAG CCTAAATGAA ATTCTTAAAA TCACCGATGG AACCAAAAAA	2400
40	AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA	2432

45 (2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

55	GACGCTGGGG GCGGGTGGGG GCGCGGGTA CCGGGCTGGA CGGCCGGCCG GCGCCCCCTC	60
	ATTAGTATGC GGACGAAGCG GCGGGCTGCG CGGAGNGACG TCCCTTGACG CCGCGGACCG	120
	AGGCAGCGGC GGCACCTGCC GGCCGAGCAA TGCCAAGTGA GTACACCTAT GTRAACTGA	180
60	GAAGTGATTG CTCGAGGCCT TCCCTGCAAT GGTACACCCG AGCTCAAAGC AAGATGAGAA	240

	GGCCCAGCTT GTTATTAAAA GACATCCTCA AATGTACATT GCTTGTGTTT GGAGTGTGGA	300
	TCCTTTATAT CCTCAAGTTA AATTATACTA CTGAAGAAATG TGACATGAAA AAAATGCATT	360
5	ATGTGGACCC TGACCATGTA AAGAGAGCTC AGAAATATGC TCAGCAAGTC TTGCAGAAGG	420
	AATGTCGTCC CAAGTTTGCC AAGACATCAA TGGCGCTGTT ATTTGAGCAC AGGTATAGCG	480
10	TGGACTIONT CCCTTTTGTG CAGAAGGSCC CCAAAGACAG TGAAGCTGAG TCCAAGTACG	540
	ATCCTCCTTT TGGGTTCCGG AAGTTCTCCA GTAAAGTCCA GACCCTCTTG GAACTCTTGC	600
	CAGAGCACGA CCTCCCTGAA CACTTGAAAG CCAAGACCTG TCGGCGCTGT GTGGTTATTG	660
15	GAAGCGGAGG AATACTGCAC GGATTAGAAC TGGGCCACAC CCTGAACCAG TTCGATGTTG	720
	TGATAAGGTT AAACAGTGCA CCAGTTGAGG GATATTCAGA ACATGTTGGA AATAAACTA	780
20	CTATAAGGAT GACTTATCCA GAGGGCGCAC CACTGTCTGA CCTTGAATAT TATTCCAATG	840
	ACTTATTTGT TGCTGTTTTA TTAAAGAGTG TTGATTTCAA CTGGCTTCAA GCAATGGTAA	900
	AAAAGGAAAC CTTGCCATTC TGGGTACGAC TCTTCTTTTG GAAGCAGGTG GCAGAAAAAA	960
25	TCCCACTGCA GCCAAAACAT TTCAGGATTT TGAATCCAGT TATCATCAAA GAGACTGCCT	1020
	TTGRACATCC TTCAGTACTC AGAGCCTCAG TCAAGGTTCT GGGGGCCGAG ATAAGAACGT	1080
30	CCCCACAATC GGTGTCAFTG CCGTTGTCTT AGCCACACAT CTGTGCGATG AAGTCAGTTT	1140
	GGCGGGTTTT GGATATGACC TCAATCAACC CAGAACACCT TTGCACTACT TCGACAGTCA	1200
	ATGCATGGCT GCTATGAACT TTCAGACCAT GCATAATGTG ACAACGGAAA CCAAGTTCCT	1260
35	CTTAAAGCTG GTCAAAGAGG GAGTGGTGAA AGATCTCAGT GGAGGCATTG ATCGTGAATT	1320
	TTGAACACAG AAAACCTCAG TTGAAAATGC AACTCTAACT CTGAGAGCTG TTTTGTACAG	1380
40	CCTTCTTGAT GTATTTCTCC ATCCTGCAGA TACTTTGAAG TGCAGCTCAT GTTTTTAACT	1440
	TTTTAATTTAA AAACACAAAA AAAATTTTAG CTCCTCCAC TTTTTTTTC CTATTTATTT	1500
	GAGGTCAGTG TTTGTTTTTG CACACCATTT TGTAATGAA ACTTAAGAAT TGAATTGGAA	1560
45	AGACTTCTCA AAGAGAATTG TATGTAACGA TGTGTWTTG ATTTTAAAGA AAGTAATTTA	1620
	ATTTGTAAAA CTTCTGCTCG TTTACACTGC ACATTGAATA CAGGTAACCTA ATTGGAAGGA	1680
50	GAGGGGAGGT CACTCTTTTG ATGGTGGCCC TGAACCTCAT TCTGGTCCC TGCTGCGCTG	1740
	CTTGGTGTGA CCCACGGAGG ATCCACTCCC AGGATGACGT GCTCCGTAGC TCTGCTGCTG	1800
	ATACTGGGTC TGCGATGCAG CGGCGTGAGG CCTGGGCTGG TTGGAGAAGG TCACAACCCT	1860
55	TCTCTGTTGG TCTGCCTTCT GCTGAAAGAC TCGAGAACCA ACCAGGGAAG CTGTCTCTGA	1920
	GGTCCCTGGT CGGAGAGGGA CATAGAATCT GTGACCTCTG ACAACTGTGA AGCCACCCTG	1980
60	GGCTACAGAA ACCACAGTCT TCCAGCAAT TATTACAATT CTTGAATTCC TTGGGGATTT	2040

TTTACTGCCC TTTCAAAGCA CTTAAGTGT AGATCTAACG TGTTCCAGTG TCTGTCTGAG 2100
 GTGACTTAAA AAATCAGAAC AAAACTTCTA TTATCCAGAG TCATGGGAGA GTACACCCTT 2160
 5 TCCAGGAATA ATGTTTGGG AAACACTGAA ATGAAATCTT CCCAGTATTA TAAATTGTGT 2220
 ATTTAAAAAA AAGAACTTT TCTGAATGCC TACTGGCGGT GTATACCAGG CAGTGTGCCA 2280
 10 GTTTAAAAAG ATGAAAAGA ATAAAACTT TTGAGGAAMA AAAAAAAAAA AAAAACTCGA 2340

15 (2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 601 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

25 AGTAGGGGAG ACTGAGACTG ACCGGTAGCC AGGCAGGCGG ACGACGCACG CCCGGACAGA 60
 CTGAGCAGGC GCCGGAGAAC CACTCACAGG TTCCCCCGC CTTTCCCTTT GAAANCTAGG 120
 CTTTTCCTTT TCCCGTGGCG CCCGAGAGAG AATGCTGGAC TCTGCCGACT TCAGCGCAAC 180
 30 TAANGATTTT TCAAGCTAGG GGACAAACGA TCAGCCCAAT CCTGAGAAGG GGGGAACCAA 240
 GCACCCCGTC CCCATCCCCC TCCCCTCCCC CGACTAACT CGGGCGCCAA ACCCAGCCCT 300
 35 TCTCTAACCA CCCTACTTCC TCCTCTCCTT TCTAGCATGG TGGCTGTATG GACAGTCTGA 360
 CAGAACAGAG ACTGACATCT CCCAATCTGC CGGCCCCCA CCTGGAACAC TACAGTGTTT 420
 TGCATTGCAC CATGACCCTG GATGTGCAAA CTGTAGTCGT TTTTGCCGTG ATTGTAGTCC 480
 40 TCCTGCTTGT CAATGTCATA CTCATGTTT TCCTGGGAAC GCGCTGAATG GAGTCCAGNC 540
 ACCTGAGCTG TCGCGAATC TCGCTTTGAT TTCATCCCGA GAGCCACCGA GAAGAAAAAA 600
 45 A 601

50 (2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

60 CTCGTGCCGA ATTCCGCACG AGAGATGGTA CTTTAAAGAG GTAATTAGGT TGCTAAGATG 60

5 GATTAACATC TTTCTCTTGA CACTGAGACT GGGTTCTCCT GGAATGGTT AGTTCCCAAG 120
 AGAGTGAGTT GTTATAAAAC AATGCTGCCT CTCTATTTT GCGCTTTTGT TTTGCACAAA 180
 CTCGGTCCCC TTCTGTTTCT CTACGATGTT TTGATGCRGC ATGAGGCAGT CATGAGAACC 240
 CACCAGATAC AGCTGCCTGA TCCTGAATTT CCCAGCCAAC AGAACCAAGT GCTAAATAAA 300
 10 ACTCTTTTTA ATAAGTTAAA AAAAAAAAAA AAAAAAAAAA AANAAANANA AAAAAAAAAA 359

15 (2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

25 GGCACGAGCT GCTGAGGCGT GAGAATGGCG TCCCGCGGCC GCGTCCGGA GCATGGCGGA 60
 CCCCCAGAGC TGTTTTATGA CGAGACAGAA GCCCGGAAAT ACGTTCGCAA CTCACGGATG 120
 ATTGATATCC AGACCAGGAT GGCTGGGCGA GCATTGGAGC TTCTTTATCT GCCAGAGAAT 180
 30 AAGCCCTGTT ACCTGCTGGA TATTGGCTGT GGCACCTGGC TGAGTGGAAG TTATCTGTCA 240
 GATGAAGGGC ACTATTGGGT GGGCCTGGAT ATCAGCCCTG CCATGCTGGA TGAGGCTGTG 300
 35 GACCGAGAGA TAGAGGGAGA CCTGCTGCTG GGGGATATGG GCCAGGGCAT CCCATTCAAG 360
 CCAGGCACAT TTGATGGTTG CATCAGCATT TCTGCTGTGC AGTGGCTCTG TAATGCTAAC 420
 AAGAAGTCTG AAAACCCTGC CAAGCGCCTG TACTGCTTTT TTGCTTCTCT TTTTCTGTGT 480
 40 CTCGTCCGGG GATCCCGAGC TGTCCTGCAG CTGTACCCTG AGAACTCAGA GCAGTTGGAG 540
 CTGATCACAA CCCAGGCCAC AAAGGCAGGC TTCTCCGGTG GCATGGTGGT AGACTACCCT 600
 45 AACAGTGCCA AAGCAAAGAA ATTCTACCTC TGCTTGTTTT CTGGGCCTTC GACCTTTATA 660
 CCAGAGGGGC TGAGTGAAAA TCAGGATGAA GTTGAACCCA GGGAGTCTGT GTTCACCAAT 720
 GAGAGGTTCC CATTAAGGAT GTCGAGGCGG GGAATGGTGA GGAAGAGTCG GGCATGGGTG 780
 50 CTGGAGAAGA AGGAGCGGCA CAGGCGCCAG GGCAGGGAAG TCAGACCTGA CACCCAGTAC 840
 ACCGCGCCGA AGCGCAAGCC CCGCTTCTAA GTCACCACGC GGTTCCTGGAA AGGCACTTGC 900
 55 CTCTGCACTT TTCTATATTG TTCAGCTGAC AAAGTAGTAT TTTAGAAAAG TTCTAAAGTT 960
 ATAAAAATGT TTTCTGCAGT AAAAAAAAAA TTCTCTGGGC CGGGCGTGGT GGCTCACACC 1020
 60 TGTAATCCCA GCACCTTGGG AGGCTGAGGT GGGAGGATCA TTTGAGGCCA GGAGTTTGAG 1080

ACCTGCCTGG GCAACATAAT GAAACTTCCT TTCCAGGGAG AAAAAAAAAA AAAAAAAAAA 1140

A 1141

5

(2) INFORMATION FOR SEQ ID NO: 55:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1560 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TCCTTCTCTG GGGCGGTCGC GTTGGCAGCG GATGCGGGAA GCCGGACTCT GGGCCTCATG 60

20 TACTACAAGT TTAGTGGCTT CACGCAGAAG TTGGCAGGAG CATGGGCTTC GGAGGCCTAT 120

AGCCCGCAGA TTNAAGCCT GTGGTTTCCA CAGAAGCACC ACCTATCATA TTTGCCACAC 180

25 CAACTAAACT GACCTCCGAT TCCACAGTGT ATGATTATGC TGGGAAAAAC AAAGTTCCAG 240

AGCTACAAAA GTTTTTCAG AAAGCTGATG GTGTGCCCCG CTACCTGAAA CGAGGCCTGC 300

CTGACCAAAT GCTTTACCGG ACCACCATGG CGCTGACTGT GGGAGGGACC ATCTACTGCC 360

30 TGATCGCCCT CTACATGGCT TCGCAGCCCA AAAACAAATG AGTTAGGCTG CAGAGGACTG 420

GTMTGTTTTT TGGCATAAAC CCTTTGAAGT TCCTTTTTC TGTATAAATT AAAATTTTTT 480

35 TTTTACTTGT GATGGCTTAA CATTTTTCGA AGAAAAATAG GAAGATATGA AGATGATGTT 540

TTGGTTTGTT TATGAAATGC ATATGGCTTG TCAGAGCTCA TTCGACAGTT AAAGCCATTG 600

TTTAAAGAAA CGGTGCTTTG CTCTGTGTTT GTGCTCCTGA TTTCCCTGGA GGTCTGGAT 660

40 GAAGGCTGAA CACAGGCTTG TTAATGTCAG TCTGTGCTGA GGACCTCAGG GACTTGAGGT 720

TGCATTTTGT AGCATGGGGT GCAGGAGCCT TTCTGGATTT GGATGTGGCT ATGGAAGAA 780

45 CACAGAAGCC AAGGTCATGT GCATGAAATG AGGAGTTTGA GTTAGTCACC TCGGGATTT 840

TTCCATTTT GCAGTAAAT GTTAAATTAA TGTAGCCTGC CTCTATTGT TGGGCAGGTA 900

ATTTCAAAGG GTTATTGCTC TCATCTCCTA TCTTTAGTGA AATCTTATGT GTAATTGTGT 960

50 GTATTTATTC CACCGTGGGA ACAGAGAATA CCTGTTTAGT GTTGCACTTT AGACTGGTGT 1020

CTGTTTGTGT AATGCAGCTG TGCCACAAAT TCTCCTTTAT CTTTTAAAAA TGTATAGCT 1080

55 TTAAATTTTG ATTTATTTTG ACTGTGGAAT AAATACATGA ATGAAAAATT TTAAGTTTGA 1140

AGTTCTTTGA ATGACCTTTC AGAGTAATTT CAGAACACCA GCAGCATCTT AAACCTGAGT 1200

CTAATTTCTT TCTTGTTAAT TAGGCACCAG ATAATCTTTA TAAATGGTC TTTAAAGCTA 1260

60 GTAATAGGAG CTTAATGGCA ATKGATGATT ACCACAKGGT TTTTATAAAA AACCTGCCTG 1320

5 CCCCTWAGTG AAAGGTACCT GTAACYCACA GTYCATTTAG AACTAATTT CCTYTGCYGT 1380
 CATGATTGGK AGACTTCACT TACCCTATAT TAATTTTGAA AAAAGGTGGA ATTTTATTAT 1440
 ATATGAAGGA ATAGTTTGTA TCTTACCATA GCACAGAACA GTGACCTCTT GCTCAGGATA 1500
 AGATGTGGTG ATTTGAAAAT ACTCATAGTA GCCTTGCACT GATACCTCTC TCNCTCTCTC 1560
 10

(2) INFORMATION FOR SEQ ID NO: 56:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1507 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 20
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

GGAACGCAGA GCGGAGCGTG GAGAGCGGAG CGAAGCTGGA TAACAGGGGA CCGATGATGT 60
 25 GCGGACCATC AGTTCTGCTG CTCTCTGTTG TACTGAGGCA CGGGGCCAG GGAAGCCAT 120
 CCCCAGACGC AGGCCCTCAT GGCCAGGGGA GGTGACCA GCGGGCCCC CTGAGCGACG 180
 CTCCCCATGA TGACGCCAC GGAAGCTTCC AGTACGACCA TGAGGCTTTC CTGGGACGGG 240
 30 AAGTGGCCAA GGAATTCGAC CAACTCACC CAGAGGAAAG CCAGGCCCGT CTGGGGCGGA 300
 TCGTGACCG CATGGACCGC GCGGGGACG GCGACGCTG GGTGTCGCTG GCCGAGCTTC 360
 35 GCGCGTGGAT CGCGCACACG CAGCAGCGGC ACATACGGA CTCGGTGAGC GCGCCTGGG 420
 ACACGTACGA CACGACCGC GACGGGCGTG TGGGTGGA GGAGCTGCGC AACGCCACCT 480
 ATGGCCACTA CGCGCCCGGT GAAGAATTT ATGACGTGGA GGATGCAGAG ACCTACAAAA 540
 40 AGATGCTGGC TCGGGACGAG CGGCGTTTC GGTGGCCGA CCAGGATGGG GACTCGATGG 600
 CCACTCGAGA GGAGCTGACA GCCTTCCTGC ACCCCGAGGA GTTCCCTCAC ATGCGGGACA 660
 45 TCGTGATTGC TGAAACCTG GAGGACCTGG ACAGAAACA AGATGGCTAT GTCCAGGTGG 720
 AGGAGTACAT CGCGGATCTG TACTCAGCCG AGCCTGGGGA GGAGGAGCCG GCGTGGGTGC 780
 AGACGGAGAG GCAGCAGTTC CGGACTTCC GGGATCTGAA CAAGGATGGG CACCTGGATG 840
 50 GGAGTGAGGT GGGCCACTGG GTGCTGCCCC CTGCCAGGA CCAGCCCCTG GTGGAAGCCA 900
 ACCACCTGCT GCACGARAGC GACACGGACA AGGAYGGCG GCTGAGCAA GCGSAAATCC 960
 55 TGGGTAATTG GAACATGTTT GTGGGCAGTC AGGCCACCA CTATGGYGAG GACCTGACCC 1020
 GGCACCACGA TGAGCTGTGA GCMCCGNGCA CCTGCCACAG CCTCAGAGGC CCGCACAATG 1080
 ACCGGAGGAG GGGCCGCTGT GGTCTGGCCC CCTCCCTGTC CAGGCCCCGC AGGAGGCAGA 1140
 60

TGCAGTCCCA GGCATCCTCC TKCCCCCTGGG CTCTCAGGGA CCCCCTGGGT CGGCTTCTGT 1200
 CCCTGTCACA CCCCCAACCC CAGGGAGGGG CTGTCATAGT CCCAGAGGAT AAGCAATACC 1260
 5 TATTTCTGAC TGAGTCTCCC AGCCCAGACC CAGGGACCCT NGGCCCAAG CTCAGCTCTA 1320
 AGAACC GCCC CAACCCCTCC AGCTCCAAAT CTGAGCCTCC ACCACATAGA CTGAAACTCC 1380
 10 CCTGGCCCCA GCCCTCTCCT GCCTGGCCTG GCCTGGGACA CCTCCTCTCT GCCAGGAGGC 1440
 AATAAAAGCC AGCGCCGGGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1500
 AAAAAAN 1507

15

(2) INFORMATION FOR SEQ ID NO: 57:

20

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

GAATTCGGCA CGAGCAGTGT CCAACACTGT AGCTGGTGCC TGCCAGGTC CCAGTGGCTG 60
 30 GGGTCACCAG GTCTGAAGAG AGATGTGCTG GCTGCGGGCA TGGGSCCAGA TCYTCTGACC 120
 AGTTTTCYTC TCCYTCTTTC TCATCCAATT GCTTATCAGC TTCTCAGAGA ATGGTTTTAT 180
 35 CCACAGCCCC AGGAACAATC AGAAACCAAG AGATGGGAAT RAAGAGGAAT GTGCTGTAAA 240
 GAAGAGTTGT CAATTGTGCA CAGAAGATAA GAAATATATG ATGAATAGAT AATTGAAAAG 300
 AGATCCTCCA GAAAGAGCAG AAGGAAGTTT CTTCAATGGC TTCCTTCAGG ATTTTAATCA 360
 40 TCCTTACAGC CTCTTTGAGA ATGATTGAAC TTCCAAATTC CCTGAAGTTA AAATTTTAAA 420
 TTCTATTAAA CATTTTTCG AGTAAAAAAA 450

45

(2) INFORMATION FOR SEQ ID NO: 58:

50

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1147 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GGCACGAGAC CCATTGAGCA GAAGGAGGCC AGGTGGGAAA GCTCCTGGGA AGAGCAGCCA 60
 60 GACTGGACAC TGGGCTGCTT GAGTCCTGAG TCACAATTCA GAATTCCTGG GCTCCCTGGG 120

	TGCATTCTAT CATTCCAGTT GAAAGTTTGC TTCCTTCCAG TCATGTGGCT CTCATTCTTA	180
	CTCTCCTTGG CTCTCATMTC AGATGCCATG GTCATGGATG AAAAGGTCAA GAGAAGCTTT	240
5	GTGCTGGACA CGGCTTCTGC CATCTGCAAC TACAATGCCC ACTACAAGAA TCACCCCAAA	300
	TACTGGTGCC GAGGCTATTT CCGTGACTAC TGCAACATCA TCGCCTTCTC CCCTAACAGC	360
	ACCAATCATG TGGCCCTGAA GGACACAGGG AACCAGCTCA TTGTCACTAT GTCCTGCCTG	420
10	AACAAAGAAG ACACGGGCTG GTACTGGTGT GGCATCCAGC GGGACTTTGC CAGGGATGAC	480
	ATGGATTTTA CAGAGCTGAT TGTAAGTAC GACAAAGGAA CCTGGCCAAT GACTTTGGTC	540
15	TGGGAAAGAC TATCAGGCAC AAAACCAGAA GCTGCAAGGC TCCCAAAGTT GTCCGCAAGG	600
	CTGACCGCTC CAGGACGTCC ATTCTCATCA TTTGCATACT GATCACGGGT TTGGGAATCA	660
	TCTCTGTAAT CAGTCATTTG ACCAAAAGGA GGAGAAGTCA AAGGAATAGA AGGGTAGGCA	720
20	ACACTTTGAA GCCCTTCTCG CGTGTCTGA CTCCAAAGGA AATGGCTCCT ACTGAACAGA	780
	TGTGACTGAA GATTTTMTTA ATTTAGTTC TAAAGTGATG CTACAACAGA ATAATCACCA	840
25	TGACAACTGG CCCACACCT CAGAGACTGA TTCTGATCTC CCAGGAATTC TGAAGTCCC	900
	TCTATCCTTG ACAACAATCA TTTGCAGCCA GGTAGCAACG GCAGTAGTCA GAGGAGCTAT	960
	GATAGACCAC ACCCAAGCAA GGCTGCCCTC AAATAACATC TCAAGATCTT AGTTCTTATG	1020
30	CATTCCATCA GTCAGAAGTG AAGAAGAGGT GGAGAATCTG GATTGGGGAC CAGGAAATCA	1080
	CTTGTATTTT GTTAGCCAAT AAATTCCTAG CCAGTGTGA ATGAAAAAA AAAAAAAAAA	1140
35	AAAAAAA	1147

40 (2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 777 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

50	GGCAGAGGCT CCTCAGAAGG GCGTGGGCTC TCCAGTCTTC CACAGTCCCC ACCATGCCCT	60
	GTTGCCTTAC CGCTGACGTA GCTCACCCAT CTTTACTTG CCTGGCTAAG ATGCATGGCA	120
	TYWCATTTCC TCCTTGTGTC ACTGCAGTCA GTCCCTCACT GCCCCATCT CCTGGAAGAG	180
55	GAGCATAAGC TTTGCAAGGT CAGCCACTTC TCTGGGTCA CACTAGTTAC ATCAAGACAG	240
	GACTCCAGCT CATATGTGCC AGTGCAGACA CTCTCATCC ACCTGGGGCC CTGGGCTTGG	300
60	GACCTGGYTC CTTGCACAGC AGARGACCCG GAGGCTGAGA GGAGCTTGCG GTTGTGTCAT	360

5 AGTCACCTGG CCAGARGGAA CGTGAGCCCC TCCCAAGCTG CAGARGGARG GARCARGCGT 420
 GGCTGTCAGC ACCGAGGTAG CAGAGAATTA ACATTCTTGT CAGCAGAGAA TGAAGCAGGA 480
 ATATAATTAA AACTTTGCCC TTGGAATAGC TGATTCATTT GAATTTTATT CCACACGTTT 540
 GAAAGAGGAA AGAAAATGTG AAGACTTGCA GCCTGGTTCT CGCCTGGCCT GGGCTGGCCC 600
 10 AGCTGTCAGG CCCGGTTCCT TTCTGAGCAT TCAGTCCACT GATGTTGACT GAGGGCCAGG 660
 AGAGACCTC AGCAGGGTAT TACCATATCA GCCTCCTATC GCTGCTGGGA GAAATTACCA 720
 15 TGAATTCAGT GGCTTAAAAC AACACACGAG CCTCTCTGAG CCTACCCTGG CTCAGGA 777

20 (2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1191 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

30 AAGANTGATT TTCCTTACTC TCCAAAGCGT CAGCATTTTG AAGTTTCTTT TATGAAAGTG 60
 GGGGCAAGAA TCAGGGTGAA AATGAGTGTA AACAAAGCCC ATCCTGTGGT CAGCACCCAC 120
 TGGAGGTGGC CAGCAGAGTG GCCTCAGATG TTCCTGCACC TGGCCCAGGA GCCCAGGACA 180
 35 GAGGTCAAAT CTAGGCCCTT TGGTCTGGCT GGATTCATCA GGCAAGATTC GAAAACAAGA 240
 AAACCTCTAG AACAAAGAAC AATCATGTCT GCAGCAGATA CGGCACTGTG GCCCTATGGC 300
 40 CATGGCAATC GTGAGCACCA AGAGAATGAG TTACAGAAAT ATCTCCAATA CAAAGACATG 360
 CATCTCCTGG ACAGTGGACA GTCGCTGGGA CACACACACA CACTTCAAGG CTCACACAAC 420
 CTAACAGCCT TAAATATCTG AAGAAACAGA ATCACGACAT TAAGTCAGCA GAGGGAGAGG 480
 45 TAGGCTGAAG CAGCAGGAGG CCAATTTTAT ATCCACAGA TTTTMTTAAA AATGACTCCC 540
 CAGCAAGGGG TGGGGAGAAA GCCACTGATT TAGGAGAGTT CTTGGCTCAG CCAACCACTG 600
 50 CGTTTATCTA CACGTTTAC AAAGGCACRG AAGTAGAGAG GGGCTGCACT CACGACCCTC 660
 CCCAGGGCCC GCACAGCCAG ACACGGTGGG TTCTTCCTTT TTCCCTTCTG GCCTTGGTGG 720
 AATTCCTACC ACGGTGGCCT CTGCCTTTGG GACAATGCCT TCATGCTCAT CCCCAGGTCA 780
 55 AGGATGGAGT CTGTTACCAT TTTCCAGGGG AAATTCCAAG GACCAGCCCC GCCTCATTAC 840
 GTTCACCCCA CAGGAAGGTG ATCTGGAAAG CCTGTAAACA CGTACTCTGG GTGGCTGAGT 900
 60 GGTGTCACCA AGCTGCTTTT GTGCAGGGCT GAAGCACAGA CAAGAGGGCA GGCAGCTGCC 960

GGAGGCCTGA AGTGGGGAGA GATCCCCGCA GGCCTGCAGG AGCCAGGGAG AACCTCCAAC 1020
 TGGATCTAAA CTGTGGGACA GCCCAGGCGT GCCCCTCTTC ACATGGCTCC CAGGCTCCCT 1080
 5 CAAAGCCCTT CCCAGGCCCT GCAGGAAGAG AGGGAGGGTG AGGAGAGGCA GGGAGGGCAG 1140
 AGGTCGCCTG AAAGCCTGGG CTCCGAATC CCTCAGCAGA GCTTTAAAGT G 1191

10

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 1580 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CCCCGCCCC CGCCACGAA GGAAGTGGCT GCTGCTCCGG CGCGGACCCA GAGCCGGTTC 60
 GGCGCGTCGA CTGCCCAGAG TCCGCGGCCG GGCGCGGGAG GAGCCAAGCC GCCATGGCCT 120
 25 ACCACAGCTT CCTGGTGGAG CCCATCAGCT GCCACGCCTG GAACAAGGAC CGCACCAGA 180
 TTGCCATCTG CCCCAACAAC CATGAGGTGC ATATCTATGA AAAGAGCGGT GCCAAATGGA 240
 30 CCAAGGTGCA CGAGCTCAAG GAGCACAACG GGCAGGTGAC AGGCATCGAC TGGGCCCCCG 300
 AGAGTAACCG TATTGTGACC TCGGCACAG ACCGCAACGC CTACGTGTGG ACGCTGAAGG 360
 GCCGCACATG GAAGCCCACG CTGGTCATCC TCGGATCAA CCGGGCTGCC CGCTGCGTGC 420
 35 GCTGGGCCCC CAACGAGAAC AAGTTTGCTG TGGGCAGCGG CTCTCGTGTG ATCTCCATCT 480
 GTTATTTCGA GCAGGAGAAT GACTGGTGGG TTTGCAAGCA CATCAAGAAG CCCATCCGCT 540
 40 CCACCGTCCT CAGCCTGGAC TGGCACCCCA ACAATGTGCT GCTGGCTGCC GGCTCCTGTG 600
 ACTTCAAGTG TCGATCTTT TCAGCCTACA TCAAGAGGT GGAGGAACGG CCGGCACCCA 660
 CCCCCTGGGG CTCCAAGATG CCCTTTGGGG AACTGATGTT CGAATCCAGC AGTAGCTGCG 720
 45 GCTGGGTACA TGGCGTCTGT TTCTCAGCCA GCGGGAGCCG CGTGGCCTGG GTAAGCCACG 780
 ACAGCACCGT CTGCCTGGCT GATGCCGACA AGAAGATGGC CGTCGCGACT CTGGCCTCTG 840
 50 AAACACTACC ACTGCTGGCG CTGACCTTCA TCACAGACAA CAGCCTGGTG GCAGCGGGCC 900
 ACGACTGCTT CCCGTGCTG TTCACCTATG ACGCCGCCGC GGGGATGCTG AGCTTCGGCG 960
 GGCGGCTGGA CGTTCCTAAG CAGAGCTCGC AGCGTGGCTT GACGGCCCCG GAGCGCTTCC 1020
 55 AGAACCTGGA CAAGAAGGCG AGCTCCGAGG GTGGCACGGC TCGGGCGCGG GGCCTAGACT 1080
 CGCTGCACAA GAACAGCGTC AGCCAGATCT CGGTGCTCAG CGGCGGCAAG GCCAAGTGCT 1140
 60 CGCAGTTCTG CACCACTGGC ATGGATGGCG GCATGAGTAT CTGGGATGTG AAGAGCTTGG 1200

5 AGTCAGCCTT GAAGGACCTC AAGATCAAAT GACCTGTGAG GAATATGTTG CCTTCATCCT 1260
 AGCTGCTGGG GAAGCGGGGA GAGGGGTCAG GGAGGCTAAT GGTTCCTTTG CTGAATGTTT 1320
 CTGGGGTACC AATACGAGTT CCCATAGGGG CTGCTCCCTC AAAAAGGGAG GGGACAGATG 1380
 GGGAGCTTTT CTTACCTATT CAAGGAATAC GTGCCTTTTT CTTAAATGCT TTCATTTATT 1440
 10 GAAAAA AAAAATGCCC CCAAAGCACT ATGCTGGTCA TGAAGTCTT CAAAATGTGG 1500
 AGGTAATAAA ATGCAACTGT GTAAAAA AAAAATAA AAATGACCCT CGCGATCTAG 1560
 15 AACTAGNCGG ACGCNTGGGT 1580

20 (2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1117 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

30 GGCACGAGGC GCGATGCAGC ACAGGCTAGA GGCTGCGCAA SGCGGGGGCC CGCCCCGGG 60
 ACCCTCCGGG CCGGGCGGTT TGGCCCCTTA GCGCCCGGGC GTCGGGGCGG TAAAAGGCCG 120
 GCAGAAGGGA GGCACCTGAG AAATGTCTTT CCTCCAGGAC CCAAGTTTCT TCACCATGGG 180
 35 GATGTGGTCC ATTGGTGCAG GAGCCCTGGG GGCTGCTGCC TTGGCATTGC TGCTTGCCAA 240
 CACAGACGTG TTTCTGTCCA AGCCCCAGAA AGCGGCCCTG GAGTACCTGG AGGATATAGA 300
 40 CCTGAAAACA CTGGAGAAGG AACCAAGGAC TTTCAAAGCA AAGGAGCTAT GGGAAAAA 360
 TGGAGCTGTG ATTATGGCCG TGCGGAGGCC AGGCTGTTTC CTCTGTGAG AGGAAGCTGC 420
 GGATCTGTCC TCCCTGAAAA GCATGTTGGA CCAGCTGGGC GTCCCCCTCT ATGCAGTGGT 480
 45 AAAGGAGCAC ATCAGGACTG AAGTGAAGGA TTTCCAGCCT TATTTCAAAG GAGAAATCTT 540
 CCTGGATGAA AAGAAAAAGT TCTATGGTCC ACAAAGGCGG AAGATGATGT TTATGGGATT 600
 50 TATCCGTCTG GGAGTGTGGT ACAACTTCTT CCGAGCCTGG AACGGAGGCT TCTCTGGAAA 660
 CCTGGAAGGA GAAGGCTTCA TCCTTGGGGG AGTTTTCGTG GTGGGATCAG GAAAGCAGGG 720
 CATTCCTCTT GAGCACCGAG AAAAGAATT TGGAGACAAA GTAAACCTAC TTTCTGTCTT 780
 55 GGAAGCTGCT AAGATGATCA AACCACAGAC TTTGGCCTCA GAGAAAAAAT GATTGTGTGA 840
 AACTGCCCAG CTCAGGGATA ACCAGGGACA TTCACCTGTG TTCATGGGAT GTATTGTTTC 900
 60 CACTCGTGTC CCTAAGGAGT GAGAAACCCA TTTATACTCT ACTCTCAGTA TGGATTATTA 960

ATGTATTTTA ATATTCTGTT TAGGCCCACT AAGGCAAAAT AGCCCCAAAA CAAGACTGAC 1020
 AAAAATCTGA AAAACTAATG AGGATTATTA AGCTAAAACC TGGGAAATAG GAGGCTTWAA 1080
 5 ATGACTGCCM GCTGGTGCRT GCTCACACTT GGCCAC 1117

10 (2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

20 CCCACGCGTG CKGGCGCCTG GCAGCCACCG CCTGGGAGGT TACTGTAAGG CCCGCAGCTC 60
 CCGCCAGCTC CCGCGGACTS CTGCCGCCTC CTTACCATGA AGCCAGTAAG TCGTCGCACG 120
 CTGGACTGGA TTTATTCAGT GTTGCTGCTT GCCATCGTTT TAATCTCCTG GGGCTGCATC 180
 25 ATCTATGCTT CGATGGTGTC TGCAAGACGA CAGCTAAGGA AGAAATACCC AGACAAAATC 240
 TTTGGGACGA ATGAAAATTT GTAACCTCTC TGGATTAAAT TATCTGAAAA TACAGTTCTT 300
 30 TCCCTCATGC TTATGTAGAT ATAAAAATAA AATTCATAAT GCAAAAAAAA AAAAAAAAAA 360
 G 361

35

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1668 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GGCACGAGGT CTGCCAAGCT ATAGACCATG GCTGTGAACA CATTTGTGTG AACAGTGACG 60
 ACTCATACAC GTGCGAGTGC TTGGAGGGAT TCCGGCTCGC TGAGGATGGG AAACGCTGCC 120
 50 GAAGAAGGAT GTCTGCAAAT CAACCCACCA TGGCTGCGAA CACATTTGTG TTAATAATGG 180
 GAATTCCTAC ATCTGCAAAT GCTCAKAGG ATTTGTTCTA GCTGAGGACG GAAGACGGTG 240
 55 CAAGAAATGC ACTGAAGGCC CAATTGACCT GGTCTTTGTG ATCGATGGAT CCAAGAGTCT 300
 TGGAGAAGAG AATTTTGAGG TCGTGAAGCA GTTTGTCACT GGAATTATAG ATTCCTTGAC 360
 AATTTCCCCC AAAGCCGCTC GAGTGGGGCT GCTCCAGTAT TCCACACAGG TCCACACAGA 420
 60

	GTTCACTCTG AGAAACTTCA ACTCAGCCAA AGACATGAAA AAAGCCGTGG CCCACATGAA	480
	ATACATGGGA AAGGGCTCTA TGA CTGGGCT GGGCC TGAAA CACATGTTTG AGAGAAGTTT	540
5	TACCCAAGGA GAAGGGGCCA GGCCCTTTCC ACAAGGGTGC CCAGAGCAGC CATTTGTGTTT	600
	ACCGACGGAC GGGCTCAGGA TGACGTCTCC GAGTGGGCCA GTAAAGCCAA GGCCAATGGT	660
10	ATCACTATGT ATGCTGTTGG GGTAGGAAAA GCCATGAGG AGGAACTACA AGAGATTGCC	720
	TCTGAGCCCA CAAACAAGCA TCTCTTCTAT GCCGAAGACT TCAGCACAAT GGATGAGATA	780
	AGTGAAAAAC TCAAGAAAGG CATCTGTGAA GCTCTAGAAG ACTCCGATGG AAGACAGGAC	840
15	TCTCCAGCAG GGGAACTGCC AAAAACGGTC CAACAGCCAA CAGTGCAACA CAGATATCTG	900
	TTTGAAGAAG ACAATCTTTT ACGGTCTACA CAAAAGCTTT CCCATTCAAC AAAACCTTCA	960
20	GGAAGCCCTT TGGAAGAAAA ACACGATCAA TGCAAATGTG AAAACCTTAT AATGTTCCAG	1020
	AACCTTGCAA ACGAAGAAGT AAGAAAATTA ACACAGCGCT TAGAAGAAAT GACACAGAGA	1080
	ATGGAAGCCC TGGAATAATCG CCTGAGATAC AGATGAAGAT TAGAAATCGC GACACATTTG	1140
25	TAGTCATTGT ATCACGGATT ACAATGAACG CAGTGCAGAG CCCCAAAGCT CAGGCTATTG	1200
	TTAAATCAAT AATGTTGTGA AGTAAACAA TCAGTACTGA GAAACCTGGT TTGCCACAGA	1260
30	ACAAAGACAA GAAGTATACA CTAAC TTGTA TAAATTTATC TAGGAAAAAA ATCCTTCAGA	1320
	ATTCTAAGAT GAATTTACCA GGTGAGAATG AATAAGCTAT GCAAGGTATT TTGTAATATA	1380
	CTGTGGACAC AACTTGCTTC TGCCTCATCC TGCCTTAGTG TGCAATCTCA TTTGACTATA	1440
35	CGATAAAGTT TGCACAGTCT TACTTCTGTA GAACACTGGC CATAGGAAAT GCTGTTTTTT	1500
	TGTAYTGGAC TTTACCTTGA TATATGTATA TGGATGTATG CATAAAATCA TAGGACATAT	1560
40	GTACTTGTGG AACAAGTTGG ATTTTTTATA CAATATTAAA ATTCACCACT TCAGAGRAAA	1620
	AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAANAAAA	1668

45

(2) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

55	GGGTCGACCC ACGCGTCCGC CCACGCGTCC GGATGGCTGC GCTGTTGCTG AGACACGTTG	60
	GTCGTCAATG CCTCCGAGCC CACTTTAGCC CTCAGCTCTG TATCAGAAAT GCTGTTCTTT	120
60	TGGGAACCAC GGCCAAAGAA GAGATGGAGC GGTCTCTGGAA TAAGAATATA GGTTCAAACC	180

5 GTCTCTGTCT TCCCCACATT ACTATCTACA GTTGGTCTCT TCCCATGGCG ATGTCCATCT 240
 GCCACCGTGG CACTGGTATT GCTTTGAGTG CAGGGGTCTC TCTTTTGGC ATGTGGGCCC 300
 TGTACTCCC TGGGAACCTT GAGTCTTATT TGGAACTTGT GAAGTCCCTG TGTCTGGGGC 360
 CAGCACTGAT CCACACAGCT AAGTTTGAC TTGTCTTCCC TCTCATGTAT CATACCTGGA 420
 10 ATGGGATCCG ACACTTGATG TGGGACCTAG GAAAAGGCCT GAAGATTCCC CAGCTATACC 480
 AGTCTGGAGT GGTGTCTCTG GTTCTTACTG TGTGTCTCTC TATGGGGCTG GCAGCCATGT 540
 GAAGAAAGGA GGCTCCCAGC ATCATCTTCC TACACATTAT TACATTCACC CATCTTTCTG 600
 15 TTTGTCTATC TTATCTCCAG CCTGGGAAAA GTTCTCTCTTA TTTGTTTAGA TCCTTTTGTA 660
 TTTTCAGATC TCCTTGGAGC AGTAGAGTAC CTGGTAGACC ATAATAGTGG AAAAGGGTCT 720
 20 AGTTTTCCCC TTGTTTCTAA AGATGAGGTG GCTGCAAAAA CTCCCCTTTT TTGCCCACAG 780
 CTGCGCTACT CTCGGCTAG AAGCAGTTAT TCTCTCTCCA TATGGGGCTT TGATTTGTGC 840
 TGAGGGTCAG CTTTTGGCTC CTCTTCTCTG AGACAGTGA AACAATGCCA GCTCTGTGGC 900
 25 TTCTGCCCTG GGGATGGGCC GGGTTGGGG GTGGTTGGT GAGGCTTTGG GTGCCACTGC 960
 CTGTGGGTTG CTGGCTTAAA GGACAATTCT CTTCAATTGGT GAGAGCCCAG GCCATTAACA 1020
 30 CCTACACAGT GTTATTGAAA GAAGAGAGGT GGGGGTGGAG GGGAAATTAGT CTGTCCCAGC 1080
 TAGAGGGAGA TAAAGAGGC TAGTTAGTTC TTGGAGCAGC TGCTTTTGAG GAGAAAATAT 1140
 ATAGCTTTGG ACACGAGGAA GATCTAGAAA ATTATCATTG AACATATTAA TGGTTATTTT 1200
 35 TTTTCTTTGG ATTTCCAGAA AAGCCTCTTA ATTTTATGCT TTCTCATCGA AGTAATGTAC 1260
 CCTTTTCTTC TGAAACTGAA TTAAATACTC ATTTTATCTT TGAAAAAAA AAAAAAACC 1320
 40 TNGGGGGGGG CCCCAGACCC NAATTGGCCC TAT 1353

45 (2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1011 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

55 CGGAAGAAAG CAGCCATCCA GACATTTTCTG AACACGTACC AGGTGTTAGC TGTGACCTTC 60
 AATGACACAA GTGATCAGAT TATTTCTGGT GGAATAGACA ATGATATCAA GGTCTGGGAC 120
 TCGCCAGAA CAAGCTAACC TACACCATGA GAGGCCATGC AGATTCAGTG ACTGGCCTGA 180
 60

	GTTTAAGTTC TGAAGGCTCT TATCTTTTGT CCAATGCAAT GGACAATACA GTTCGTGTCT	240
	GGGATGTCCG GCCATTTGCC CCCAAAGAGA GATGTGTAAA GATATTTCAA GGAAATGTGC	300
5	ACAACPTTGA AAAGAACCTT CTGAGATGTT CTTGGTCACC TGATGGAAGC AAAATAGCAG	360
	CTGGCTCAGC CGACAGGTTT GTTTATGTGT GGGATACCAC AAGCAGGAGA ATATTGTATA	420
10	AGCTGCCCCG CCATGCTGGC TCCATCAATG AAGTGGCTTT CCACCCTGAT GAGCCCATCA	480
	TTATCTCAGC ATCGAGTGAC AAGAGACTGT ATATGGGAGA GATTCACTGA AGATATGGAC	540
	TGGAAGACTC CAAGGCCGCT TGTCTTTGAG ACCTCAGACT GCATAAGTGA TGCCAAATGT	600
15	TGGATGTCCA GGYTAGCACC CTCCTTCAG ATGACCATTG CTAGCAAGAA ACAGGAGGCC	660
	GTGGCCATAT TCCAAAACC ACTTCTGTCC CATTTACCA GGATGACTAA GGCAAGCTCC	720
20	CTGTGGCCTC TAAAAACCAC CTGCCAGATT TCAGGGACTG TTTTTTTTTT TCTTTTCTT	780
	TTTTCTGTGT TTCTAATGCA GGCCCAATGT GACAAATTG TTGGTTGGGA TTTTTTTTTT	840
	TTTTGTAACT TGGCTGTAT GATATTTTCT TTCTGTATTT CTCTATATCA TTTGTATTA	900
25	AAAGCCAAAT AGATGCCTTT TTACAAGARM AAAAAAAAAA AAAAAAAAAA NNAAAAAAAA	960
	CTGGGAGGGG GGGCCCGGTA CCCAAATCGC CGGATATGAT CGTAAACAAT C	1011

30

(2) INFORMATION FOR SEQ ID NO: 67:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1193 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

	GGCCGGGCGG TGCGCACTGC GGGCGCATCC CTGCCCCGGC GCCGTCCGTG CCCGCGGGAC	60
45	CTGACAGCCG GGTGAGAGG CGAACTGTGC TCAGGCCCGG GCTGGACGCA GAGCCAGAGC	120
	TGTCCCAGAG GGAGCAGAGG GTCCTGGAAA GGAAGCTGAA AAAGGAACGG AAGAAAGAGG	180
	AGAGGCAGCG TCTGCGGGAG GCAGGCCCTG TGGCCAGCA CCCGCCTGCC AGGCGCTCGG	240
50	GGGCCGAACT GGCCTGGGAC TACCTCTGCA GATGGGCCCA AAAGCACAAG AACTGGAGGT	300
	TTCAGAAGAC GAGGCAGACG TGGCTCCTGC TGCACATGTA TGACAGTGAC AAGGTTCCCG	360
55	ATGAGCACTT CTCCACCCTG CTGGCCTACC TGGAGGGGCT GCAGGGCCGG GCCCAGAGC	420
	TGACGGTGCA GAAGGCGGAA GCCTGATGCG GGAGCTGGAT GAGGAGGGCT CTGATCCCCC	480
	CCTGCCGGGG AGGGCCAGC GCATCCGACA GNTGCTGCAG CTGCTCTCCT AGTGGGTTCA	540
60	GCGCGGGGCG GGGCCGCTGC CCAGTGCAGG GCTGCCTCAG ACCACACAGG GTGCAGCTCC	600

TCCGGCGGTG GGGGCCGGGT TCACCAGCAG GGCAGCGGCT GAGCAAGGGC TTTCAGCTCC 660
 TCCGGTGGTG GGGGCCGGGA TCACCAGCAC CAGAGCCTCG CAAGGGCCCC TTCCCTCCTC 720
 5 CAGACCCTCC TTGGCCGGTG ACGCTGTGAC AGTGATGGCA GGTTCAGTGC CTCAGCGCA 780
 GAGCGTGGAT GCTCTGGAAT CACCCGGACC CCTGGCCTTG GAGGGACCCT CCAGCCCCAG 840
 10 GAATCTGCTT TGGAGGGAAA TGTCTATTTT TCTACCGGGA ATATTTTAGA GATTGGGGCA 900
 TGCTGGCTCC TCCCGCCAGC TGCAAACCTG CACCTTCCGC CTGATTCCCG ATCCCCCTGC 960
 GTGGGCCGCA TTCCTGGTCC CCTGCCTGCG TCCATCGAGG GGCCTGGCTG TGGCCTGTTT 1020
 15 TCCTTTGACC CCACACAGCG TCATTGCGGG TCATGGGGAG CCCCTGGTGG GAGCTTGTGG 1080
 AGTCGGATCA CGTACCTGTG CAGAAACCGC CTCTGTGGCT GCATTTGAAA TAAAACCCGA 1140
 20 CCCAGCAGCA AAAAAAAAAA AAAAAANCNC NAGGGGGGGC CCGNACCCA ATT 1193

25 (2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

35 GAATTCGGCA CGAGTTGGCA CATGATGCAA AATGCATTTT TCAGAGTAGA TTGCAGTCAA 60
 AAATGTTGGA AACTACTAAG CATGTGCARA TAGCATGCAT GCTGCTGCTG ACCTGCCAGA 120
 TATTTCTCCC TTCTCCCTT TCTCCCTCAT TTATTCATTC ATTAAGTGAT TCATTCATCC 180
 40 CATTAAAAAA ATTATATGTA TGTMTTGTGC AAAGCACCTT ACTCAAGGCT GCGGGGTACA 240
 AAAGTATATC AGAAGCCTTG GGCTMTGACM WACTTCTCTG TAGTAGTGCT AGATTTGTGT 300
 45 GGATCTGCCA CACTTACTCC AGGCCTCTTG TGACCTGTGC TTGCAATTAA TCTCTTAGGC 360
 TAAGCCACAT ACCTTTTTCAT TATACAATCT TTGCTGATGC TAAGGACAGA TTCCAAAGTG 420
 CCCTCCTTAT AATTTTGTGA TTTAATGCAA AGTGTAATCA AGAATAGGCC ATTGTTAGGT 480
 50 CAATTGCTTT TCTGTATTTA TCTTTTCAAA CAATAAATAA TCAGTGGGAT GAAAAAGGGC 540
 CGGAAAAAAA AAAAAAAAAA 560

55

(2) INFORMATION FOR SEQ ID NO: 69:

- 60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1657 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

	CGGACNGAGC CGCCGCGGG CACTTCCTGT GGAGCCGCA GCGGGTGCGG GCGCCGACGG	60
10	GCGAGAGCCA GCGAGCGAGC GAGCGAGCCG AGCCGAGCCT CCCGCCGTCG CCATGGGCCA	120
	GAACGACCTG ATGGGCACGG CCGAGGACTT CGCCGACCAG TTCCTCCGTG TCACAAAGCA	180
15	GTACCTGCCC CACGTGGCGC GCCTCTGTCT GATCAGCACC TTCCTGGAGG ACGGCATCCG	240
	TATGTGGTTC CAGTGGAGCG AGCAGCGCGA CTACATCGAC ACCACCTGGA ACTGCGGCTA	300
	CCTGCTGGCC TCGTCCTTCG TCTTCCTCAA CTGCTGGGA CANTGACTGG CTGCGTCCTG	360
20	GTGTTGAGCA GGAACCTTCG GCAGTACGCC TGCTTCGGGC TCTTTGAAT CATAGCTCTG	420
	CAGACGATTG CCTACAGCAT TTTATGGGAC TTGAAGTTTT TGATGAGGAA CCTGGCCCTG	480
25	GGAGGAGGCC TGTGCTGCT CCTAGCAGAA TCCCGTTCTG AAGGGAAGAG CATGTTTGC	540
	GGCGTCCCCA CCATGCGTGA GAGCTCCCC AAACAGTACA TGCAGCTCGG AGGCAGGGTC	600
	TTGCTGGTTC TGATGTTTAT GACCTCCTT CACTTTGACG CCAGCTTCTT TTCTATTGTC	660
30	CAGAACATCG TGGGCGACAG CTCTGATGAT TTTAGTGGC ATTGGTTTTA AAACCAAGCT	720
	GGCTGCTTTG ACTCTTTGTT TGTGGCTCTT TGCCATCAAC GTATATTTC ACGCCTTCTG	780
35	GACCATTTCA GTCTACAAGC CCATGCATGA CTTCTGAAA TACGACTTCT TCCAGACCAT	840
	GTGCGTGATT GGGGGCTTGC TCCTGGTGGT GGGCCTGGC CCTGGGGGTG TCTCCATGGA	900
	TGAGAAGAAG AAGGAGTGGT AACAGTCACA GATCCCTACC TGCCTGGCTA AGACCCGTGG	960
40	CCGTCAAGGA CTGTTTCGGG GTGGATTCAA CAAACTGCC AGCTTTTATG TATCCTCTTC	1020
	CCTTCCCTC CCTTGGTAAA GGCACAGATG TTTTGAGAAC TTTATTGCA GAGACACCTG	1080
45	AGAATCAATG GCTTCAGGAC ATGGGTCTC TTCTCCTGTG ATCATTCAAG TGCTCACTGC	1140
	ATGAAGACTG GCTGTCTCA GTGTTTCAAC CTCACCAGG CTGTCTCTTG GTCCACACCT	1200
	CGCTCCCTGT TAGTGCCGTA TGACAGCCCC CATCAAATGA CCTTGGCCAA GTCACGGTTT	1260
50	CTCTGTGGTC AAGGTTGGTT GGCTGATTGG TGGAAAGTAG GGTGGACCA AGGAGGCCAC	1320
	GTGAGCAGTC AGCACCAGTT CTGCACCAGC AGCGCTCCG TCCTAGTGGG TGTTCCTGTT	1380
55	TCTCCTGGCC CTGGGTGGGC TAGGGCCTGA TTCGGAAGA TGCCTTTGCA GGGAGGGGAG	1440
	GATAAGTGGG ATCTACCAAT TGATTCTGGC AAAACAATTT CTAAGATTTT TTTGCTTTAT	1500
	GTGGGAAACA GATCTAAATC TCATTTTATG CTGTATTTA TATCTTAGTT GTGTTTGAAA	1560
60	ACGTTTIGAT TTTTGAAAC ACATCAAAT AAATAATGGC GTTGTGTGTA AAAAAAAAAA	1620

AAAAAACTC GRGGGGGGC CCGGTACCCA AATCGCC

1657

5

(2) INFORMATION FOR SEQ ID NO: 70:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 711 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

GGCACGAGCG AAGACCCTGT TCGGACCCTG CCCCGATTCC AGACTCAGGT AGATCGTCGG 60
CATACCCTCT ACCGTGGACA CCAGGCAGCC CTGGGGCTGA TGGAGAGAGA TCAGGTATCC 120
20 CCCAGGGAGT AGGGGCTACC TTGAGGGGAT GATAGACCTC CCCCCTCCC AGTGKKAECT 180
TGGAAATATG AAGGAACTAG GGAGTGGAAAG AGATTTCAGA GCTGGGGAGA GGAGTTCCTC 240
25 CCTTCAAAGC CAGCAACTGC CTTTGGGGAA TGTCGGGGGG TCTCTCCTTT CTCCTGCTTG 300
TTTRAGGTGG TACACAGTCC CCCCTTCAMC TGGSGGGAAG CTGTNCCGA CARACTCATC 360
TCAGCTTTCC CTTGGGGCAG GATCGGGGGC AGCAGCTCCA GCAGAAACAG CAGGATCTGG 420
30 AGCAGGAAGG CCTCGAGGCC ACACAGGGGC TGCTGGCCGG CGAGTGGGCC CCACCCCTCT 480
GGRAGCTGGG CAGCCTCTTC CAGGCCTTCG TGAAGAGGGA GAGCCAGGCT TATGCGTAAG 540
35 CTTCATAGCT TCTGCTGGCC TGGGGTGGAC CCAGGACCCC TGGGGCCTGG GTGCCCTGAG 600
TGGTGGTAAA GTGGAGCAAT CCCTTCACGC TCCTTGCCCA TGTTCTGAGC GGCCAGCTTG 660
GCCTTTGCCT TAATAAATGT GCTTTATTTT CAAAAA AAAA AAAAAC T 711
40

45 (2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 935 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

GGCACAGGGT GAAAGCCAGC TAAACCCCAA GTGGAGAAGT GAAAGACATG GTTGTTCCTA 60
55 TAAGTTTATT GCTCACATTA TGAAAGAAGC CATAGTCATG AGTGAACCAC TCCCTAGGTT 120
GATAAGGAAA CCAACACGGA AGATCTCTTT CTGGAAGAAG CAGCCAGCCT CGTGAAGGAG 180
60 CGGCCAGCC GCCGGGCGG AGGGTCGCCT TTTGTTCGGA GTGGCACGAT TGTCCGTTC 240

	CAGACATTCT CGCCTGGAGC ACGAAGCCAG TATGTTTGCA GACTTTATCG TAGTGACAGC	300
5	GACAGTTCAA CGCTGCCCCG GAAGTCCCCC TTTGTCCGAA ATACTTTGGA AAGACGAACC	360
	CTTCGCTATA AGCAGTCATG CAGGTCTTCC CTGGCTGAGC TCATGGCCCCG CACCTCCCTG	420
	GACTTGGAGC TGGATCTCCA GGCCTCGAGA ACACGGCAGA GGCAGCTGAA TGAGGAGCTC	480
10	TGCGCCCTCC GTGAGCTGCG GCAGCGGTTN GGAGGACGCC CAGCTCCGTG GCCAGACTGA	540
	CCTCCCACCC TGGGTGCTTC GGGACGAGCG GCTCCGTGGC CTGCTGCGGG AGCCGAGCGG	600
15	CAGACAAGAC AGACCAAACCT TGACTACCGT CATGAGCAGG CGGCTGAGAA GATGCTGAAG	660
	AAGGCCTCCA AGGAGATCTA CCAGCTGCGT GGCAGAGCCA CAAAGAGCCC ATCCAAGTGC	720
	AGACCTTTAG GGAGAAGATA GCATTCTTCA CAAGGCCAAG GATCAACATA CCTCCTCTCC	780
20	CAGCCGACGA CGTCTGATGG AGTGCAATGT GCACATGAAG TATTTATCCA CCTGTTTAT	840
	TTTCATGAAG TTCTTAGACT AGCTGAATTT GTCTTTAAAA TATTTGTGCA AAGCTATTAA	900
25	TATACACATT TTGTAAAAA AAAAAAAAAA AACT	935

30 (2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

40	GCAGGGGCGA GGGYTGGGG ACCGCGGGC GGACGGGAGC GAGTATGTCC GCTCTGACTC	60
	GGCTGGCGTC TTTCGCTCGC GTTGGAGGCC GCCTTTTCAG AAGCGGCTGC GCACGGACTG	120
	CTGGAGATGG TGGAGTCCGT CATGCCGTG GTGGTGTGCA CATGAGCCC CGGTATAGAC	180
45	AGTTCCCCCA GCTGACCAGA TCCCAGGTGT TCCAGAGCGA GTTCTTCAGC GGACTCATGT	240
	GGTTCTGGAT TCTCTGGCGC TTTTGGCATG ACTCAGAAGA GGTGCTGGGT CACTTTCCGT	300
50	ATCCTGATCC TTCCAGTGG ACAGATGAAG AATTAGGTAT CCTCCTGAT GATGAAGACT	360
	GAAGGTGTAG ACTCAGCCTC ACTCTGTACA AGAGCCAGGT GAGAATTTCA AGGATTATCG	420
	ACTTCATATT GCACATTAAA GTTACAAATT AAAGTGGCTT GGTCAAGAAT GARAAAAAA	480
55	AAAAAAATTT GGGGGGGGGC CCCN	504

60 (2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 620 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

10 GAATTCGGCA CGAGGAGGAG GGGAGGCGGG GTAAGTTTGG TGGGAAACTC TGTAATTTCC 60
WTTTTTACTT TCACAGCAAT AGTGCAGAAT CCAGAATGGA TGTCTCTTT GTAGCCATCT 120
TTGCTGTGCC ACTTATCCTG GGACAAGAAT ATGAGGATGA AGAAAGACTG GGAGAGGATG 180
15 AATATTATCA GGTGGTCTAT TATTATACAG TCACCCCCAG TTATGATGAC TTTAGTGCAG 240
ATTTACCAT TGATTACTCC ATATTGAGT CAGAGGACAG GCTGAACAGG TTGGATAAGG 300
20 ACATAACAGA AGCAATAGAG ACTACCATTA GTCTTGAAAC AGCACGTGCA GACCATCCGA 360
AGCCTGTAAC TGTGAAACCA GTAACAACGG AACCTCAGAG TCCAGATCTG AACGATGCCG 420
TGTCCAGTTT GCGAAGTCCT ATTCCCCTCC TCCTGTCGTG TGCCTTTGTT CAGGTGGGGA 480
25 TGTATTTTAT GTAGAAGGTG GAAGAAGGCT GCTATGACTC TTTGGATGGG AGTCTGGCAA 540
GAGGAAATTG GAAGATAAAA TAAATAATAA GTGAAATAAA AAAAAAAAAA AAAAAGTCTGA 600
30 GGGGGGGCCC GGTACCCAAT 620

35 (2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 581 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

45 ACAAGGTGTG TGTAAAGTTT ATGTTTGTA ACTGAATTCT ATCTTAAATC CAAAAAGAAC 60
TCGGGAGTAA TTCATTTTTG TAGCATAAAG ATCCCTAAGT TTTATTTTGA AATATCTGAT 120
TTTTACACGT TAAAAAATAA CAGGGCATCG AGAGGATTCC TAGGTGACAT CCAGACTCCT 180
50 TTAGCTTTGT GTGTGTGGCA CCGGTAGTC TGCTTCTCTC TCCTTTCTTG CACTGCTTCA 240
CACAGCCATG CCCTGCCAGC CCGGCAGGT GCCTTCCTGT CAATGTACAT TTGGGCTTCT 300
55 GCTCATGCTG CCCTCCCTCC CCTCCCCTGC CTCCAACCC CGCCCCCTTT GTTCCTCCAT 360
GGAGTACTTC CATGGGTGTG CCTCCCCAG CCAAGCCATA ATAGGTGGTT TCCCCTTCGC 420
TTCTGTAGCC CTTGCAGACA TCCTCTGTTT ACAGTAGGTG TTGACTTACT TCCCCTCTCC 480
60

CCGSTAAAGC CATAAACTCC TTAAGGACAG GTAGCATTCCT TAGTATCTTC GTTCTTCTCA 540
 ATGACCAGTA GACCATTTAAA CATGTAGCAA ACAAATGTGA A 581

5

(2) INFORMATION FOR SEQ ID NO: 75:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1843 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

AAACCCAACN CCCTCCGGTC CCCNAAAGAA AGCCCAGCCC AAATCCCAAG CCGGCAGTGA 60
 20 GCCCGCGAAC AAGGCCCTCA AGACGCCCAG NCGAACAAGC AGCCCCCAGG AGCCCCCGCA 120
 AGAGAACTCC CTGGCGGCCC AAGCGGGCAG CTCTGTGTCG GCAGAACTCA GCCACCGAGA 180
 25 GCGCAGACAG CATCGAGATT TATGTCCCGG AGNCCCAGAC CAGGCTCTGA GACCATGCAG 240
 GAGGAAAGAA ACGATTTTAA ATCATTTAAA ACACAAAAAC TAAGTGGGAA CGGAACAGAG 300
 TTTTCTCAAC CTCTGTCTATG GTTATCTGTG CTAGAGACCC TGAGCCAACT TTCAAATTGA 360
 30 CGCATACAAG GGCTCACAAT TTGGCTTTTT TGGGTCCCTC CCAGCTTTAG GTTATGAAGA 420
 TTTTACTCAC AAAAAAATC AACAAAAATC ACGAACTAG AAACTTTTTT TTTTCTCTTT 480
 GCTGGCCGTG GTGGACTAGA TAGATGGACG TCGGCAACTC CCGGCCAGC CTCCATACTG 540
 35 CGGTCTTTTT ACTCGTTCTA TCTGATGAGA ACTCTCTCTA GCTTGTTTAC AAGATGACGA 600
 CAGTCCAAGG GCAGCCTTGG GCACCTGCCA TCTCTCTCTA TTCCCCAGCT ATCCCCGCTC 660
 40 TGACCTTGAT TTTCATTTCT ATGTTTTTCT CTTCTCTCTA CAGAGCTCAC ACAGTGGTCA 720
 CCATTGTGGC AAGCGGCTTT CTGGGTCTCA GCCCTCTCTG CGGTTGAGGG CCCAGAGGAC 780
 45 AGAGAGATGG ACATGCGTCC CCTCCCTCCC CCGCCAAGT GCTCACACAC AACCTCACGC 840
 GCACACACAC ACACGCAGAT GGAGGCGCCT CACTGGGAGG TGCCCCGCCA GCCCTGGGCA 900
 GTGTCAGGCA GGACTCACTC ACCGCTGAGC AGATGAGAGA AGTTTATAGTC TTGGCGGGTG 960
 50 GAAATGAGAC GAAGCCACAG TTATCACA CTAGACTCCT GCCCTTTTAT TTTCTCCAGC 1020
 CCTTCTTTCC TTCAGCAAAA TCTAGGACTC CCGAGTGGCT TCCAGGGGGC CGTCAGTCTT 1080
 55 CAGCCGCGCC TGTGTCCGGT GCCCGAGGGG CGGGCGGGCG TGTCTGTATG TATGTGTACA 1140
 TATGCACATA GACCTTAGAG TGTATAGTTA ACAAACGCCC ATCTGCTCAC CCATGCCAC 1200
 CCAGCGCCGC CGCCGCTGGC TCTCGGGGCA CCTGGCAGGA GGCGGGTGTG TGAATAGCAT 1260
 60 ATATTTTTTAC ATGTACTATA TCTAGGTGTG TGTACAAGTG TGTGTAAAAA TATATACCTT 1320

GTGTGTAAGC AGCCCTTTTT TTTTITGGTC TCCACCCCCC TCCCCCGCC CCGCACTCCT 1380
 AAGGGCCCAT CTGCCCAGCC TCTGAGTTTT CTGTTCTATT TTTTTTTTAA CCCCAATTAT 1440
 5 CCTTCTCTCT CTCTGCCCC CGCATCCAC TCCAGGGTG TCACGAGCCC TGAGCTGCAA 1500
 TGGCCCGGGC CTGCAGGGCG GGGTAGGGGA GGGCARGGCT SAGCCCCGAA GCCAGCTCAG 1560
 10 TACCTGAGGG GCTGCTCTAT GCTGTGTATG CGCCTCTCTG GCATCCGAGA CATCCTCTTG 1620
 GTGGCGCTTG CTNGCAGGGG ACCCCCCCCC CGTCCCCAGG TGAACCAAGG GTCTGCTCCG 1680
 GGGCCCATTT CCAGCTTGGC CGCCGTCTGT GACCTTGGGC AAGTCACTTG ACCTCTGTGT 1740
 15 GCCTCAACTT CCTCCTCTGT AAAACGGGGA CAGTCCCTGC CCCTCCCTAC CTCACAGGCA 1800
 TGTGTGAGA ATAAATGAGG TAACGTGTAA AAAAAAAAAA AAT 1843

20

(2) INFORMATION FOR SEQ ID NO: 76:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1441 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

TCGACCCACG CGTCCGGCTC CCCGAGCCCT GCCAACCATG GTGAACITGG GTCTGTCCCG 60
 35 GGTGGACGAC GCCGTGGCTG CCAAGCACCC GGGACTCGGG GAGTATGCCG CATGCCAGTC 120
 ACACGCCTTC ATGAAGGGCG TTTTCACCTT CGTCACAGGC ACCGGCATGG CCTTTGGCTT 180
 GCAGATGTTT ATTCAGAGGA AGTTTCCATA CCCTTTGCAG TGGAGCCTCC TAGTGGCCGT 240
 40 GGTTCAGGC TCTGTGGTCA GCTACGGGGT GACGAGAGTG GAGTCGGAGA AATGCAACAA 300
 CCTCTGGCTC TTCCTGGAGA CCGGGCAGCT CCCCAAAGAC AGGAGCACAG ATCAGAGAAG 360
 45 CTAGGAGAGC TCCAGCAGGG GCACAGAGGA TTGGGGGCAG GAGGAGTCTG GAACACAGCC 420
 TTCATGCCCC CTGACCCCAG GCCGACCTC CCCACACCTT AGGGTACCCC AGTCGTATCC 480
 TCTGTCCGCA TGTKTGGCCA GGCCTGACAA ACACCTGCAG ATGGCTGCTG CCCCACCTG 540
 50 GGACCTGCCC AGRAGGTTGG AGCAGAAAGG GCTCTCCCTG GGGTGGTGT TCTCCTCTAG 600
 GGTATTGGGA TGCATGTTCT GCACTGCCAG CAGAGAGGT GTGTCTGGG GCCACCACCT 660
 55 ATGGGACACG GGGTCGAAGG GGCCTGTACA CTCTGTCATT TCCTTTCTAG CCCCTGCATC 720
 TCCAACAAGT CCAAGGTGAC AGCTGGTGCT AGGGGCGTGG GGTAAATAAA TGGCTTATCC 780
 TTCTCTCCAC CCAAGTTTCC ACCTGACCAG GTGAAAAACA AATCAGAAGG GTAAGATGAT 840
 60

	GACAGGTCAC ATGAAACCTT TATTACCCTA CAGTTGATAT ATGAGGATCA CATGCAAGTT	900
	ACATACTGAG GATGTACAGG GAAGTTCCCA GCGCTGAACC CCAGAATTAG ACGTTCGCAT	960
5	CAGCCCCGTA GGCCACGTGG ACACCACCAC AGCCTCTCTG TATGGGGGTC TGCCTCTGTA	1020
	GCACTTGGCA TGTAGGGGCA GAGCAAAAGG GGCCANGCTG GCCAGAGCCT GGCTGCTGGG	1080
10	NAGARGAGGG ACTTGTGGGS CACGCCACNT GCCTATCATT CCCAYTCAT CTATTAGCCA	1140
	AAGTCACTCC CCAGAGGCAG AGCTAGCCCG TTGTAGCCGT GTCTGTGTGG AGGGAAAGCT	1200
	TCTGAGTGGG CAAGCCTACA CACAGCCCCG AGCCCCAAGA GGAGGAAGAG GTGGAGACCA	1260
15	GACGGAACCT CCACAAGTCC ATCATGGTTA CAGCTGGCTT CCCCAGCA CCGAAGACCC	1320
	ACAGCATNGG CCCTGCTGCC CCCGACCCAG CTCAGCTGCC ANGCCTCACC TTGCCAGGAA	1380
20	TTGAAAGAAA GTTATTGAGT ACTAATTGGC CTCAGAGTNA CAGGAAGCTC AAGTTAAAGT	1440
	G	1441
25	(2) INFORMATION FOR SEQ ID NO: 77:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 910 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:	
	GGCAGAGCTG GCCTTCGACT CGCTATGTCC ACTAACAATA TGTCGGACCC ACGGAGGCCG	60
	AACAAAGTGC TGAGGTGAGG ACCCCAGCGT CGTGGGCACG GGTTCGGGTT GTGGGTGTGG	120
40	ATCGGGGCCC TGGGAAGCGC CTGTCTATCC CGGGGGCAGG ACCTGAGCGC CCCTGACCCT	180
	CGAGCCTGTC GCAGGTACAA GCCCCGCCG AGCGAATGTA ACCCGGCCTT GGACGACCCG	240
45	ACGCCGGA CTATGAACCT GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAG	300
	CTGAAGTGGT GTGCTTGGGT CGCTGTCTAC TGCTCCTTCA TCAGCTTTGC CAACTCTCGG	360
	AGCTCGGAGG ACACGAAGCA AATGATGAGT AGCTTCATGT GAGACTTGCC CTACAGAACA	420
50	AGTGACTCTT GAGTAAGGGG TGGGGGGACC CCAGCCTGGC CATCCTAGAC TGACACCTCT	480
	CTCCTGTCTT CATGCTGTCC ATCTCTGCCG TGGTGATGTC CTATCTGCAG AATCCTCAGC	540
55	CCATGACGCC CCCATGGTGA TACCAGCCTA GAAGGGTCAC ATTTTGGACC CTGTCTATCC	600
	ACTAGGCCTG GGCTTTGGCT GCTAAACCTG CTGCCTTCAG CTGCCATCCT GGACTTCCCT	660
	GAATGAGGCC GTCTCGGTGC CCCAGCTGG ATAGAGGGAA CCTGGCCCTT TCCTAGGGAA	720
60	CACCCTAGGC TTACCCCTCC TGCCTCCCTT CCCCTGCCTG CTGCTGGGGG AGATGCTGTC	780

	CATGTTTCTA GGGGTATTCA TTTGCTTTCT CGTTGAAACC TGTGTTAAT AAAGTTTTTC	840
	ACTCTGAAAA AAAAAAAAAA AAAAAAAAAAC TYGRGGGGGG GCCCGGAACC CAATTCSCCG	900
5	GATAGTGAGT	910
10	(2) INFORMATION FOR SEQ ID NO: 78:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 2776 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:	
20	TCGACCCACG CGTCCGGGCG GGCAGTGATG GCGGCTGGTG ATGGGGACGT GAAGCTAGGC	60
	ACCCCTGGGGA GTGGCAGCGA GAGCAGCAAC GACGGCGGCA GCGAGAGTCC AGGCGACGCG	120
25	GGAGCGGCAG CGRAAGGGGG AGGCTGGGCG GCGGCGGCGT TGGCGCTTCT GACGGGGGGC	180
	GGGGAAATGC TGCTGAACGT GCGGCTGGTG GCTCTGGTGC TGCTGGGGGC CTACCGGCTG	240
	TGGGTGCGCT GGGGGCGGCG GGGTCTGGGG GCCGGGGCCG GGGCGGGCGA GGAGAGCCCC	300
30	GCCACCTCTC TGCCTCGCAT GAAGAAGCGG GACTTCAGCT TGGAGCAGCT GCGCCAGTAC	360
	GACGGCTCCC GCAACCCGCG CATCCTGCTC GCGGTCAATG GGAAAGTCTT CGACGTGACC	420
35	AAAGGCAGCA AGTTCTACGG CCCGGCGGGT CCATATGGAA TATTTGCTGG TAGGGATGCC	480
	TCCAGAGGAC TGGCCACATT TTGCCTAGAT AAAGATGCAC TTAGAGATGA ATATGATGAT	540
	CTCTCAGATT TGAATGCAGT ACAAATGGAG AGTGTTGAG AATGGGAAAT GCAGTTTAAA	600
40	GAAAAATATG ATTATGTAGG CAGACTCCTA AAACCAGGAG AAGAACCATC AGAATATACA	660
	GATGAAGAAG ATACCAAGGA TCACAATAAA CAGGATTGAA CTTTGTAAC AACCAAAGTC	720
45	AGGGGCCTTC AGAACTGCAA TTCTTACTCC CTTTCACAGA CTGTCCGGAG TCTTTGGGTT	780
	TGATTACCT GCTGCGAAAA ACATTCAACA AATTGTGTAC AAGATAAATT AATCTCACTA	840
	TGAAGATTTG AATAACTAGA CATTATTTAT GCTGCCAAAC TCATTTGTTG CAGTTGTTTG	900
50	TAATGTCTAG TGGGGCTTCA TCATCCTGAA AAGAAGGAGA CAGGGATTTT TTTAAAGAGC	960
	AAGAAAGTCA CAATATTACT TCTTTCCTTC CTTTTCCTT TCTTTCCTTT CTTCTTCTC	1020
55	TTTCTTCTT TTTAAAATAT ATTGAAGACA ACCAGATATG TATTTGCTAC TCAAGTGATC	1080
	AGATCTCCTC AAGAAACATC AAGGGACTCC TGTGTCACAT ACTGTGTTTT TATTTTAAAC	1140
60	TGGGTGAGGG AGGCGACCTG ATCAGGGGAG GTGGGGGTAC ACATCAATTT GAGTTGTTCA	1200

	GGCTACTGAA ACATTAAAAT GTGAATTCCC AAACCTTTCT TTTTGGCTTT GTCAGGGAAA	1260
	AGAAAAATAT CTTTATAAAG AAATCTTTGG AAATTAGGAG AAGGAATTC AGGTGGGTTT	1320
5	AAGTCAGAGC TAGTTCCCCA ACAGAAAGAT CATTTGAAAC CAGTTTTTAT CCCTTCTCTT	1380
	TCCTTCCCTT TCCCTAAATC AAATCAATAT TAATTGTGCC TTATTTCACT TAACATAGAC	1440
10	TTGAATTATT TTTAGGGAAA GCCCCTATAA TGAATTCAGA AATCACTACA AGCAGCATT	1500
	AGACTGAAGT TGAATATTC TGTGACCAT AAAACCTTGA TATCATTCTG TGTATATAGA	1560
	ATGTAAAAGG AATATTACAG TGTAACTGC CATATATGTA ATATACACAA ACTCAATTAG	1620
15	CATTGTAATG GCCAAATGCA TTCCCCATG CTTTCTGTT TTCAAAAAA TTGAAAAACA	1680
	AATCAACTCT TATCCCCAAC AGCTGCCTAA TTTTAGGAGT CTGACCCTCC ACATCTCACT	1740
20	GGTGTGGGTG CATGGGGCTG TGGAGTGGGT GTCAGTATGG ATGTGTCTGA ATGTGTGAGG	1800
	CCTTGAAGG GACTCTTTCT GCAGATACTG TAAATACAAG TACCATTTTA ATAAAGCATG	1860
	TACAATAAAC CAAAATAAGC TTGAGTTGGA CTTTATATAC AGAACTGTAA GCCAGTGCAT	1920
25	TATGATACAG TTGTAAGATT GTGCATTTGA TTCAAGATAA GGAAAAATCT TGGAAATGAA	1980
	AAGCAGGCAC KGGTTAACCA AGTTGTACAC ATTGTACCAC ATTCAGCATA ACTTTAGGAA	2040
30	GAAATTCAC TTTGTGAACA TTCTCCAGAA ATCCAAGATT ATTCAGGTAA GAATTGGTAT	2100
	ATTAAATGTA CATCTTTTTA CTTTCTATTT TGATGCCAAC TGATTATACT AGACAATTAG	2160
	CACTCCAGGT GGTATATGAA CACAAAACAG TAAAAGAATA TTGCACTGAT AGATACTAAA	2220
35	TTATTTATTTT ATTAGGTTGA AAAAGCCCTT ACTAAAAGCC CCTCATATAT CAATTACTTT	2280
	ATTTCAATTAT GACTACTTAG GTTCCGGGCT GGGGACAAGT TCACTTAAAA AGGCAATGTT	2340
40	ATTTAACAGG TCACCAGTTA AGACTTCTGC TTTGTAGATA CATGCAGAAG CCATCAAACA	2400
	AGGGGGRGCT TTAACTGCA ACAATAAGCT AAAGTATGTA AAATACTACA TTCTATTTCAG	2460
	TCTTGGAGTG TTTTGTAGAA AGTTATCTTC AGCCAAATCT TTGCTGAAGA CTGGTTGTGG	2520
45	AGTGTGGTA AATGCTTTGT GTTTTATGT AAAATATTTT CTAAACAAAA AATGTTAAAA	2580
	GTACATGTCC TCTGTAGTAA ACTGATATCT ATATATATGA ATCATTCAG CCTAAAGTCT	2640
50	AGTAATAAAC TGTACTTGTG AATAGAGAAA CCCTAAATAT TCATGCAGWA AAAATTATGC	2700
	GGTCTGTAA GAAAAATGAG TAATTTGTGT TTTGGACTTG AAATAAACAG TGTCTGTAG	2760
	ATAATTCCTC AACTTC	2776

55

(2) INFORMATION FOR SEQ ID NO: 79:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1525 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

	CCGCTGCTGA TAACTATGGC ATCCCCCGGG CCTGCAGGAA TTCGGCACGG AGCTACGGCG	60
10	CCGCCTGGCT CCTGCTGNCA CCTGCAGGCT CGTCGCGGGT GGAGCCCACC CAAGACATCA	120
	GCATCAGCGA CCAGCTGGGG GGCAGGACG TGCCCGTGTT CCGGAACCTG TCCCTGCTGG	180
	TGGTGGGTGT CGGCGCCGTG TTCTCACTGC TATTTCCACCT GGGCACCCGG GAGAGGCGCC	240
15	GGCCGCATGC GGASGAGCCA GGCAGACACA CCCCCCTGTT GGGCCCTGCC ACGGCCCAGC	300
	CCCTGCTGCT CTGGAAGCAC TGGCTCCGGG AGCSGGCTTT CTACCAGGTG GGCATACTGT	360
20	ACATGACCAC CAGGCTCATC GTGAACCTGT CCCAGACCTA CATGGCCATG TACCTCACCT	420
	ACTCGCTCCA CTGCCCCAAG AAGTTCATCG CGACCATTCC CCTGGTGATG TACCTCAGCG	480
	GCTTCTGTGC CTCCTTCCTC ATGAAGCCCA TCAACAAGTG CATTTGGAGG AACATGACCT	540
25	ACTTCTCAGG CTCCTGGTG ATCCTGGCCT TTGCCGCTG GGTGGCGCTG GCGGAGGGAC	600
	TGGGTGTGGC CGGTACGCA GCGGCTGTGC TGCTGGGTGC TGCTGTGCC ACCATCCTCG	660
30	TCACCTCGCT GGCCATGACG GCCGACCTCA TCGGTCCCA CACGAACAGC GGACTKTCGT	720
	GTACGGCTCC ATGAGCTTCT TGGATAAGGT GGCCAATGGG CTGGCAGTCA TGGCCATCCA	780
	GAGCCTGCAC CTTTGCCCCCT CAGAGCTCTG CTGCAGGGCC TGCGTGAGCT TTTACCACTG	840
35	GGCGATGGTG GCTGTGACGG GCGGCGTGGG CGTGGCCGCT GCCCTGTGTC TCTGTAGCCT	900
	CCTGCTGTGG CCGACCCGCC TGGACGCTG GGACCGTGAT GCGCGGCCCT GACTCCTGAC	960
40	AGCCTCCTGC ACCTGTGCAA GGGAACTGTG GGGACGCACG AGGATGCCCC CCARGGCCTT	1020
	GGGGAAAAGC CCCCCTGCC CTTCACTCTT CTCTGGACCC CCACCCTCCA TCCTCACCCA	1080
	GCTCCCGGGG GTGGGGTCCG GTGAGGGCAG CAGGGATGCC CGCCAGGGAC TTGCAAGGAC	1140
45	CCCCTGCGTT TTGAGGGTGT CCCATTCTCA ACTCTAATCC ATCCCAGCCC TCTGGAGGAT	1200
	TTGGGGTGCC CTTCTCGGCA GGGAAACAGGA AGTAGGAATC CCAGAAGGGT CTGGGGGAAC	1260
50	CCTAACCTTG AGCTCAGTCC AGTTCACCCC TCACCTCCAG CCTGGGGGTC TCCAGACACT	1320
	GCCAGGGCCC CTTAGGACG GCTGGAGCCT GGAGGAGACA GCCACGGGGT GGTGGGCTGG	1380
	GCCTGGACCC CACCGTGGTG GGCAGCAGGG CTGCCCCGCA GGCTTGGTGG ACTCTGCTGG	1440
55	CAGCAAATAA AGAGATGACG GCAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1500
	AAAAAAAAAA AAACCCACCG TCCGC	1525
60		

(2) INFORMATION FOR SEQ ID NO: 80:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1563 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

	AATTCGGCAC GAGNCAGAAA CCTGCGGAAA ATGGTAGCGA TGGCGGCTGG GCCGAGTGGG	60
15	TGTCTGGTGC CGGCGTTTGG GCTACGGTTG TTGTTGGCGA CTGTGCTTCA AGCGGTGTCT	120
	GCTTTTGGGG CAGAGTTTTC ATCGGAGGCA TGCAGAGAGT TAGGCTTTTC TAGCAACTTG	180
20	CTTGCAGCT CTTGTGATCT TCTCGGACAG TTCAACCTGC TTCAGCTGGA TCCTGATTGC	240
	AGAGGATGCT GTCAGGAGGA AGCACAATTT GAAACCAAAA AGCTGTATGC AGGAGCTATT	300
	CTTGAAGTTT GTGGATGAAA ATTGGGAAGG TTCCCTCAAG TCCAAGCTTT TGTTAGGAGT	360
25	GATAAACCCA AACTGTTTCAG AGGACTGCAA ATCAAGTATG TCCGTGGTTC AGACCCGTGA	420
	TTAAAGCTTT TGGACGACAA TGGGAACATT GCTGAAGAAC TGAGCATTTCT CAAATGGAAC	480
30	ACAGACAGTG TAGAAGAATT CCTGAGTGAA AAGTTGGAAC GCATATAAAT CTGCTTAA	540
	TTTGTCTCTA TCCTTTTGTT ACCTTATCAA ATGAAATATT ACAGCACCTA GAAAATAATT	600
	TAGTTTGTCT TGCTTCCATT GATCAGTCTT TTAATTGAGG CATTAAATAT CTAATTAAAT	660
35	CGTGAAATGG CAGTATAGTC CATGATATCT AAGGAGTTGG CAAGCTTAAC AAAACCCATT	720
	TTTATAAAT GTCCATCCTC CTGCATTTGT TGATACCACT AACAAAATGC TTTGTAACAG	780
40	ACTGCGGTT AATTATGCAA ATGATAGTTT GTGATAATTG GTCCAGTTTT ACGAACAACA	840
	GATTTCTAAA TTAGAGAGGT TAACAAGACA GATGATTACT ATGCCTCATG TGCTGTGTGC	900
	TCCTTGAAAG GAATGACAGC AGACTACAAA GCAAATAAGA TATACTGAGC CTCAACAGAT	960
45	TGCCTGCTCC TCAGAGTCTC TCCTATTTTT GTATTACCCA GCTTCTTTT TAATACAAAT	1020
	GTTATTTATA GTTTACAATG AATGCACTGC ATAAAAACTT TGTAGCTTCA TTATTGTAAA	1080
50	ACATATTCAA GATCCTACAG TAAGAGTGAA ACATTCACAA AGATTGCGT TAATGAAGAC	1140
	TACACAGAAA ACCTTTCTAG GGATTTGTGT GGATCAGATA CATACTGGC AAATTTTGA	1200
	GTTTACATT CTTACAGAAA AGTCCATTTA AAAGTGATCA TTTGTAAGAC CAAAATATAA	1260
55	ATAAAAAGTT TCAAAAATCT ATCTGAATTT GGAATCTTTC TGGTTTGTTC TTTCATGTTT	1320
	AAAAATGATG TTTTTCATG CATTTTTTTC ATGTAAGCCC TTTTTTTAGC CAAAATGTAA	1380
60	AAATGGCTGT AATATTTAAA ACTTATAACA TCTTATTGTT GGTAATAGTG CTTTATATTT	1440

GTCTGATTTT ATTTTCAAA GTTTTTCAT TTATGAACAC ATTTTCATG GTATATTAT 1500
TAAGGAATAT CTCTGATAT AGAATTTTAA TATTAATAAT GATTTTCTT TGCTTAAAA 1560
5 AAA 1563

10 (2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 1020 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

20 TGCACGCTGG CCATGTGGGN GTTGGGCCAC TGCACCCCC GCGCTGCAC GGGCCGAAG 60
CTGGCCCCGC TGGGCTGGT GCGCTGCCTG CGCCTGGGCC ACAGATTCGG CGGTCTGGTG 120
CTGAGCCCCG TGGGCAAGCA GTACGCGTCC CCCGAGACA GACAGCTGGT GGCGCAGTCT 180
25 GGGGTCGCCG TCATCGACTG CTCCTGGGCC AGGCTGGACG AGACACCGTT TGGGAAGATG 240
CGAGGGAGCC ACTTGCGCCT GTTGCCCTAC CTGGTGGCCG CCAACCCCGT GAACTATGGC 300
30 CGGCCCTACA GACTTTCCTG CGTGAAGCG TTTGCTGCCA CCTTCTGCAT CGTAGGCTTT 360
CCAGACCTTG CTGTCATTTT GCTGCGGAAG TTTAAATGGG GCAAGGGCTT CTGACCTG 420
AACCGCCAGC TCCTGGACAA GTACGCGGCC TGCGGCAGCC CGGAGGAGGT GCTGCAGGCG 480
35 GAGCAGGAGT TCTTGGCCAA TGCCAAGGAG AGCCCCCAGG AGGAGGAGAT CGATCCCTTC 540
GATGTGGATT CAGGGAGAGA GTTTGAAAC CCCAACAGGC CTGTGGCCAG CACCCGGCTG 600
40 CCCTCGGACA CTGATGACAG TGATGCGTCT GAGGACCCAG GGCCTKCGC CGAGCGCGGA 660
GGAGCCAGCA GCAGCTGCTG TGAAGAGGAG CAGACGCAGG GACGGGGGGC TGAGGCCAGG 720
GCCCCGGCTG AGGTTTGAA AGGAATCAAG AAACGGCAGA GAGACTGAGG GTTGCAGACA 780
45 CATATATTTT TGAGGCTGGG TGACGAGAAA ATCTAGAGAC ATGAGGGACA TAAATGGGCC 840
TGGCAGCCTC GGCTCTTTGC GGCTGCTGGC AGGACTGAGC TGTCCGGGTT CTCCCCACAC 900
50 TTCCAGCACA GCTGTGCTCT GTGCTCTGCC TCGGCGCTCT CGCAAATGAA GCTGCAGGCC 960
AAGAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAG GGGGGGGGGC 1020

55

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 770 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

	TCGACCCACG CGTCCGGGCC GCCGTAGCGC GTCTTGGGTC TCCCGGCTGC CGCTGCTGCC	60
10	GCCGCCCGCT CGGGTCGTGG AGCCAGGAGC GACGTCACCG CCATGGCAGG CATCAAAGCT	120
	TTGATTAGTT TGTCCTTTGG AGGAGCAATC GGA CTGATGT TTTTTRATGCT TGGATGTGCC	180
	CTTCCAATAT ACAACAAATA CTGGCCCCTC TTTGTCTAT TTTTTTACAT CCTTTCACCT	240
15	ATTCCATACT GCATAGCAAG AAGATTAGTG GATGATACAG ATGCTATGAG TAACGCTTGT	300
	AAGGAACTTG CCATCTTTCT TACAACGGGC ATTGTCGTGT CAGCTTTTGG ACTCCCTATT	360
20	GTATTTGCCA GAGCACATCT GATTGAGTGG GGAGCTTGTG CACTTGTCT CACAGGAAAC	420
	ACAGTCATCT TTGCAACTAT ACTAGGCTTT TTCTTGGTCT TTGGAAGCAA TGACGACTTC	480
	AGCTGGCAGC AGTGGTGAAA AGAAATTACT GAACTATTGT CAAATGGACT TCCTGTCAAT	540
25	TGTTGGCCAT TCACGCACAC AGGAGATGGG GCAGTTAATG CTGAATGGTA TAGCAAGCCT	600
	CTTGGGGGTA TTTTAGGTGC TCCCTTCTCA CTTTATTGT AAGCATACTA TTTTCACAGA	660
30	GACTTGCTGA AGGATTAAAA GGATTTTCTC TTTTGGAAAA AAAAAAAAAA AAAAAACYGA	720
	GGGGGGGCCC GTWCCCATTC SCCCATATG AATTCNTTT TTACAATCCC	770

35

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 481 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

45	GAATTCGGCA CGAGCATAGT GTTAACCACT AGAATTCACCT GCCCTTCCTA TCCAAAAATG	60
	ACACTACTGA TCAITTTTCT TCCTTTTSCT TTTACAACAT TMACAAATTC AGGTGGCTCT	120
50	TTCCCAGTAC GGTAGGCTGA TTCGTATGGA TGCACCACGG TTGGTGA CTG CCCCCACCCC	180
	ACAGAGTTTC TGGCGTTCAT TCGGTTGAAC CCAAGGCCAG CAAGGGCTGA CTGGGAACAA	240
55	ACCGAACACT AGGCCGTGAA CCAATCGTCT CTCGTTGCC GGGAGCGAMC CCGGGGGCCT	300
	TTCACTCTCC CAAGGACTCC ANGGGGGGGC CGGTACCCA ATTCCGCCCC TATAGTGAAT	360
	CCGTNATPAC AATTCCACNT GGGCCGTCCN TTTTACAAA CGTTCCGTTG AACTGGGAAA	420
60	AACCCCTTGG CGGTTTACCC CAACTTTAAT CCGCCTTTGC AAGCACATCC CCCCCCTTTT	480

C

481

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(2) INFORMATION FOR SEQ ID NO: 84:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 644 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

GCTGGGATAG AGCATGAAAG GAGAACTGCT CCCTTTTCTG TTTCTCACAG TTTGGTTATG 60
GCTTTATAAA CTTKTATTTG GTGAAAGCCC CAGATACCCA AATGTCATTG GCAAAACTTA 120
20 TTTTPTTTTC TGGACAGATC AGATTTCTAG AGAGAGCAGA TTTCTAGAGA GATTAGCATT 180
CATAGTAAGT GAAAATTGTC TAATTTTTTT AATCCATGCT ATTACTGGGC AGTAGGTCTA 240
25 ATTTTTTTTG ACAAAAAATA GATCTATTTT CCTTATATAT TGATTTAGAA TCTTAAGTTA 300
GAATTTTATA GAAGAAATGT CTGAGCAGTT CTATGTATGG AGGAGCAATT CAGCTTTTCA 360
GCAGCAACTT TATCTTTTGC CACTAGAGGG AGATCTGTGG TTGCTTTCTC CTTTGGAGAA 420
30 TAGCTGCTTT GCTTTTATTT TTAATTCTA AGGTTGGAAT AGAACTTATT CTCAAAATTC 480
CTTTAGTGTT ATTAAATATT TTCATTTATT AGTCAAAGGT AAGTTAATTA AGCTTGTTTA 540
35 ATGATGCCAA TCTTATGCTT TTCTGTAATC TTCAATTTTT AATAAATGTG AGTTAGATAC 600
TAAGTGAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA 644

40

(2) INFORMATION FOR SEQ ID NO: 85:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GGCACGAGTG CGCAGCGGTG GGGCTCTCTC CTTGTCAATC GGCGCCGCGT GCGGGCTGGT 60
GGCTCTGTGG CAGCGGCGGC GGCAGGACTC CGGCACTATG AGCGGCTTCA GCACCGAGGA 120
55 GCGCGCCGCG CCNTTCTCCC TGGAGTACCG AGTCTTCCTC AAAAATGAGA AAGGACAATA 180
TATATCTCCA TTTCATGATA TTCCAATTTA TGCAGATAAG GATGTGTTTC ACATGGTAGT 240
60 TGAAGTACCA CGCTGGTCTA ATGCAAAAAT GGAGATTGCT ACAAAGGACC CTTTAAACCC 300

	TATTAAACAA GATGTGAAAA AAGGAAACT TCGCTATGTT GCGAATTTGT TCCCGTATAA	360
5	AGGATATATC TGGAACATATG GTGCCATCCC TCAGACTTGG GAAGACCCAG GGCACAATGA	420
	TAAACATACT GGCTGTTGTG GTGACAATGA CCCAATTGAT GTGTGTGAAA TTGGAAGCAA	480
	GGTATGTGCA AGAGGTGAAA TAATTGGCGT GAAAGTTCTA GGCATATTGG CTATGATTGA	540
10	CGAAGGGGAA ACCGACTGGA AAGTCATTGC CATTAAATGTG GATGATCCTG ATGCAGCCAA	600
	TTATAATGAT ATCAATGATG TCAAACGGCT GAAACCTGGC TACTTAGAAG CTAATGTGGA	660
15	CTGGTTTAGA AGGTATAAGG TTCCTGATGG AAAACCAGAA AATGAGTTTG CGTTTAATGC	720
	AGAATTTAAA GATAAGGACT TTGCCATTGA TATTATTAAA AGCACTCATG ACCATTGGAA	780
	AGCATTAGTG ACTAAGAAAA CGAATGGAAA AGGAATCAGT TGCATGAATA CAACTTTGTC	840
20	TGAGAGCCCC TTCAAGTGTG ATCCTGATGC TGCCAGAGCC ATTGTGGATG CTTTACCACC	900
	ACCCTGTGAA TCTGCCTGCA CAGTACCAAC AGACGTGGAT AAGTGGTTCC ATCACCAGAA	960
25	AAACTAATGA GATTTCTCTG GAATACAAGC TGATATTGCT ACATCGTGT CATCTGGATG	1020
	TATTAGAAGT AAAAGTAGTA GCTTTTCAAA GCTTTAAATT TGTAGAACTC ATCTAACTAA	1080
	AGTAAATTCT GCTGTGACTA ATCCAATATA CTCAGAATGT TATCCATCTA AAGCATTTT	1140
30	CATATCTCAA CTAAGATAAC TTTTAGCACA TGCTTAAATA TCAAAGCAGT TGTCATTTGG	1200
	AAGTCACTTG TGAATAGATG TGCAAGGGGA GCACATATTG GATGTATATG TTACCATATG	1260
35	TTAGGAAATA AAATTATTTT GCTGAAAAAA AAAAAAAAAA AACCNCGGGG GGGGCCCCGG	1320
	TCCCCATTTG GCCCTTTGGG GGGNGGTTTT A	1351

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(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2527 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

	CTCTTGCTAC CTTCCCGGCG CAGAGAACCC CGGCTGCTCA GCGCGCTCCG GGGTCATGGA	60
	GATCCCCGGG AGCCTGTGCA AGAAAGTCAA GCTGAGCAAT AACGCGCAGA ACTGGGGAAT	120
55	GCAGAGAGCA ACCAATGTCA CCTACCAAGC CCATCATGTC AGCAGGAACA AGAGAGGTCA	180
	GGTGGTGGGG ACCAGAGGTG GCTTTCGTGG TTGCACAGTT TGGCTAACAG GCTTGTCTGG	240
60	AGCGGGAAAG ACTACTGTGA GCATGGCCTT GGAGGAGTAC CTGGTTTGTC ATGGTATTC	300

	ATGCTACACT CTGGATGGTG ACAATATCG TCAAGGTCTC AATAAAAAATC TTGGCTTTAG	360
	TCCTGAAGAC AGAGAAGAGA ATGTTTCGACG CATCGCAGAA GTTGCTAAAC TGTTCGAGA	420
5	TGCTGGCTTA GTGTGCATCA CAAGTTTCAT ATCACCTTAC ACTCAGGATC GCAACAATGC	480
	AAGGCAAATT CATGAAGGTG CAAGTTTACC GTTTTGTGAA GTATTGTGTG ATGCTCCTCT	540
10	GCATGTTTGT GAACAGAGGG ATGTCAAAGG ACTCTACAAA AAAGCCCGGG CAGGAGAAAAT	600
	TAAAGGTTTC ACTGGGATCG ATTCTGAATA TGAAAAGCCA GAGGCCCTG AGTTGGTGCT	660
	GAAAACAGAC TCCTGTGATG TAAATGACTG TGTCCAGCAA GTTGTGGAAC TTCTACAGGA	720
15	ACGGGATATT GTACCTGTGG ATGCATCTTA TGAAGTAAAA GAACTATATG TGCCAGAAAA	780
	TAAACTTCAT TTGGCAAAAA CAGATGCGGA AACATTACCA GCACTGAAAA TTAATAAAGT	840
20	GGATATGCAG TGGGTGCAGG TTTTGGCAGA AGGTTGGGCA ACCCCATTGA ATGGCTTTAT	900
	GAGAGAGAGG GAGTACTTGC AGTGCCTTCA TTTTGATTGT CTTCTGGATG GAGGTGTCAT	960
	TAACTTGTCG GTACCTATAG TTCTGACTGC GACTCATGAA GATAAAGAGA GGCTGGACGG	1020
25	CTGTACAGCA TTTGCTCTGA TGTATGAGGG CCGCCGTGTG GCCATTCTTC GCAATCCAGA	1080
	GTTTTTTGAG CACAGGAAAG AGGAGCGCTG TGCCAGACAG TGGGGAACGA CATGCAAGAA	1140
30	CCACCCCTAT ATTAAGATGG TGATGGAACA AGGAGATTGG CTGATTGGAG GAGATCTTCA	1200
	AGTCTTGGAT CGAGTTTATT GGAATGATGG TCTTGATCAG TATCGTCTTA CTCCTACTGA	1260
	GCTAAAGCAG AAATTTAAAG ATATGAATGC TGATGCTGTC TTTGCATTTC AACTACGCAA	1320
35	CCCAGTGCAC AATGGACATG CCCTGTTAAT GCAGGATACC CATAAGCAAC TTCTAGAGAG	1380
	GGGCTACCGG CGCCCTGTCC TCCTCCTCCA CCCTCTGGGT GGCTGGACAA AGGATGACGA	1440
40	TGTTCCCTTG ATGTGGCGTA TGAAGCAGCA TGCTGCAGTG TTGGAGGAAG GAGTTCTGAA	1500
	TCCTGAGACG ACAGTGGTGG CCATCTTCCC ATCTCCCATG ATGTATGCTG GACCAACTGA	1560
	GGTCCAGTGG CATTGCAGAG CACGGATGGT TGCAGGAGCC AACTTTTACA TTGTTGGACG	1620
45	AGACCCTGCT GGCATGCCTC ATCCAGAAAC AGGGAAGGAT CTTTATGAGC CAAGTCATGG	1680
	TGCCAAAGTG CTGACGATGG CCCCTGGTTT AATCACTTTG GAAATAGTTC CCTTTCGAGT	1740
50	TGCAGCTTAC AACAAGAAAA AGAAGCGTAT GGACTIONTAT GACTCTGAAC ACCATGAAGA	1800
	CTTTGAATTT ATTTTCAGGAA CACGAATGCG CAAACTTGCT CGAGAAGGCC AGAAACCACC	1860
	TGAAGGTTTC ATGGCTCCCA AGGCTTGGAC CGTGCTGACA GAATACTACA AATCCTTGGA	1920
55	GAAAGCTTAG GCTGTAAACC CAGTCACTCC ACCTTTGACA CATTACTIONT AACAAGAGGG	1980
	GACCACATAG TCTCTGTTGG CATTTCTTTG TGGTGTCTGT CTGGACATGC TTCCTAAAAA	2040
60	CAGACCATTT TCCTTAACCT GCATCAGTTT TGGTCTGCCT TATGAGTTCT GTTTTGAACA	2100

	AGTGTAACAC ACTGATGGTT TTAATGTATC TTTTCCACTT ATTATAGTTA TATTCCTACA	2160
	ATACAATTTT AAAATTGTCT TTTTATATTA TATTTATGCT TCTGTGTCAT GATTTTTTCA	2220
5	AGCTGTTATA TTAGTTGTAA CCAGTAGTAT TCACATTAAA TCTTGCTTTT TTTCCCCTTA	2280
	AAAAAAGAAA AAAATTACCA AACAATAAAC TTGGCTAGAC CTTGTTTGA GGATTTTACA	2340
10	AGACCTTTGT AGCGATTAGA TTTTTTTTCT ACATGAAAA TAGAACTGC TTCCTTTCTT	2400
	CTTCCAGTC AGCTATTGGT CTTTCCAGCT GTTATAATCT AAAGTATTCT TATGATCTGT	2460
	GTAAGCTCTG AATGAACCTC TTTACTCAAT AAAATTAATT TTTGGCTTC TTAACAAAAA	2520
15	AAAAAAA	2527

20 (2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 2566 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

30	CCCAAGAATT CGGCACGAGC GNGGCAWAAK TGGGATTTCT GAAACCTGTA GGCCCCAAGC	60
	CCATCAACTT GCCCAAAGAA GATTCCAAAC CTACATTTCC CTGGCCTSCT GGAAACAAGC	120
35	CATCTCTTCA CAGTGTA AAC CAAGACCATG ACTTAAAGCC ACTAGGCCGA AATCTGGGCC	180
	TACTCCTCCA ACCTCAGAAA ATGAACAGAA GCAAGCKTTT CCCAAATTGA CTGGGGTTAA	240
	AGGGAAATTT ATGTCAGCAT CACAAGATCT TGAACCCAAG CCCCTCTTCC CCAAACCCGC	300
40	CTTTGGCCAG AAGCCGCCCC TAAGTACCGA GAACTCCCAT GAAGACGAAA GCCCCATGAA	360
	GAATGTGTCT TCATCAAAAG GGTCCCCAGC TCCCCTGGGA GTCAGGTCCA AAAGCGCCCC	420
45	TTTAAACCA GCAAGGGAAG ACTCAGAAAA TAAAGACCAT GCAGGGGAGA TTTCAAGTTT	480
	GCCCTTTCTT GGAGTGGTTT TGAAACCTGC TGCGAGCAGG GGAGGCCAG GTCTCTCCAA	540
	AAATGGTGAA GAAAAAAGG AAGATAGGAA GATAGATGCT GCTAAGAACA CCTTCCAGAG	600
50	CAAAATAAAT CAGGAAGAGT TGGCCTCAGG GACTCCTCCT GCCAGGTTCC CTAAGGCCCC	660
	TTCTAAGCTG ACAGTGGGGG GGCCATGGGG CCAAAGTCAG GAAAAGGAAA AGGGAGACAA	720
55	GAATTCAGCC ACCCCGAAAC AGAAGCCATT GCCTCCCTTG TTTACCTTGG GTCCACCTCC	780
	ACCAAAACCC AACAGACCAC CAAATGTTGA CCTGACGAAA TTCCACAAAA CCTCTCTGG	840
	AAACAGTACT AGCAAAGGCC AGACGTCTTA CTCAACAAC TCCCTGCCAC CACCTCCACC	900
60	ATCCCATCCG GCCAGCCAAC CACCATTGCC AGCATCTCAC CCATCACAAC CACCAGTCCC	960

	AAGCCTACCT CCCAGAAACA TTAAACCTCC GTTTGACCTA AAAAGCCCTG TCAATGAAGA	1020
	CAATCAAGAT GGTGTCACGC ACTCTGATGG TGCTGGAAAT CTAGATGAGG AACAAGACAG	1080
5	TGAAGGAGAA ACATATGAAG ACATAGAAGC ATCCAAAGAA AGAGAGAAGA AAAGGAAAAA	1140
	GGAAGAAAAG AAGAGGTTAG AGCTGGAGAA AAAGGAACAG AAAGAGAAAAG AAAAGAAAAGA	1200
10	ACAAGAAATA AAGAAGAAAT TTAAACTAAC AGGCCCTATT CAAGTCATCC ATCTTGCAAA	1260
	AGCTTGTTGT GATGTCAAAG GAGGAAAGAA TGAAGTGAAG TTCAAGCAAG GAGAGCAAAAT	1320
	TGAAATCATC CGCATCACAG ACAACCCAGA AGGAAAATGG TTGGGCAGAA CAGCAAGGGG	1380
15	TTCATATGGC TATATTAAAA CAACTGCTGT AGAGATTGAC TATGATTCTT TGAACTGAA	1440
	AAAAGACTCT CTTGGTGCCC CTTCAAGACC TATTGAAGAT GACCAAGAAG TATATGATGA	1500
20	TGTTGCAGAG CAGGATGATA TTAGCAGCCA CAGTCAGAGT GGAAGTGGAG GGATATTCCC	1560
	TCCACCACCA GATGATGACA TTTATGATGG GATTGAAGAG GAAGATGCTG ATGATGGCTC	1620
	CACACTACAG GTTCAAGAGA AGAGTAATAC GTGGTCCTGG GGGATTTTGA AGATGTTAAA	1680
25	GGGAAAAGAT GACAGAAAAG AAAGTATACG AGAGAAACCT AAAGTCTCTG ACTCAGACAA	1740
	TAATGAAGGT TCATCTTTCC CTGCTCCTCC TAAACAATTG GACATGGGAG ATGAAGTTTA	1800
30	CGATGATGTG GATACCTCTG ATTTCCCTGT TTCATCAGCA GAGATGAGTC AAGGAACTAA	1860
	TGTTGGAAAA GCTAAGACAG AAGAAAAGGA CCTTAAGAAG CTAAAAAGC AGRAAAAARA	1920
	ARAAAAAGAC TTCAGGAAAA AATTAAATA TGATGGTGAA ATTAGAGTCC TATATTCAAC	1980
35	TAAAGTTACA ACTTCCATAA CTTCTAAAAA GTGGGGAACC AGAGATCTAC AGGTAAACC	2040
	TGGTGAATCT CTAGAAGTTA TACAAACCAC AGATGACACA AAAGTTCTCT GCAGAAATGA	2100
40	AGAAGGGAAA TATGGTTATG TCCTTCGGAG TTACCTAGCG GACAAATGAT GAGAGATCTA	2160
	TGATGATATT GCTGATGGCT GCATCTATGA CAATGACTAG CACTCAACTT TGGTCATTCT	2220
	GCTGTGTTCA TTAGGTGCCA ATGTGAAGTC TGGATTTTAA TTGGCATGTT ATTGGGTATC	2280
45	AAGAAAATTA ATGCACAAAA CCACTTATTA TCATTTGTTA TGAAATCCCA ATTATCTTTA	2340
	CAAAGTGTTC AAAGTTTGAA CATAGAAAAT AATCTCTCTG CTTAATTGTT ATCTCAGAAG	2400
50	ACTACATTAG TGAGATGTAA GAATTATTAA ATATTCCATT TCCGCTTTGG CTACAATTAT	2460
	GAAGAAGTTG AAGGTACTTC TTTTAGACCA CCAGTAAATA ATCCTCCTTC AAAAAATAAA	2520
55	AATAAAAAAA AAAAAAAA ACTCGAGGGG GGGCCCGGTA CCAAT	2566

(2) INFORMATION FOR SEQ ID NO: 88:

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

10 GAATTCGGCA CGAGGCTTTC TGTGTCCTCT GTGGCTGCTT TAGTGTGCCA CCAGGGGCAG 60
 ACTTGGGTGG GTTGCAGCAG AGATGGCATG GCCCTCAAGG TCCAAGATGT TTA CTCTCTT 120
 GCCGGTCCTC TGTATCTCT GGTCTTTGTG GTTCCACAG TTTCTTGGA TCCAGGAGTT 180
 15 AAAGGCAGTC CTGAGGGATG ATGGCCTCAT CTCGCGAGTT GCVTGAATG CTGAATTTC 240
 GACGTGCTAA AGGAGGGTTG CAGACATTGT GTGGWATGCA TTCAGACCCC AGATGTGGGT 300
 GCAGGAAGGC AGGCATGGCA CAGCCAGGTA GAGACTGGTT TCCAGGCCCA AGCAGCCTTC 360
 20 AGCAGCTGTG CGCCTTGTTT CTGATGTTGT TTGGGAGTAA GAATAATGTA GACATGGGGG 420
 GTCATGARGC TCAATAAAAA CTCAAGGAA ACCTCCCATG GCATGGTTGG GCGCAGTGAC 480
 25 TCATGCCTGT AACCCAGCA CTGTGGAATG CCAAGGTGGA AGGATCGCTT GAGGCCAAGA 540

30 (2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1863 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

40 TCGACCCACG CGTCCGGCGA GATCCCTACC GCAGTAGCCG CCTCTGCCGC CGCGGAGCTT 60
 CCCGAACCTC TTCAGCCGCC CGGAGCCGCT CCCGGAGCCC GGCCGTAGAG GCTGCAATCG 120
 CAGCCGGGAG CCCGAGCCC GCGCCCCGAG CCCGCCGCG CCCTTCGAGG GCGCCCCAGG 180
 45 CCGCGCCATG GTGAAGGTGA CGTTCAACTC CGCTCTGGCC CAGAAGGAGG CCAAGAAGGA 240
 CGAGCCCAAG AGCGGCGAGG AGGCGCTCAT CATCCCCCCC GACGCCGTCG CGGTGGACTG 300
 50 CAAGGACCCA GATGATGTGG TACCAGTTGG CCAAGAAGA GCCTGGTGTT GGTGCATGTG 360
 CTTTGGAATA GCATTTATGC TTGCAGGTGT TATTCTAGGA GGAGCATACT TGTACAAATA 420
 TTTTGCACTT CAACCAGATG ACGTGTACTA CTGTGGAATA AAGTACATCA AAGATGATGT 480
 55 CATCTTAAAT GAGCCCTCTG CAGATGCCCC AGCTGCTCTC TACCAGACAA TTGAAGAAAA 540
 TATTAAAAATC TTGAAGAAG AAGAAGTTGA ATTTATCAGT GTGCCTGTCC CAGAGTTTGC 600
 60 AGATAGTGAT CTGCCAACA TTGTTTCATGA CTTTAACAAG AAAC TTACAG CCTATTTAGA 660

TCTTAACCTG GATAAGTGCT ATGTGATCCC TCTGAACACT TCCATTGTTA TGCCACCCAG 720
 AAACCTACTG GAGTTACTTA TTAACATCAA GGCTGGAACC TATTTGCCTC AGTCCTATCT 780
 5 GATTCATGAG CACATGGTTA TTAGTGATCG CATTGAAAC ATTGATCACC TGGGTTTCTT 840
 TATTTATCGA CTGTGTCATG ACAAGGAAAC TTACAACTG CAACGCAGAG AAACATATTA 900
 10 AGGTATTCAG AAACGTGAAG CCAGCAATTG TTTCGCAATT CGGCATTTTG AAAACAAATT 960
 TGCCGTGGAA ACTTTAATTT GTTCTTGAAC AGTCAAGAAA AACATTATTG AGGAAAATTA 1020
 ATATCACAGC ATAACCCAC CCTTTACATT TTGTGCAGTG ATTATTTTTT AAAGTCTTCT 1080
 15 TTCATGTAAG TAGCAAACAG GGCTTTACTA TCTTTTCATC TCATTAATTC AATTAAAACC 1140
 ATTACCTTAA AATTTTTTTC TTTGGAAGTG TGGTGTCTTT TATATTTGAA TTAGTAACTG 1200
 20 TATGAAGTCA TAGATAATAG TACATGTCAC CTTAGGTAGT AGGAAGAATT ACAATTTCTT 1260
 TAAATCATTT ATCTGGATTT TTATGTTTAA TTAGCATTTT CAAGAAGACG GATTATCTAG 1320
 AGAATAATCA TATATATGCA TACGTAAAAA TGGACCACAG TGAATTATTT GTAGTTGTTA 1380
 25 GTTGCCCTGC TACCTAGTTT GTTAGTGCAT TTGAGCACAC ATTTTAATTT TCCTCTAATT 1440
 AAAATGTGCA GTATTTTCAG TGTCAAATAT ATTTAACTAT TTAGAGAATG ATTTCCACCT 1500
 30 TTATGTTTAA ATATCCTAGG CATCTGCTGT AATAATATTT TAGAAAATGT TTGGAATTTA 1560
 AGAAATAACT TGTGTTACTA ATTTGTATAA CCCATATCTG TGCAATGGAA TATAAATATC 1620
 ACAAAGTTGT TTAAGTAGAC TGCGTGTGT TTTTCCCGTA TAATAAAACC AAAGAATAGT 1680
 35 TTGGTTCTTC AAATCTTAAG AGAATCCACA TAAAGAAGA AACTATTTTT TAAAAATTCA 1740
 CTTCTATATA TACAATGAGT AAAATCACAG ATTTTTCCTT TAAATAAAAA TAAGTCATTT 1800
 40 TAATAACTAA ACCAGATTCT TTGTGATACT ATTAANGTAA CATTTAGCCC CAAAAAATAA 1860
 AAA 1863

45

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 2478 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

GGCACAGCGG CACGAGGTGA GCTGAGCCGG TGGGTGAGCG GCGGCCACGG CATCCTGTGC 60
 TGTGGGGGCT ACGAGGAAAG ATCTAATTAT CATGGACCTG CGACAGTTTC TTATGTGCCT 120
 60

	GTCCCTGTGC ACAGCCTTTG CCTTGAGCAA ACCCACAGAA AAGAAGGACC GTGTACATCA	180
	TGAGCCTCAG CTCAGTGACA AGGTTTCAAA TGATGCTCAG AGTTTGTATT ATGACCATGA	240
5	TGCCTTCTTG GGTGCTGAAG AAGCAAAGAC CTTTGATCAG CTGACACCAG AAGAGAGCAA	300
	GGAAAGGCTT GGAAAGATTG TAAGTAAAT AGATGGCGAC AAGGACGGGT TTGTCACTGT	360
10	GGATGAGCTC AAAGACTGGA TTAAATTTGC ACAAAGCGC TGGATTTACG AGGATGTAGA	420
	GCGACAGTGG AAGGGGCATG ACCTCAATGA GGACGGCCTC GTTTCCTGGG AGGAGTATAA	480
	AAATGCCACC TACGGCTACG TTTTAGATGA TCCAGATCCT GATGATGGAT TTAACATAA	540
15	ACAGATGATG GTTAGAGATG AGCGGAGGTT TAAATGGCA GACAAGGATG GAGACCTCAT	600
	TGCCACCAAG GAGGAGTTCA CAGCTTTCCT GCACCCTGAG GAGTATGACT ACATGAAAGA	660
20	TATAGTAGTA CAGGAAACAA TGGAAGATAT AGATAAGAAT GCTGATGGTT TCATTGATCT	720
	AGAAGAGTAT ATTGGTGACA TGTACAGCCA TGATGGGAAT ACTGATGAGC CAGAATGGGT	780
	AAAGACAGAG CGAGAGCAGT TTGTTGAGTT TCGGGATAAG AACCGTGATG GGAAGATGGA	840
25	CAAGGAAGAG ACCAAAGACT GGATCCTTCC CTCAGACTAT GATCATGCAG AGGCAGAAGC	900
	CAGGCACCTG GTCTATGAAT CAGACCAAAA CAAGGATGGC AAGCTTACCA AGGAGGAGAT	960
30	CGTTGACAAG TATGACTTAT TTGTTGGCAG CCAGGCCACA GATTTTGGGG AGGCCTTAGT	1020
	ACGGCATGAT GAGTTCTGAG CTRCGGAGGA ACCCTCATTT CCTCAAAAGT AATTTATTTT	1080
	TACAGCTTCT GGTTCACAT GAAATTGTTT GCGCTACTGA GACTGTTACT ACAAACTTT	1140
35	TAAGACATGA AAAGGCGTAA TGAAAACCAT CCCGTCCCA TTCCTCCTCC TCTCTGAGGG	1200
	ACTGGAGGGA AGCCGTGCTT CTGAGGAACA ACTCTAATTA GTACACTTGT GTTTGTAGAT	1260
40	TTACACTTTG TATTATGTAT TAACATGGCG TGTTTATTTT TGTATTTTTC TCTGGTTGGG	1320
	ACTATGATAT GAAGGATCAA GATCCTCAAC TCACACATGT AGACAAACAT TAGCTCTTTA	1380
	CTCTTTCTCA ACCCCTTTTA TGATTTAAT AATTCCTACT TAACTAATTT TGTAAGCCTG	1440
45	AGATCAATAA GAAATGTTCA GGAGAGAGGA AAGAAAAAA ATATATGCTC CACAATTTAT	1500
	ATTTAGAGAG AGAACACTTA GTCTTGCCCTG TCAAAAAGTC CAACATTTCA TAGGTAGTAG	1560
50	GGCCACATA TTACATTTCAG TTGCTATAGG TCCAGCAACT GAACCTGCCA TTACCTGGGC	1620
	AAGGAAAGAT CCCTTTGCTC TAGGAAAGCT TGGCCCAAAT TGATTTTCTT CTTTTCCTCC	1680
	CTGTAGGACT GACTGTTGGC TAATTTTGTG AAGCACAGCT GTGGTGGGAA GAGTTAGGGC	1740
55	CAGTGTCTTG AAAATCAATC AAGTAGTGAA TGTGATCTCT TTGCAGAGCT ATAGATAGAA	1800
	ACAGCTGGAA AACTAAAGGA AAAATACAAG TGTTTTCGGG GCATACATTT TTTTCTGGG	1860
60	TGTGCATCTG TTGAAATGCT CAAGACTTAA TTATTTGCCT TTTGAAATCA CTGTAAATGC	1920

CCCCATCCGG TTCCTCTTCT TCCCAGGTGT GCCAAGGAAT TAATCTTGGT TTCACTACAA 1980
 TTAAAATTCA CTCCTTTCCA ATCATGTCAT TGAAAGTGCC TTTAACGAAA GAAATGGTCA 2040
 5 CTGAATGGGA ATTCTCTTAA GAAACCCTGA GATTAAAAAA AGACTATTTG GATAACTTAT 2100
 AGGAAAGCCT AGAACCTCCC AGTAGAGTGG GGATTTTTTTT CTTCTTCCCT TTCTCTTTTG 2160
 GACAATAGTT AAATTAGCAG TATTAGTTAT GAGTTTGGTT GCAGTGTTCT TATCTTGTGG 2220
 10 GCTGATTTCC AAAAACCACA TGCTGCTGAA TTTACCAGGG ATCCTCATAC CTCACAATGC 2280
 AAACCACTTA CTACCAGGCC TTTTCTGTG TCCACTGGAG AGCTTGAGCT CACACTCAAA 2340
 15 GATCAGAGGA CCTACAGAGA GGGCTCTTTG GTTTGAGGAC CATGGCTTAC CTTTCCTGCC 2400
 TTTGACCCAT CACACCCCAT TTCCTCCTCT TTCCCTCTCC CCGCTGCCAA TTCCTGCAGC 2460
 CCGGGGGAAC CACTAGTT 2478
 20

(2) INFORMATION FOR SEQ ID NO: 91:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2058 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

TCGGCCTTGC TTTTGTGGYC TTCCTCTGTG GCCAGAGCGT TTTCATCACC AAGCCTCCTG 60
 35 ATGGCAGTNC CTTACCGAT ATGTTCAAGA TACTGACGTA TTCCTGCTGT TCCCAGAAGC 120
 GAAGTGAGA GCGCCAGAGT AATGGTGAAG GCATTGGAGT NTTTCAGCAA TCTTCTAAAC 180
 40 AAAGTCTGTT TGATTCATGT AAGATGTCTC ATGGTGGGCC ATTTACAGAA GAGAAAGTGG 240
 AAGATGTGAA AGCTCTGGTC AAGATTGTCC CTGTTTCTTT GGCTTTGATA CCTTACTGGA 300
 CAGTGATTTT CCAAATGCAG ACAACATATG TTTTACAGAG TCTTCATTTG AGGATTCCAG 360
 45 AAATTTCAAA TATTACAACC ACTCCTCACA CGCTCCCTGC AGCCTGGCTG ACCATGTTTG 420
 ATGCTGTGCT CATCCTCCTG CTATCCCTC TGAAGGACAA ACTGGTCGAT CCCATTTTGA 480
 50 GAAGACATGG CCGCTCCCA TCCTCCCTGA AGAGGATCGC CGTGGGCATG TTCTTTGTCA 540
 TGTGCTCRGC CTTTGCTGCA GGAATTTTGG AGAGTAAAAG GCTGAACCTT GTTAAAGAGA 600
 AAACCATTA TACAGACCATC GGCAACGTCG TCTACCATGC TGCCGATCTG TCGCTGTGGT 660
 55 GGCAGGTGCC GCAGTACTTG CTGATTGGGA TCAGCGAGAT CTTTGCAAGT ATCGCAGGCC 720
 TGAATTTGC ATACTCAGCT GCCCCAAGT CCATGCAGAG TGCCATAATG GGCTTGTCT 780
 60 TTTTCTTCTC TGGCGTCGGG TCGTTCGTGG GTTCTGGACT GCTGGCACTG GTGTCTATCA 840

	AAGCCATCGG ATGGATGAGC AGTCACACAG ACTTTGGTAA TATTAACGGC TGCTATTTGA	900
5	ACTATTACTT TTTCTTCTG GCTGCTATTC AAGGAGCTAC CCTCCTGCTT TTCCTCATTA	960
	TTTCTGTGAA ATATGACCAT CATCGAGACC ATCAGCGATC AAGAGCCAAT GGCGTGCCCA	1020
	CCAGCAGGAG GGCCTGACCT TCCTGAGGCC ATGTGCGGTT TCTGAGGCTG ACATGTCAGT	1080
10	AACTGACTGG GGTGCACTGA GAACAGGCAA GACTTTAAAT TCCCATAAAA TGTCTGACTT	1140
	CACTGAAACT TGCATGTTGC CTGGATTGAT TTCTTCTTTC CCTCTATCCA AAGGAGCTTG	1200
15	GTAAGTGCCT TACTGCAGCG TGTCTCCTGG CACGCTGGGC CCTCCGGGAG GAGAGCTGCA	1260
	GATTTGAGT ATGTCGCTTG TCATTCAAGG TCTCTGTGAA TCCTCTAGCT GGGTTCCCTT	1320
	TTTTACAGAA ACTCACAAAT GGAGATTGCA AAGTCTTGGG GAACTCCACG TGTTAGTTGG	1380
20	CATCCCAGTT TCTTAAACAA ATAGTATCAC CTGCTTCCCA TAGCCATATC TCACTGTAAA	1440
	AAAAAAATTT AATAAACTGT TACTTATATT TAAGAAAGTG AGGATTTTTT TTTTTTAAAG	1500
25	ATAAAAGCAT GGTGAGATGC TGCAAGGATT TTACATAAAT GCCATATTTA TGGTTTCCTT	1560
	CCTGAGAACA ATCTTGCTCT TGCCATGTTT TTGATTTAG GCTGGTAGTA AACACATTTT	1620
	ATCTGCTGCT TCAAAAAGTA CTTACTTTTT AAACCATCAA CATTACTTTT CTTCTTTAAG	1680
30	GCAAGGCATG CATAAGAGTC ATTTGAGACC ATGTGTCCCA TCTCAAGCCA CAGAGCAACT	1740
	CACGGGGTAC TTCACACCTT ACCTAGTCAG AGTGCTTATA TATAGCTTTA TTTTGGTACG	1800
35	ATTGAGACTA AAGACTGATC ATGGTTGTAT GTAAGGAAAA CATTCCTTTG AACAGAAATA	1860
	GTGTAATTAA AAATAATTGA AAGTGTTAAA TGTGAACTTG AGCTGTTTGA CCAGTCACAT	1920
	TTTGTATATG TTACTGTACG TGTATCTGGG GCTTCTCCGT TTGTTAATAC TTTTCTGTGA	1980
40	TTTGTGCTG TATTTTGGC ATAACCTTAT TATAAAAAGC ATCTCAAATG CGAAAWAAAA	2040
	AAAAAAAAAA AAAAAAAC	2058

45

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

	GGCACAGGAG CGACCCGGGA GAAGGAGGGC CAMGAKCGG AAGCGGAGGA GTCTCCAGGA	60
60	GACCCGGGGA CAGCATCGCC CAGGCCCTG TTTGCAGGCC TTTCAGATAT ATCCATCTCA	120

CAAGACATCC CCGTAGAAGG AGAAATCACC ATTCCATATGA GATCTCGCAT CCGGGAGTTT 180
 GACAGCTCCA CATTAAATGA ATCTGTTCGC AATACCATCA TCGTGATCT AAAAGCTGTT 240
 5 GGGAAAAAAT TCATGCATGT TTTGTACCCA AGGAAAAGTA ATACTCTTTT GAGAGATTGG 300
 GATTGTGGG GCCCTTTGAT CCTTTGTGTG AACTCTGCAT TAATGCTGCA AAGAGACTCT 360
 GCAGATAGTG AAAAAGATGG AGGGCCCCAA TTTGCAGAGG TGTTCATCAT TGTCTGGTTT 420
 10 GGTGCAGTTA CCATCACCTT CAACTCAAAA CTTCTTGGAG GGAACATATC TTTTTTTCAG 480
 AGCCTCTGTG TGCTGGGTTA CTGTATACTT CCCTTGACAG TAGCAATGCT GATTTGCCGG 540
 15 CTGGTACTTT TGGCTGATCC AGGACCTGTA AACTTCATGG TTCGGCTTTT TGTGGTGATT 600
 GTGATGTTTG CCTGGTCTAT AGTTGCCTCC ACAGCTTTCC TTGCTGATAG CCAGCCTCCA 660
 AACCGCAGAG CCCTAGCTGT TTATCCTGTT TTCTGTTTT ACTTTGTCAT CAGTTGGATG 720
 20 ATCTCACCT TTAATCCTCA GTAAATCAGG AATGGGAAAT TAAAACCAG TGAATTGAAA 780
 GCACATCTGA AAGATGCAAT TCACCATGGA GCTTTGTCTC TGGCCCTTAT TTGTCTAATT 840
 25 TTGGAGGTAT TTGATAACTG AGTAGGTGAG GAGATTAAAA GGGAGCCATA TAGCACTGTC 900
 ACCCCTTATT TGAGGAACTG ATGTTTGAAA GGCTGTCTT TTCTCTCTTA ATGTCATTTT 960
 TTTAAAAATA CATGTGCATA CTACACACAG TATATAATGC CTCCTTAAGG CATGATGGAG 1020
 30 TCACCGTGGT CCATTTGGGT GACAACCACT GACTTGGGAA GCACATAGAT ACATCTTACA 1080
 AGTTGAATAG AGTTGATAAC TATTTTCAGT TTTGAGAATA CCAGTTCAGG TGCAGCTCTT 1140
 35 AAACACATTG CCTTATGACT ATTAGAATAT GCCTCTCTT TCATAAATAA AAATACATGG 1200
 TCTATATCCA TTTCTTTTA TTTCTCTCTC TTAAGCTTAA AAAGGCAATG AGAGAGGTTA 1260
 GGAGTGGGTT CATAACCGA GAATGAGAAA ACATGCATTA ACCAATATTC AGATTTTGAT 1320
 40 CAGGGGAAAT TCTAYACTTG TTGCAAAAAA AAAAAAAAAA AACTCGAGG GGGGCCCGT 1380
 ACCCAATCGC NGTATATGAT CGNAAACAAT C 1411

45

(2) INFORMATION FOR SEQ ID NO: 93:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

GCTTTGGCTT TTTTGGCGG ACTGGGCGC CCTCCGGAAG CGTTTCCAAC TTTCAGAAG 60
 60 TTTCTCGGGA CGGGCAGGAG GGGGTGGGGA CTGCCATATA TAGATCCCGG GAGCAGGGGA 120

	GCGGGCTAAG AGTAGAATCG TGTCGCGCTC GAGAGCGAGA GTCACGTCCC GCGCTAGCC	180
5	CAGCCCGACC CAGGCCCACC GTGGTGACG CAAACCACTT CCTGGCCATG CGCTCCCTCC	240
	TGCTTCTCAG CGCCTTCTGC CTCTGGAGG CGGCCCTGGC CGCCGAGGTG AAGAAACCTG	300
	CAGCCGCAGC AGCTCCTGGC ACTGCGGAGA AGTTGAGCCC CAAGGCGGCC ACGCTTGCCG	360
10	AGCGCAGCCG GCCTGGCCTT CAGCTTGATC CAGGCCATGG CCAAGGACCA GGCAGTGGAG	420
	AACATCCTGG TGTCACCCGT GGTGGTGGCC TCGTCGCTGG GGCTCGTGTC GCTGGGCGGC	480
15	AAGGCGACCA CGGCGTCGCA GGCCAAGGCA GTGCTGAGCG CCGAGCAGCT GCGCGACGAG	540
	GAGGTGCACG CCGGCCTGGG CGAGCTGCTG CGCTCACTCA GCAACTCCAC GGCGCGCAAC	600
	GTGACCTGGA AGCTGGGCAG CCGACTGTAC GGACCCAGCT CAGTGAGCTT CGCTGATGAC	660
20	TTCTGTGCGCA GCAGCAAGCA GCACTACAAC TCGGAGCACT CCAAGATCAA CTTCCGCGAC	720
	AAGCGCAGCG CGCTGCAGTC CATCAACGAG TGGGCCGCGC AGACCACCGA CGGCAAGCTG	780
25	CCCGAGGTCA CCAAGGACGT GGAGCGCAGG GACGGCGCCC TGTTAGTCAA CGCCATGTTT	840
	TTCAAGCCAC ACTGGGATGA GAAATTCAC CACAAGATGG TGGACAACCG TGGCTTCATG	900
	GTGACTCGGT CCTATACCGT GGGTGTCTATG ATGATGCACC GGACAGGCCT CTACAACTAC	960
30	TACGACGACG AGAAGGAAAA GCTGCAAATC GTGGAGATGC CCCTGGCCCA CAAGCTCTCC	1020
	AGCCTCATCA TCCTCATGCC CCATCACGTG GAGCCTCTCG AGCGCCTTGA AAAGCTGCTA	1080
35	ACCAAAGAGC AGCTGAAGAT CTGGATGGGG AAGATGCAGA AGAAGGCTGT TGCCATCTCC	1140
	TTGCCCAAGG GTGTGGTGGA GGTGACCCAT GACCTGCAGA AACACCTGGC TGGGCTGGGC	1200
	CTGACTGAGG CCATGACAA GAACAAGGCC GACTTGTCAC GCATGTCAGG CAAGAAGGAC	1260
40	CTGTACCTGG CCAGCGTGT CCACGCCACC GCCTTTGAGT TGGACACAGA TGGCAACCCT	1320
	TTGACCAGAA TTACGGGCGG AGGAGTGCAG ACCCAAGTGT TCTACGCCGA CCACCCCTTC	1380
45	ATTTCTTAGT GCGGGACACC CAAAGCGGTC CCTGCTATTC ATTGGGCGCC TGGTCCGGCC	1440
	TAAGGGTGAC AAGATGCGAG ACGAGTTATA GGCCTCAGGG TGCACACAGG ATGGCAGGAG	1500
	GCATCCAAAG GCTCCTGAGA CACATGGGTG CTATTGGGGT TGGGGGGGAG GTGAGGTACC	1560
50	AGCCTTGAT ACTCCATGGG GTGGGGTGA AAAGCAGACC GGGGTTCCTG TGTGCCTGAG	1620
	CGGACTTCCC AGCTAGAATT CACTCCACTT GGACATGGGC CCCAGATACC ATGATGCTGA	1680
55	GCCCGGAAAC TCCACATCCT GTGGGACCTG GGCCATAGTC ATTCTGCCTG CCCTGAAAGT	1740
	CCCAGATCAA GCCTGCCTCA ATCAGTATTC ATATTTATAG CCAGGTACCT TCTCACCTGT	1800
	GAGACCAAAT TGAGCTAGGG GGGTCAGCCA GCCCTCTTCT GACACTAAAA CACCTCAGCT	1860
60	GCCTCCCCAG CTCTATCCCA ACCTCTCCCA ACTATAAAAC TAGGTGCTGC AGCCCTGGG	1920

ACCAGGCACC CCCAGAATGA CCTGGCCGCA GTGAGGCGGA TTGAGAAGGA GCTCCCAGGA 1980
GGGGCTTCTG GGCAGACTCT GGTCAAGAAG CATCGTGTCT GCGTTGTGG GGATGAACTT 2040
5 TTTGTTTTGT TTCTTCCTTT TTTAGTTCTT CAAAGATAGG GAGGGAAGGG GGAACATGAG 2100
CCTTGTGTC TATCAATCCA AGAACTTATT TGTACATTTT TTTTTCAT AAAACTTTTC 2160
10 CAATGACAAA AAAAAAAAAA AAAAAA 2187

15 (2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 757 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

25 GACAGTACGG TCGATTCCC GGGTCGACCC ACGCGTCCGC GGACGGTGAA GAAGGTGAAG 60
ATGGCGGTGG CCAGGGCCCG GGTCTTGGGA GTCCAGTGGC TGCAAAGGGC ATCCCGGAAC 120
GTGATGCCGC TGGGCGCACG GACAGCCTCC CACATGACCA AGGACATGTT CCCGGGGCCC 180
30 TATCCTAGGA CCCAGAAGA ACGGGCCGCC GCCCCAAGA AGTATAATAT GCGTGTGGAA 240
GACTACGAAC CTTACCCGGA TGATGGCATG GGGTATGGCG ACTACCCGAA GCTCCCTGAC 300
35 CGCTCACAGC ATGAGAGAGA TCCATGGTAT AGCTGGGACC AGCCGGGCCT GAGGTGAAC 360
TGGGTGAAC CGATGCACTG GCACCTAGAC ATGTACAACA GGAACCGTGT GGATACATCC 420
CCCACACCTG TTTCTTGGCA TGTATGTGT ATGCAGCTCT TCGGTTTCCT GGC'TTTCATG 480
40 ATATTCATGT GCTGGGTGGG GGACGTGTAC CCTGTCTACC AGCCTGTGGG ACCAAAGCAG 540
TATCCTTACA ATAATCTGTA CCTGGAACGA GCGGTGATC CCTCAAAGA ACCAGAGCGG 600
45 GTGGTCACT ATGAGATCTG AGGAGGCTTC GTGGGCTTTT GGGTCCTCTA ACTAGGACTC 660
CCTCATTCCT AGAAATTTAA CCTTAATGAA ATCCCTAATA AAACTCAGTG CTGTGTAA 720
AAAAAAAAA AAAAAAAAAA AAAAAGGGGG GCCCCNN 757
50

55 (2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 2394 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

5	GGCACGAGCA CTCCTGCACT TCCCCACCCC CACGACCGAA CCTGGCTTCG CTAACGCCCT	60
	CCCAGCTCCC TCGGCCTGA CTTCCGGTTT CCTCGCGCGT CCCTGGCGCC GAGCCGCGGA	120
	CAGCAGCCCC TTTCCTGGCT GAGAGCTCAT CCACACTTCC AATCACTTTC CGGAGTGCTT	180
10	CCCCCTCCCTC CGGCCCGTGC TGGTCCCGAC GGCGGGCCTG GGTCTCGCGC GCGTATTGCT	240
	GGGTAACGGG CCTTCTCYCG CGTCGGCCCG GCCCCCTCTG CCTCGGCTCG TCCCTCCTTC	300
15	CAGAACGTCC CGGGCTCCTG CCGAGTCAGA AGAAATGGGA CTCCCTCCGC GACGTGCCCCG	360
	GAGCAGCTCC CTTGCTGTG GAAGCGGCGG TGTCTTCGAA GAAACCGGAA GCCCGTGGTG	420
	ACCCCTGGCG ACCCGGTTTG TTTCGGTCC GTTTCCAAAC ACTAAGGAAT CGAAACTCGG	480
20	CGGCCTTGGG GGCGGCCCTA CGTAGCCTGG CTTCTGGTTG TCATGGATGC ACTGGTAGAA	540
	GATGATATCT GTATTCTGAA TCATGAAAAA GCCCATAAGA GAGATACAGT GACTCCAGTT	600
25	TCAATATATT CAGGAGATGA ATCTGTTGCT TCCCATTTTG CTCTTGTCAC TGCATATGAA	660
	GACATCAAAA AACGACTTAA GGATTCAGAG AAAGAGAACT CTTTGTATAA GAAGAGAATA	720
	AGATTTTGGG AAGAAAAGCT AATAGCTCGA TTTGAAGAAG AAACAAGTTC CGTGGGACGA	780
30	GAACAAGTAA ATAAGGCCTA TCATGCATAT CGAGAGGTTT GCATTGATAG AGATAATTG	840
	AAGAGCAAAC TGGACAAAAT GAATAAAGAC AACTCTGAAT CTTTGAAAGT ATTGAATGAG	900
35	CAGCTACAAT CTAAAGAAGT AGAACTCCTC CAGCTGAGGA CAGAGGTGGA AACTCAGCAG	960
	GTGATGAGGA ATTTAAATCC ACCTTCATCA AACTGGGAGG TGGAAAAGTT GAGCTGTGAC	1020
	CTGAAGATCC ATGGTTTGGA ACAAGAGCTG GAACTGATGA GGAAAGAATG TAGCGATCTC	1080
40	AAAATAGAAC TACAGAAAGC CAAACAAACG GATCCATATC AGGAAGACAA TCTGAAGAGC	1140
	AGAGATCTCC AAAAATAAG CATTTCAAGT GATAATATGC AGCATGCATA CTGGGAAC TG	1200
45	AAGAGAGAAA TGTCTAATTT ACATCTGGTG ACTCAAGTAC AAGCTGAACT ACTAAGAAAA	1260
	CTGAAAACCT CAACTGCAAT CAAGAAAGCC TGTGCCCTG TAGGATGCAG TGAAGACCTT	1320
	GGAAGAGACA GCACAAAAC GCACTTGATG AATTTTACTG CAACATACAC AAGACATCCC	1380
50	CCTCTCTTAC CAAATGGCAA AGCTCTTTGT CATAACACAT CTTCCCTTTT ACCAGGAGAT	1440
	GTAAAGGTTT TATCAGAGAA AGCAATCCTC CAATCATGGA CAGACAATGA GAGATCCATT	1500
55	CCTAATGATG GTACATGCTT TCAGGAACAC AGTTCTTATG GCAGAAATTC TCTGGAAGAC	1560
	AATTCCTGGG TATTTCCAAG TCCTCCTAAA TCAAGTGAGA CAGCATTTGG GGAAACTAAA	1620
	ACTAAAACCT TGCCTTTACC CAACCTTCCA CCACTGCATT ACTTGATCA ACATAATCAG	1680
60	AACTGCCTTT ATAAGAATTA ATTTGGAAGA GATTCACGAT TTCACCATGA GGACACTTAT	1740

CTCTTTCAGT GGTCTCCCA AGAAATTATT TAACAACTG AANGGAGATT TTGATTAAAA 1800
 TTTTGCAGAG GTCTTCAGTA TCTATATTTG AACACACTGT ACAATAGTAC AAAAACCAAC 1860
 5 ATAGTTGGTT TTCTAGTATG AAAGAGCACC CTCTAGCTCC ATATTCTAAG AATCTGAAAT 1920
 ATGCTACTAT ACTAATTAAT AAGTAACTT AAGGTGTTTA AAAAAGCTCTG CCTTCTATAT 1980
 10 TAATGTAAA ATTTTGCCTC TCAGAAGAAT GGAATTGCAG ATTGTAGACG TGGTTTACA 2040
 AAATGTGAAA TGTCTAAATA TCTGTTTATA AAAATAAAAG GAAACATGT TTCTTCAAAT 2100
 TGCATAATGG AACAAATGGC AATGTGAGTA GGTACATTT CTGTTGTTAT AATGCGTAAA 2160
 15 GATATTGAAA ATATAATGAA ATAAAAGCAT CTTAGGTTAT ACCATCTTTA TATGCTATTG 2220
 CGTTTCAATA TTTAAGATTT AAAGTGATTT TTTGGTCACA GTGTTTGTGTT GATAAAATTT 2280
 20 TTTTAGAATT GAAGTTTGAA TTCTAAGACT TGAAACAACC TGATCACTGA AGCCAACCTT 2340
 GTCCAGCAC ATTCCTTAAG TCCTAATTGG GGAAAAAAA AAAAAAAAC TCGA 2394

25

(2) INFORMATION FOR SEQ ID NO: 96:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 672 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

AGTGCTCTGT TGCCAGGCT GGAGTGCCTT AGTGTAATGT CAGTCCACTG CAACCTCCAC 60
 CCCCAGGTTT AAGCAATTCT CATGCCTCAG CCTCCAAGT AGCTGAAATT ACTGGCATGC 120
 40 ACCACCACAC CCAGCTGATG TTTATTTATT TATTTATATA TTTATTTATT TTAGGTGTTT 180
 TTTTMTTTT TTTTGTAGAC GGAGTCTTGC TCTGTGCCC TGGGTGTGGT TACGTGGRAT 240
 45 TACCATYCTG GGTGACTCAC TGAAATGTAC TCMCAGTGAG TCATGCCTTC MAATGACATC 300
 TCAAGTTCTG CCTGCTTGA GATACATCTG GGGATCTTAA GGGGTGAGGG ACTACTCAAC 360
 AAGAAGGAAT TTAGCCTGTC TTTTAAATA AACGGCATTT CTMTTCTTA KAAAAATGGG 420
 50 AAATTCCTCA ATTCTCTAAT ACAGGGACAC TGAGATAACA AAGAGGAAAG TGTCTGGTTG 480
 GAGGTGGGA RGCCACCCTG GGTCTCTCC TACAAAAATG GAAAGAAAA GAACGGTGAR 540
 55 AAATCMAGCA AAGCACAARA AAKTTTCCCT TTGCTAAAAG GGAAAGATG CCCCMAATG 600
 CCCATAACA TGAAGTGGG ATAAGGAGGA RAATGTCTCT YCTTGGCACC CCCAAACAAA 660
 CGTTAATTAC CC 672
 60

(2) INFORMATION FOR SEQ ID NO: 97:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1419 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

15	TAAGAACAGA ACAGCAAGTA TGAACCACAT GGAACCTAAA ACATATGGGT GTGAAGTCCA	60
	CTTATGTAGA CAAAACCTAT AATTTCCTAAA CTGTTGTCTA GTATACAGTG ATCAGTTGCT	120
	CTCTGTTCAA GTCATTCCAC ACATTTCCCT ATTTTAGGCT ATTATAATAT AGAAAGAAAA	180
20	TGGGAAGCAT TAGTTGGAGC TAGAAAATGA ACTGTATATT ATTGCTATAT TTGCTAATAC	240
	CAACTATMTC AATAAGTGTT GTACCATATG TAGCATTAAT TATAAATAC ATAAAGAAT	300
	GTACAGAAAA TAGCTTTTAT TGAGTAATAT TACATMTCAT TTATACTGTA GCAATATATT	360
25	TGTAGGTATA CTCTGTAAGG GCTTTAAATA AAAGAGGTCC ATTAATACTT CCTTATAAAA	420
	ATTCTAGTCT GTTTCATTAC TGCCCAGATG TTTTAGAGAT AAATATTTAT GCAGAAGGTA	480
30	TTTTKGAAAG TCYCCYTTTG TCTGATAGAG TTTAACNAGA TATTTAAATT TAGTGCCYNA	540
	GAAATCCCAC AAGTCACGGT CTAAACACAC TTAGAATACT ACAGCATAAA TCTGTTAGCA	600
	TTANTTGCCA AATAAGACAG TTGGGATCCC AAACCCCAAG TCCTTGAGCA ATGTTTTTCC	660
35	TCAAAAAGCT GCTATNCCAA TGATATAGGA AAAWACATTG TGTTCCTCCTA AACACACTTT	720
	TCTTTTAAA TGTGCTTCAT TGTTTGATTT GGTCTGCCT AAATTCACA AGCTAGGCCA	780
40	ATGAAGGCTG AATCAAAGAC ATTTCATCCA CCAATATCAT GTGTAGATAT TATGTATAGA	840
	AAATAAAATA AATTATGGCT CTAACCTCTG TGTGCTGTT TATCTTGTTA TTTTCGGCG	900
	TTATACTAAT GNGTTTATTG AGAGCATTTT ACCTTCCAGA CTTCTCATGG CTAACCTTTG	960
45	GTCTGWATTT TGSTCCTTAG ATGKGAATAT TTCCTATTAG TYTGCTYCCT GCWACGCAAT	1020
	GACTGCATTT CTATCATMTC TCAGTTTGTT AGWATATGTG GATAGTATTC TACTGTATAA	1080
50	ATGATPGCAA AGTTTATCAA AAACAAATTA TTATATGTAG CTTTCTACA GTGCTTTGCT	1140
	AAACCATGTA GTACTAGTTA AGTSTTCCTT GAAAATAAAG ATACACTCTT ATAGGGGACA	1200
	GTTCTGTTC ACTCCCAGGA AACTTTTTTA AAAGATGACA CTGAATGTTT ATTGCACTTT	1260
55	AGTGCACTGA AGTGGCAATA AAACCTAACA TGAATCAAGG TTGTTTATGG CAGATGCATG	1320
	TGTTGCTTTA CAGAGTTTAG CAAAAGCTCT TAATTTTATG TCATACTGTA TTCTACTGAA	1380
60	TAATAAAGCT AACATTATTC AATAATAAAA TGGAAAAAA	1419

5 (2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1487 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

15 GCGACCGCGC CCCTTTCAGC TAGCTCGCTC GCTCGCTCTG CTTCCCTGCT GCCGGCTGCG 60
CATGGCKWIG GCGTTGGCGG CGCTGGCGGC GGTGAGCCG GCCTGCGCAG CCGGTACCAG 120
CAGTTGCAGA ATGAAGAAGA GTCTGGAGAA CCTGAACAGG CTGCAGGTGA TGCTCCTCCA 180
20 CCTTACAGCA GCATTTCTGC AGAGAGCGCA GTTTTCCACC TATTTCCCTG GATATTTTGA 240
TGGTCAGTAC TGGCTCTGGT GGGTGTTCCT TGTTTTAGGC TTTCTCCTGT TTCTCAGAGG 300
25 ATTTATCAAT TATGCAAAAG TTCGGAAGAT GCCAGAACT TTCTCAAATC TCCCCAGGAC 360
CAGAGTTCTC TTTATTTATT AAAGATGTTT TCTGGCAAAG GCCTTCCTGC ATTTATGAAT 420
TCTCTCTCAA GAAGCAAGAG AACACCTGCA GGAAGTGAAT CAAGATGCAG AACACAGAGG 480
30 AATAATCACC TGCTTTAAAA AAATAAAGTA CTGTTGAAAA GATCATTTCT CTCTATTTGT 540
TCCTAGGTGT AAAATTTTAA TAGTTAATGC AGAATTCTGT AATCATTGAA TCATTAGTGG 600
35 TTAATGTTTG AAAAAGCTCT TGCAATCAAG TCTGTGATGT ATTAATAATG CCTTATATAT 660
TGTTTGTAGT CATTTTAAGT AGCATGAGCC ATGTCCCTGT AGTCGGTAGG GGGCAGTCTT 720
GCTTTATTCA TCCTCCATCT CAAAATGAAC TTGGAATTAA ATATTGTAAG ATATGTATAA 780
40 TGCTGGCCAT TTAAAGGGG TTTTCTCAA AGTTAAACTT TTGTTATGAC TGTGTTTTTG 840
CACATAATCC ATATTTGCTG TTCAAGTTAA TCTAGAAATT TATCAATTC TGTATGAACA 900
45 CCTGGAAGCA AAATCATAGT GCAAAAATAC ATTTAAGGTG TGGTCAAAAA TAAGTCTTTA 960
ATTGGTAAAT AATAAGCATT AATTTTATAT AGCCTGTATT CACAATTCTG CGGTACCTTA 1020
TTGTACCTAA GGGATTCTAA AGGTGTTGTC ACTGTATAAA ACAGAAAGCA CTAGGATACA 1080
50 AATGAAGCTT AATTACTAAA ATGTAATTCT TGACACTCTT TCTATAATTA GCGTTCTTCA 1140
CCCCACCCC CACCCCACC CCCCTTATTT TCCTTTTGTC TCCTGGTGAT TAGGCCAAAG 1200
55 TCTGGGAGTA AGGAGAGGAT TAGGTACTTA GGAGCAAAGA AAGAAGTAGC TTGGAACTTT 1260
TGAGATGATC CCTAACATAC TGTACTACTT GCTTTTACAA TGTGTTAGCA GAAACCAGTG 1320
GGTTATAATG TAGAATGATG TGCTTTCTGC CCAAGTGGTA ATTCATCTTG GTTTGCTATG 1380
60

TTAAAACTGT AAATACAACA GAACATTAAT AAATATCTCT TGTGTAGCAC CTTTAAAAAA 1440
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAAN CCCGGGGGGG GGCCCCN 1487

5

(2) INFORMATION FOR SEQ ID NO: 99:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1653 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

GCGACCGCGC CCTTCAGCTA GCTCGCTCGC TCGCTCTGCT TCCCTGCTGC CGGCTGCGCA 60
20 TGGCTTNGGC GTTGGCGGCG CTGGCGGCGG CTCGAGCCGC CTGCGSAGCC GGTACCAGCA 120
GTTGCAGAAT GAAGAAGAGT CTGGAGAACC TGAACAGGCT GCAGGTGATG CTCCTCCACC 180
25 TTACAGCAGC ATTTCTGCAG AGAGCGCACA TNATTTTGAC TACAAGGATG AGTCTGGGTT 240
TCCAAAGCCC CCATCTTACA ATGTAGCTAC AACACTGCCC AGTTATGATG AAGCGGAGAG 300
GACCAAGGCT GAAGCTACTA TCCCTTTGGT TCCTGGGAGA GATGAGGATT TTGTGGGTCG 360
30 GGATGATTTT GATGATGCTG ACCAGCTGAG GATAGGAAAT GATGGGATTT TCATGTTAAC 420
TTTTTTCATG GCATTCCTCT TTAAGTGGAT TGGGTTTTTC CTGTCTTTTT GCCTGACCAC 480
35 TTCAGCTGCA GGAAGGTATG GGGCCATTTC AGGATTTGGT CTCTCTCTAA TTAAATGGAT 540
CCTGATTGTC AGGTTTTCCA CCTATTTCCC TGCATTTATG AATTCTCTCT CAAGAAGCAA 600
GAGAACACCT GCAGGAAGTG AATCAAGATG CAGAACACAG AGGAATAATC ACCTGCTTTA 660
40 AAAAAATAAA GTACTGTTGA AAAGATCATT TCTCTCTATT TGTTCCCTAGG TGTAATAATT 720
TAATAGTTAA TGCAGAATTC TGTAATCATT GAATCATTAG TGGTTAATGT TTGAAAAAGC 780
45 TCTTGCAATC AAGTCTGTGA TGTATTAATA ATGCCTTATA TATTGTTTGT AGTCATTTTA 840
AGTAGCATGA GCCATGTCCT TGTAGTCGGT AGGGGGCAGT CTTGCTTTAT TCATCCTCCA 900
TCTCAAAATG AACTTGGAAT TAAATATTGT AAGATATGTA TAATGCTGGC CATTTTAAAG 960
50 GGGTTTTCTC AAAAGTTAAA CTTTGTATAT GACTGTGTTT TTGCACATAA TCCATATTTG 1020
CTGTTCAAGT TAATCTAGAA ATTTATTCAA TTCTGTATGA ACACCTGGAA GCAAAATCAT 1080
55 AGTGCAAAAA TACATTTAAG GTGTGGTCAA AAATAAGTCT TTAATTGGTA AATAATAAGC 1140
ATTAATTTTT TATAGCCTGT ATTCACAATT CTGCGGTACC TTATGTACC TAAGGGATTC 1200
TAAAGGTGTT GTCAGTGTAT AAAACAGAAA GCACTAGGAT ACAAATGAAG CTTAATTACT 1260
60 AAAATGTAAT TCTTGACACT CTTTCTATAA TTAGCGTTCT TCACCCCCAC CCCCACCCCC 1320

ACCCCCCTTA TTTTCCTTTT GTCTCCTGGT GATTAGGCCA AAGTCTGGGA GTAAGGAGAG 1380
 GATTAGGTAC TTAGGAGCAA AGAAAGAAGT AGCTTGGAAC TTTTGAGATG ATCCCTAACA 1440
 5 TACTGTACTA CTGCTTTTCA CAATGTGTGA GCAGAAACCA GTGGGTTATA ATGTAGAATG 1500
 ATGTGCTTTC TGCCCAAGTG GTAATTCATC TTGGTTTGCT ATGTTAAAAC TGTAATAACA 1560
 10 ACAGAACATT AATAAATATC TCTTGTGTAG CACCTTTTAAW AAAAAAAAAA AAAAAAAAAA 1620
 AAAAAAAAAA AAAAAANCCCG GGGGGGGGCC CCN 1653

15

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 1145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

TTTTMTTTTT TTTTMTTTTT TTGACTGAAC TAAGTGCGTT TTTTATTAGA GAAAGCCAGA 60
 ATTACAAAAG ACTTCCCTTT TCTTGGGGTA TGGCTGTCTC AGCACAATAC TCAACATAAC 120
 30 TGCAGAACTG ATGTGGCTCA GGCACCCTGG TTTTAATTCC TTGAGGATCT GGCAATTGGC 180
 TTACGCAAAA GGTCAACATT TGAGGTCCTG CCTTACTAAT TATGTGCTGC CCAACAAC TA 240
 35 AATTTGTAAT TTGTTTTTCT CTAGTTTGAG CAGGGTCTGA ATTTTTTCAT TTATTCCTTT 300
 TTTTGCCAGC AGACAGACTT GAGTCTGTAA AGACAAGCAA ATACACTGAC AGAAGTTTAC 360
 CATAGTTTCT AAAATGTAAA AAAGAAAACC CCCAAAAGAC TCAAGAAAAT TAGACCACAA 420
 40 ATTTTGCAAT GTTCATTGTA GCACTATTGG TAATAAATA ACAAATGTTT GTGCATTTTT 480
 ATGTGAAGAT CCTTCTCGTA TTTCATTGGG AAAGATGAGC AAGAGGTCTG CTTCTTCAT 540
 45 TTTACTTCCC CTTCTGTTTT TGAAAGGCAG TTTCGCCAAG CTTAATGCAA GAATATCTGA 600
 CTGTTTAGAA GAAAGATATT GCCACAATCT CTGGATGGTT TTCCAGGGTT GTGTTATTAC 660
 TGAGCTTCAT CTTTCCAGAA TGAGCAAAAC ACTGTCCAGT CTTTGTACG ATTTTGTAAT 720
 50 AAATGTGTAC ATTTTMTTCA AATTTTTGGA CATCACATGA ATAAAGGTAT GTATGTACGA 780
 ATGTGTATAT ATTATATATA TGACATCTAT TTTGGAAAAT GTTTGCCCTG CTGTACCTCA 840
 55 TTTTAGGAG GTGTGCATGG ATGCAATATA TGAAAATGGG ACATTCTGGA ACTGCTGGTC 900
 AGGGGACTTT GTGCCCTGT GCACTAAAAG GGCCAGATTT TCAGCAGCCA AGGACATCCA 960
 TACCCAAGTG AATGTGATGG GACTTAAAAG AAGTGAAGT AGACAATTCA CTCTGGCTGT 1020
 60

TTGAACAGCA GCGTTTCATA GGAAGAGAAA AAAAGATCAA TCTTGTATTT TCTGACCACA 1080
TAAAGGCTTC TTCTCTTTGT AATAAAGTAG AAAAGCTCTC CTCAAAAAAA AAAAAAAAAA 1140
5 AAAAA 1145

10 (2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 734 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

20 TACCCGGCGG ATTCAGGAA GGTAAATTTA GTCCTATAAT TTTCAGCTTA ATTATAAACA 60
AAGGAACAAA TAAGTGGAAG GGCAGCTATT ACCATTCGCT TAGTCAAAAC ATTCGGTTAC 120
TGCCCTTTAA TACTCTCTA TCATCAGCAC TTCCACCATG TATTACAAGT CTTGACCCAT 180
25 CCCTGTCGTA ACTCCAGTAA AAGTTACTGT TACTAGAAAA TTTTATCAA TTAAGTGACA 240
AATAGTTTCT TTTTAAAGTA GTTCTTCCA TCTTTATTTCT GACTAGCTTC CAAAATGTGT 300
30 TCCCTTTTGT AATCGAGGTT TTTTGTGTTT GTTTGTGTTT CTGAAAAAAT CATACAACTT 360
TGTGCTTCTA TTGCTTTTGT GTGTTTGTGTT AAGCATGTCC CTGGCCCAA ATGGAAGAGG 420
AAATGTTTAA TTAATGCTTT TTAGTTTAAA TAAATGAAT CATTTATAAT AATCAGTGTT 480
35 AACAAATTAG TGACCCCTGG TAGGTTAAAG GTTGCATTAT TTATACTTGA GATTTTTTTC 540
CCCTAACTAT TCTGTTTTTT GTACTTTAAA ACTATGGGGG AAATATCACT GGTCTGTCAA 600
40 GAAACAGCAG TAATTATTAC TGAGTTAAAT TGAAAAGTCC AGTGACCAG GCATTTCTTA 660
TATAAATAAA ATTGGTGGTA CTAATGTGAA AAAAAAAAAA AAAAAAACT CGAGGGGGGC 720
CCGGTACCCT ATTA 734
45

50 (2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 713 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

60 CCGCGGGAAC GCTGTCCTGG CTGCCGNCAC CCGAACAGCC TGTCTGGTG CCGCGGCTCC 60

	CTGCCCCGCG CCCAGTCATG ACCCTGCGCC CCTCACTCCT CCCGCTCCAT CTGCTGCTGC	120
	TGCTGCTGCT CAGTGCGGCG GTGTGCCGGG CTGAGGCTGG GCTCGAAACC GAAAGTCCCG	180
5	TCCGGACCCT CCAAGTGGAG ACCCTGGTGG AGCCCCAGA ACCATGTGCC GAGCCCGCTG	240
	CTTTTGAGAGA CACGCTTCAC ATACACTACA CGGGAAGCTT GGTAGATGGA CGTATTATTG	300
	ACACCTCCCT GACCAGAGAC CCTCTGGTTA TAGAACTTGG CCAAAGCAG GTGATTCCAG	360
10	GTCTGGAGCA GAGTCTTCTC GACATGTGTG TGGGAGAGAA GCGAAGGGCA ATCATTCCCTT	420
	CTCACTTGGC CTATGGAAAA CGGGGATTTT CACCATCTGT CCCAGCGGAT GCAGTGGTGC	480
15	AGTATGACGT GGAGCTGATT GCACTAATCC GAGCCAACTA CTGGCTAAAG CTGGTGAAGG	540
	GCATTTTGCC TCTGGTAGGG ATGGCCATGG TGCCACCCTC CTGGGCCTCA TTGGGTATCA	600
	CCTATACAGA AAGGCCAATA GACCCAAAGT CTCCAAAAAG AAGCTCAAGG AAGAGAAACG	660
20	AAACAAGAGC AAAAAGAAAT AATAAATAAT AAATTTTAAA AACTTAAAA AAA	713
25	(2) INFORMATION FOR SEQ ID NO: 103:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1080 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:	
35	CCGATGTGGA CATCATCCTG TCTATCCCCA TGTTCTGCG CCTGTACCTG ATCGCCCGAG	60
	TCATGCTGCT GCACAGAAGC TCTTCACCGA TGCCTCGTCC CGCAGCATCG GGGCCCTCAA	120
40	CAAGATCAAC TTCAACACCC GCTTTGTCAT GAAGACGCTC ATGACCATCT GCCCTGGCAC	180
	TGTGCTGCTC TGTTTCAGCA TCTCTCTGTG GATCATGTCT GCCTGGACCG TCCGTGTCTG	240
	TGAAAGTCCT GAATCACCAG CCCAGCCTTC TGGCTCATCA CTTCTGCTT GGTACCATGA	300
45	CCAGCAGGAC GTAAC TAGTA ACTTCTGGG TGCCATGTGG CTCATCTCCA TCACATTCTT	360
	TTCCATTGGT TATGGGGACA TGGTGCCCCA CACATACTGT GGGAAAGGTG TCTGTCTCCT	420
50	CACTGGCATC ATGGGTGCAG GCTGCACTGC CTTGTGGTG GCCGTGGTGG CCCGAAAGCT	480
	GGAACTCACC AAAGCGGAGA AGCACGTTCA TAANTTCATG ATGGACACTC AGCTACCAA	540
	GCGGATCAAG AATGYTGCAG CCAATGTCCT TSGGAAACA TGGTTAATCT ATAAACACAC	600
55	AAAGYTGATA AAGAAGATTG ACCATGCCAA AGTGAGGAAC ACCAGAGGAA GTTCYTCCAA	660
	GTATCCACCA GTTGAGGAGC GTCAAGATGG AACAGAGGAA GCTGAGTGAC CAAGCCAACA	720
60	NTCTGGTGGA CCTTTCCAAG ATGCAGAAATG TCMTGTATGA CTTAATCACA GAACTCAATG	780

ACCGGAGCGA AGACCTGGAG AAGCAGATTG GCAGCCTGGA GTCGAAGCTG GAGCATCTCA 840
5 CCGCCAGCTT CAACTCCCTG CCGCTGCTCA TCGCCGACAC CCTGCGCCAG CAGCAGCAGC 900
AGCTCCTGTC TGCCATCATC GAGGCCCGGG GTGTCAGCGT GGCAGTGGGC ACCACCCACA 960
CCCCAATCTC CGATAGCCCC ATTGGGGTCA GCTCCACCTC CTTCCTCGACC CCGTACACAA 1020
10 GTTCAAGCAG TTGCTAAATA AATCTCCCCA CTCCAGAAGC ATTAAAAAAA AAAAAAAAAA 1080

15 (2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 489 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

25 GGCACGAGAG GCTTTGAAGC ATTTTGTGCT GTGCTCCCTG ATCTTCAGGT CACCACCATG 60
AAGTTCCTTAG CAGTCCCTGGT ACTCTTGGGA GTTTCATCTT TTCTGGTCTC TGCCCAGAAT 120
30 CCGACAACAG CTGCTCCAGC TGACACGTAT CCAGCTACTG GTECTGCTGA TGATGAAGCC 180
CCTGATGCTG AAACCACTGC TGCTGCAACC ACTGCGACCA CTGCTGCTCC TACCACTGCA 240
ACCACCGCTG CTTCTACCAC TGCTCGTAAA GACATTCCAG TTTTACCCAA ATGGGTGGG 300
35 GATCTCCCGA ATGGTAGAGT GTGTCCCTGA GATGGAATCA GCTTGAGTCT TCTGCAATTG 360
GTCACAATA TTATGCTTC CTGTGATTTC ATCCAACCTAC TTACCTTGCC TACGATATCC 420
40 CCTTTATCTC TAATCAGTTT ATTTCTTTTC AAATAAAAAA TAACTATGAG CAACAAAAAA 480
AAAAAAAAA 489

45

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 640 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

55 GCGGTCGCCG CTGTTGTTGT GGTCCCCATG GAGCTGCCGT AGCGGACCCA GCACAGCCAG 60
GAGCGTCCCG GATGAGCTCA GCCGCGGCCG ACCACTGGGC GTGGTTGCTG GTGCTCAGCT 120
60 TCGTGTGTTG ATGCAATGTT CTTAGGATCC TCCTCCCGTC CTTCTCATCC TTCATGTCCA 180

5 GGGTGCTGCA GAAGGACGCG GAGCAGGAGT CACAGATGAG AGCGGAGATC CAGGACATGA 240
 AGCAGGAGCT CTCCACAGTC AACATGATGG ACGAGTTTGC CAGATATGCC AGGCTGGAAA 300
 GAAAGATCAA CAAGATGACG GATAAGCTCA AAACCCATGT GAAAGCTCGG ACAGCTCAAT 360
 TAGCCAAGAT AAAATGGGTG ATAAGTGTCTG CTTTCTACGT ATTGCAGGCT GCCCTGATGA 420
 10 TCTCACTCAT TTGGAAGTAT TATTCTGTCC CTGTGGCTGT CGTGCCGAGT AAATGGATAA 480
 CCCTYTAGAC CGCCTGGTAG CCTTTCYAY TAGAGTAGCA GGTGGTGTG GAATTACTGT 540
 TGGATTTART CTGTACAAAT TGTCTATTG TGCTTCACCG TYCASTGAAC AGGAGGTGGT 600
 15 ACAGCCGGAG TTAACAAACG TTTCCNTTCC AGTTTAAAT 640

20

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1529 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

30 GGGCACNAGA TGGAGCTGCC GTAGCGGACC CAGCACAGCC AGGAGCGTCC GGGATGAGCT 60
 CAGCCGCGGC CGACCACTGG GCGTGGTTCG TGGTGCTCAG CTTCGTGTTT GGATGCAATG 120
 35 TTCTTAGGAT CCTCTCCCG TCCTTCTCAT CCTTCATGTC CAGGGTGCTG CAGAAGGACG 180
 CGGACAGGAG TCACAGATGA GAGCGGAGAT CCAGGACATG AAGCAGGAGC TCTCCACAGT 240
 CAACATGATG GACGAGTTTG CCAGATATGC CAGGCTGGAA AGAAAGATCA ACAAGATGAC 300
 40 GGATAAGCTC AAAACCCATG TGAAAGCTCG GACAGCTCAA TTAGCCAAGA TAAATGGGT 360
 GATAAGTGTC GCTTCTACG TATTGCAGGC TGCCCTGATG ATCTCACTCA TTTGGAAGTA 420
 45 TTATTCTGTC CCTGTGGCTG TCGTGCCGAG TAAATGGATA ACCCCTCTAG ACCGCTGGT 480
 AGCCTTTCCT ACTAGAGTAG CAGGTGGTGT TGAATTACC TGTGGATTT TAGTCTGTAA 540
 CAAAGTTGTC GCTATTGTGC TTCATCCGTT CAGCTGAACA GGAGGATGGA TACAGCCGCG 600
 50 AGTAAAAAAA CGGATTTCTT CTCTCTAGCT TAAATCTGA TTTACACTGT TTTGTTTTTT 660
 AAGAAACAAA AGTGCATAGT TTAGATTTTT TTTTGTGTA ATATGTTTGT TCTTGACTT 720
 55 TATGAGATAG TCTTATAAGA ATCAGATTTT TCTACACCTG TCATTGAGCC AAGAAAGTCC 780
 AGTTTATGAC ACGTATGTAC TAGTGAACAC CGTCTCGAT CTGTACGAAA TGTGAAATGT 840
 TTAGGGACAT CTCCATGCTG TCACTTGTGA TTTGCCCTCT TATGTATTTT GGTCAATATG 900
 60

	CCAACTGGAA AGTCAAAATTTTCTAACAAC TTTAAGTAAG TTCTTTGAAG ACTTAGTGCT	960
	GTTTTTAATC CAGTTTAGAA AGTAACTTAA TTTTAATACC RCTACTAAAA ATTGAAAAAT	1020
5	TTCTTCTTTA ATCACATTCA ATATGTTAA AAGAACAACA CTAATTGACA TTGCGTGGGC	1080
	TTTTTCTCCC TTGTTTAAA ATGTCATTG TTGAGCAAGA GTTGATAGT ATTATCTACT	1140
10	TACTTGAGGC TGTTAATTTT TCATTACAGT GTTTTGTAAG TGTATCCACG AGACCATGAT	1200
	GCATTGTTTT GTGCTCAACT TGTGTTTGT ATTTAAAGCA TTTTGAATGA AGTGTATTTT	1260
	ATAAGCATTT AATATTTATG CTCTTTAGAA TGGAACACAG AAAACAAACC TTATAAGTCC	1320
15	TGATTAATCT GAACCAATAA CCTGTGTGGC CTACAAAGTA TAATTCTATT AAATGTTCTT	1380
	TAAACACTT TTTTCTAATT AAAATCTTTG CAAATGCTTG TGTAACCTCC TGCCTTACAG	1440
20	CTACTGTGTT GCTGTGAGCC ACCCGCAACT GACAAGTGGC TGTAACTGA GTCACCATAT	1500
	CCCAGTAAAG CTGAATTTTC TCACTAAAA	1529

25

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2435 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

35

	ATGAAGGGTC GTTGGTGGGA AAGATGGCGG CGACTCTGGG ACCCCTTGGT CGTGGCAGCA	60
	GTGGCGRCGA TGTGTCGG CTCGGGATGG GTCCAGGATG TTAATCTTTC TTCTTTTGTT	120
40	GGGGTCTGGG CAGGGGCCAC AGCAAGTCGG GCGGGTCAA ACGTTCGAGT ACTTGAAACG	180
	GGAGCACTCG CTGTCGAAGC CCTACCAGGG TGTGGGCACA GGCAGTTCCT CACTGTGGAA	240
45	TCTGATGGGC AATGCCATGG TGATGACCCA GTATATCCGC CTTACCCAG ATATGCAAAG	300
	TAAACAGGGT GCCTGTGGA ACCGGGTGCC ATGTTTCCTG AGAGACTGGG AGTTGCAGGT	360
	GCACTTCAAA ATCCATGGAC AAGGAAAGAA GAATCTGCAT GGGGATGGCT TGGCAATCTG	420
50	GTACACAAAG GRWTCGGATG CAGCCAGGGC CTGTNTTTGG GAAACATGGA CAAATTTGTG	480
	GGGCTGGGAG TATTTGTAGA CACCTACCCC AATGAGGAGA AGCAGCAAGA GCGGGTATTC	540
55	CCCTRCMTCT CAGCCATGGT GAACAACGGC TCCCTCAGCT ATGATCATGA GCGGGATGGG	600
	CGGCCTACAG AGCTGGGAGG CTGCASAGCC ATGTGCCGA ATCTTCATTA CGACACCTTC	660
	CTGGTGATTC GCTACGTCAA GAGGCATTTT ACGATAATGA TGGATATTGA TGGCAAGCAT	720
60	GAGTGGAGGG ACTGCATTGA AGTGCCCGGA GTCCGCCTGC CCCGCGGCTA CTACTTCGGC	780

	ACCTCCTCCA TCACTGGGGA TCTCTCAGAT AATCATGATG TCATTTCCTT GAAGTTGTTT	840
	GAAC TGACAG TGGAGAGAAC CCCAGAAGAG GAAAAGCTCC ATCGAGATGT GTTCTTGCCC	900
5	TCAGTGGACA ATATGAAGCT GCCTGAGATG ACAGCTCCAC TGCCGCCCCCT GAGTGGCCTG	960
	GCCCTCTTCC TCATCGTCTT TTTCTCCCTG GGTGTTTTCT GTATTGCCA TAGTCATTGG	1020
10	TATCATACTC TACAACAAAT GGCAGGAACA GAGCCGAAAG CGCTTCTACT GAGCCCTCCT	1080
	GCTGCCACCA CTTTTGTGAC TGTCACCCAT GAGGTATGGA AGGAGCAGGC ACTGGCCTGA	1140
	GCATGCAGCC TGGAGAGTGT TCTTGTCTCT AGCAGCTGGT TGGGGACTAT ATTCTGTAC	1200
15	TGGAGTTTGG AATGCAGGGA CCCCGCATTC CCATGGTTGT GCATGGGGAC ATCTAACTCT	1260
	GGTCTGGGAA GCCACCCACC CCAGGGCAAT GCTGCTGTGA TGTGCCTTTC CCTGCAGTCC	1320
20	TTCCATGTGG GAGCAGAGGT GTGAAGAGAA TTTACGTGGT TGTGATGCCA AAATCACAGA	1380
	ACAGAATTTC ATAGCCCAGG CTGCCGTGTT GTTTGACTCA GAAGGCCCTT CTACTTCAGT	1440
	TTTGAATCCA CAAAGAATTA AAACTGGTA ACACCACAGG CTTTCTGACC ATCCATTCTG	1500
25	TGGGTTTTGC ATTTGACCCA ACCCTCTGCC TACCTGAGGA GCTTTCTTTG GAAACCAGGA	1560
	TGGAACTTC TTCCCTGCCT TACCTTCCTT TCACTCCATT CATGTCTCTC TCTGTGTGCA	1620
30	ACCTGAGCTG GGAAAGGCAT TTGGATGCCT CTCTGTTGGG GCCTGGGGCT GCAGAACACA	1680
	CCTGCGTTTC ACTGGCCTTC ATTAGGTGGC CCTAGGGAGA TGGCTTCTTG CTTTGATCA	1740
	CTGTTCCTTA GCATGGGTCT TGGGTCTATT GGCATGTCCA TGGCCTTCCC AATCAAGTCT	1800
35	CTTCAGGCCC TCAGTGAAGT TTGGCTAAAG GTTGGTGTAA AAATCAAGAG AAGCCTGGAA	1860
	GACATCATGG ATGCCATGGA TTAGCTGTGC AACTGACCAG CTCCAGGTTT GATCAAACCA	1920
40	AAAGCAACAT TTGTCATGTG GTCTGACCAT GTGGAGATGT TTCTGGACTT GCTAGAGCCT	1980
	GCTTAGCTGC ATGTTTTGTA GTTACGATTT TTGGAATCCC ACTTTGAGTG CTGAAAGTGT	2040
	AAGGAAGCTT TCTTCTTACA CCTTGGGCTT GGATATTGCC CAGAGAAGAA ATTTGGCTTT	2100
45	TTTTTTNCTT AATGGACAAG AGACAGTTGC TGTCTCATG TTCCAAGTCT GAGAGCAACA	2160
	GACCTCATC ATCTGTGCCT GGAAGAGTTC ACTGTCATTG AGCAGCACAG CCTGAGTGCT	2220
50	GGCTCTGTC AACCTTATT CCACTGCCTT ATTTGACAAG GGGTTACATG CTGCTCACCT	2280
	TACTGCCCTG GGATTAAATC AGTTACAGGC CAGAGTCTCC TTGGAGGGCC TGGAACTCTG	2340
	AGTCCTCCTA TGAACCTCTG TAGCCTAAAT GAAATCTTA AAATCACCGA TGGAAACCAA	2400
55	AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAN	2435
60		

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 805 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

10 ATGAAACTTA AGAATTGAAT TGGAAAGACT TCTCAAAGAG AATTGTATGT AACGATGTTG 60
TATTGATTTT TAAGAAAGTA ATTTAATTTG TAAAACTTCT GCTCGTTTAC ACTGCACATT 120
15 GAATACAGGT AACTAATTGG AAGGAGAGGG GAGGTCACTC TTTTGATGGT GGCCCTGAAC 180
CTCATCTCTGG TTCCCTGCTG CGCTGCTTGG TGTGACCCAC GGAGGATCCA CTCCCAGGAT 240
20 GACGTGCTCC GTAGCTCTGC TGCTGATACT GGGTCTGCGA TGCAGCGGCG TGAGGCCTGG 300
GCTGGTTGGA GAAGGTCACA ACCCTTCTCT GTTGGTCTGC CTTCTGCTGA AAGACTCGAG 360
AACCAACCAG GGAAGCTGTC CTGGAGGTCC CTGGTCCGAG AGGGACATAG AATCTGTGAC 420
25 CTCTGACAAC TGTGAAGCCA CCCTGGGCTA CAGAAACCAC AGTCTTCCCA GCAATTATTA 480
CAATCTTGA ATTCCTTGGG GATTTTTTAC TGCCCTTTCA AAGCACTTAA GTGTTAGATC 540
TAACGTGTTT CAGTGTCTGT CTGAGGTGAC TTAAAAATC AGAACAAAAC TTCTATTATC 600
30 CAGAGTCATG GGAGAGTACA CCCTTTCCAG GAATAATGTT TTGGGAAACA CTGAAATGAA 660
ATCTTCCCAG TATTATAAAT TGTGTATTTA AAAAAAGAA ACTTTTCTGA ATGCCTACTG 720
35 GCGGTGTATA CCAGGCAGTG TGCCAGTTTA AAAAGATGAA AAAGAATAAA AACTTTTGAG 780
GAACAAAAAA AAAAAAAAAA AAATT 805

40

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

50 GGCACGAGAG GCGCCAGTCG CAGGTGTGCT GCTGAGGCGT GAGAATGGCG TCCCGCGGCC 60
GGCGTCCGGA GCATGGCGGA CCCCAGAGC TGTMTTATGA CGAGACAGAA GCCCGGAAAT 120
55 ACGTTCGCAA CTCACGATG ATTGATATCC AGACCAGGAT GGCTGGGCGA GCATTGGAGC 180
TTCTTTATCT GCCAGAGAAT AAGCCCTGTT ACCTGCTGGA TATTGGCTGT GGCCTGGGC 240
60 TGAGTGGAAG TTATCTGTCA GATGAAGGGC ACTATTGGGT GGGCCTGGAT ATCAGCCCTG 300

5 CCATGCTGGA TGAGGCTGTG GACCGAGAGA TAGAGGGAGA CCTGCTGCTG GGGGATATGG 360
 GCCAGGGCAT CCCATTCAAG CCAGGCACAT TTGATGGTTG CATCAGCATT TCTGCTGTGC 420
 AGTGCTCTG TAATGCTAAC AAGAAGTCTG AAAACCCTGC CAAGCGCCTG TACTGCTTTT 480
 TTGCTTCTCT TTTTCTGTCT CTCGTCCGGG GATCCCAGGC TGTCTGCAG CTGTACCCTG 540
 10 AGAACTCAGA GCAGTTGGAG CTGATCACAA CCCAGGCCAC AAAGGCAGGC TTCTCCGGTG 600
 GCATGGTGGT AGACTACCCT AACAGTGCCA AAGCAAAGAA ATTCTACCTC TGCTTGTMTT 660
 CTGGGCCTTC GACCTTTATA CCAGAGGGGC TGAGTGAAAA TCAGGATGAA GTTGAACCCA 720
 15 GGGAGTCTGT GTTCACCAAT GAGAGGTTCC CATTAAAGAT GTCGAGGCGG GGAATGGTGA 780
 GGAAGAGTCG GGCATGGGTG CTGGAGAAGA AGGAGCGGCA CAGGCGCCAG GGCAGGGAAG 840
 20 TCAGACCTGA CACCCAGTAC ACCGGCCGCA AGCGCAAGCC CCGCTTCTAA GTCACCACGC 900
 GGTTCCTGAA AGGCACTTGC CTCTGCACTT TTCTATATTG TTCAGCTGAC AAAGTAGTAT 960
 TTTAGAAAAG TTCTAAAGTT ATAAAAATGT TTTCTGCACT AAAAAAAAAG TTCTCTGGGC 1020
 25 CGGGCGTGGT GGCTCACANC TGTAATCCCA GCACCTTGGG AGGCTGAGGT GGGAGGATCA 1080
 TTTGAGGCCA GGAGTTTGAG ACCTGCCTGG GCAACATAAT GAACTTCCT TTCCAGGGAG 1140
 30 AAAAAAAAAA AAAAAAAAAA ACTCGA 1166

35 (2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 586 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

45 AGAGCGGACG AAGCTGGATA ACAGGGGACC GATGATGTGG CGACCATCAG TTCTGCTGCT 60
 TCTGTTGCTA CTGAGGCACG GGGCCCAGGG GAAGCCATCC CCAGACGCAG GCCCTCATGG 120
 CCAGGGGAGG GTGCACCAGG CGGCCCCCCT GAGCGACGCT CCCCATGATG ACGCCCACGG 180
 50 GAACTTCCAG TACGACCATG AGGCTTTCCT GGGACGGGAA GTGGCCAAGG AATTCGACCA 240
 ACTCACCCCA GAGGAAAGCC AGGCCCGTCT GGGGCGGATC GTGGACCGCA TGGACCGCGC 300
 55 GGGGGACGGC GACGGCTGGG TGTCGCTGGC CGAGCTTCGC GCGTGATCG CGCACACGCA 360
 GCAGCGGCAC ATACGGGACT CGGTGAGCGC GGCCTGGGAC ACGTACGACA CGGACCGCGA 420
 CGGGCGTGTG GGTGGGAGG AGCTGCGCAA CGYACCTAT GGCCACTASG SGCCCCGRTGA 480
 60

AGAATTTTCAT GACGTGGAGG ATGCAGAGAC YTACAAAAAG ATGCTGGYTC GGGACGAGCG 540
GCGTTTCCGG GTGGCCGACC AGGATGGGGA CTCGATGGCC ACTCGA 586

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(2) INFORMATION FOR SEQ ID NO: 111:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1134 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

ACCCATTGAG CAGAAGGAGG CCAGGTGGGA AAGCTCCTGG GAAGAGCAGC CAGACTGGAC 60
20 ACTGGGCTGC TTGAGTCTCG AGTCACAATT CAGAATTCCT GGGCTCCCTG GGTGCATTCT 120
ATCAFTCCAG TTGAAAGTTT GCTTCCTTCC AGTCATGTGG CTCTTCATTC TACTCTCCTT 180
25 GGCTCTCATT TCAGATGCCA TGGTCATGGA TGAAAAGGTC AAGAGAAGTT TGTGCTGGAC 240
ACGGCTTCTG CCATCTGCAA CTACAATGCC CAYTACAAGA ATCACCCTAA ATACTGGTGC 300
CGAGGYTATT TCCGTGAYTA CTGCAACATC ATCGCCTTCT CCCCTAACAG CACCAATCAT 360
30 GTGGCCCTGA AGGACACAGG GAACCAGCTC ATTGTCACTA TGTCTGCCT GAACAAANAA 420
GACACGGGCT GGTACTGGTG TGGCATCCAR CGGGACTTTG CMAGGGATGA CATGGATTTT 480
ACAGAGCTGA TTGTAAGTGA CGACAAAGGA ACCCTGGCCA ATGACTTTTG GTCTGGGAAA 540
35 GACCTATCAG GCAACAAAAC CAGAAGCTGC AAGGCTCCCA AAGTTGTCCG CAAGCTGACC 600
GCTCCAGGAC GTCCATTCTC ATCATTTGCA TACTGATCAC GGGTTTGGGA ATCATCTCTG 660
40 TAATCAGTCA TTTGACCAAA AGGAGGAGAA GTCAAAGGAA TAGAAGGGTA GGCAACACTT 720
TGAAGCCCTT CTCGCGTGTC CTGACTCCAA AGGAAATGGC TCCTACTGAA CAGATGTGAC 780
TGAAGWTTTT TTTAATTTAG TTNCATAAAG TGATGNCTAC AACAGAWTAA TCACCCATGA 840
45 CAACTGGCCC CACACCTCAG AGACTGATTC TGATCTCCCA GGAATTCTGA AGGACCCTCT 900
ATCCTTGACA ACAATCATTT GCAGCCAGGT AGCAACGGCR GTAGTCAGAG GAGCTATGAT 960
50 AGACCACACC CAAGCAAGGC TGCCCTCAA TAACATCTCA AGATCTTAGT TCTTATGCAT 1020
TCCATCAGTC AGAAGTGAAG AAGAGGTGGA GAATCTKGAT TGGGGACCAG GAAATCACTT 1080
55 GTATTTTGTT AGCCAATAAA TTCCTAGCCA GTGTGAATG AAAAAAAAAA AAAA 1134

60

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

10 CACTTTAAAG CTC TGCTGAG GGAGTTCGGA GCCCAGGCTT TCAGGCGACC TCTGCCCTCC 60
 CTGCCTCTCC TCACCCTCCC TCTCTTCCTG CAGGGCCTGG GAAGGGCTTT GAGGGAGCCT 120
 GGGAGCCATG TGAAGAGGGG CAGCCCTGGG CTGTCCACACA GTTTAGATCC AGTTGGAGGT 180
 15 TCTCCCTGGC TCCTGCAGGC CTGCGGGGAT CTCTCCCCAC TTCAGGCCTC CGGCAGCTGC 240
 CTGCCCTCTT GTCTGTGCTT CAGCCCTGCA CAAAAGCAGC TTGGTGACAC CACTCAGCCA 300
 CCCAGAGTAC GTGTTTACAG GCTTTCCAGA TCACCTTCCT GTGGGTGAA CGTAATGAGG 360
 20 CGGGGCTGGT CCTTGGAATT TCCCCTGGAA AATGGTAACA GACTCCATCC TTGACCCGGG 420
 GATGAGCATG AAGGCATGTG CCCAAAGGCA GAGGCCACCG TGGTAGGAAT TCCACCAAGG 480
 25 CCAGAAGGGA AAAAGGAAGA ACCCACCCTG TCTGGCTGTG CGGGCCCTGG GGAGGGTCGT 540
 GAGTGCAGCC CCTCTCTACT TCTGTGCCTT TGTAACACGT GTAGATAACC GCAGTGGTTG 600
 GCTGAGCCAA GAACTCTCCT AAATCAGTGG CTTTCTCCCC ACCCCTTGCT GGGGAGTCAT 660
 30 TTTTAAAAAA ATCTGTGGGA TATAAAATTG GCCTCCTGCT GCTTCAGCCT ACCTCTCCCT 720
 CTGCTGACTT AATGTCGTGA TTCTGTTTCT TCAGATATTT AAGGCTGTTA GGTGTGTGA 780
 35 GCCTTGAAGT GTGTGTGTGT GTCCCAGCGA CTGTCCACTG TCCAGGAGAT GCATGTCTTT 840
 GTATTGGAGA TATTCTGTGA ACTCATCTCT TGGTGCTCA CGATTGCCAT GGCCATAGGG 900
 CCACAGTGCC GTATCTGCTG CAGACATGAT TGTTCCTTGT TCTAGAGGTT TTC'TTGTTTT 960
 40 CGAATCTTGC CTGATGAATC CAGCCAGACC AAGGGGCCTA GATTTGACCT CTGTCTGGG 1020
 CTCTGGGCC AGGTGCAGGA ACATCTGAGG CCACTCTGCT GGCCACCTCC AGTGGGTGCT 1080
 45 GACCACAGGA TGGGCTTTGT TTACACTCAT TTTCACCCTG ATTCTTGCCC CCACTTTCAT 1140
 AAAAGAACT TCAAAATGCT GACGCTTTGG AGAGTAAGAA AATCAATCTT GGCTGGGCAC 1200
 GGTGGCTCCT GCCTGTGATC CTAGACTTT GGGAGGCTGA AGCTGAAGGA TCACTTGAGC 1260
 50 TCAGGAGTTG GAGACCAACC CTGGCAACAT AACAAGACCC TGTCTCTACA AAAAAAAAAA 1320
 AAAAAAACT CGA 1333

55

(2) INFORMATION FOR SEQ ID NO: 113:

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1015 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

	GGCACGAGCG GCACGAGCGG CACGAGGTGA CTTCAAGTGT CGGATCTTTT CAGCCTACAT	60
10	CAAGGAGGTG GAGGAACGGC CGGCACCCAC CCCGTGGGCT CCAAGATGCC CT'TGGGGAA	120
	CTGATGTTTC AATCCAGCAG TAGCTGCGGC TGGGTACATG GCGTCTGTTT CTCAGCCAGC	180
15	GGGAGCCGCG TGGCCTGGGT AAGCCACGAC AGCACCGTCT GCCTGGCTGA TGCCGACAAG	240
	AAGATGGCCG TCGCGACTCT GGCTCTGAA AACTACCAC TGCTGGCGCT GACCTTCATC	300
	ACAGACAACA GCCTGGTGGC AGCGGGCCAC GACTGCTTCC CGGTGCTGTT CACCTATGAC	360
20	CCCCCGCGG GGATGCTGAG CTTCCGCGGG CGGCTGGACG TTCCTAAGCA GAGCTCGCAG	420
	CTGGGCTTGA CGGCCCGCGA GCGCTTCCAG AACCTGGACA AGAAGGCGAG CTCCGAGGGT	480
25	GGCACGGCTG CGGGCGCGGG CCTAGACTCG CTGCACAAGA ACAGCGTCAG CCAGATCTCG	540
	GTGCTCAGCG GCGGCAAGGC CAAGTGCTCG CAGTTCTGCA CCACTGGCAT GGATGGCGGC	600
	ATGAGTATCT GGGATGTGAA GAGCTTGGAG TCAGCCTTGA AGGACCTCAA GATCAAATGA	660
30	CCTGTGAGGA ATATGTTGCC TTCATCCTAG CTGCTGGGGA AGCGGGGAGA GGGGTCAGGG	720
	AGGCTAATGG TTGCTTTGCT GAATGTTTCT GGGGTACCAA TACGAGTTCC CATAGGGGCT	780
35	GCTCCCTCAA AAAGGGAGGG GACAGATGGG GAGCTTTTCT TACCTATTCA AGGAATACGT	840
	GCCTTTTCT TAAATGCTTT CATTTATTGA AAAAAAAAAA AAATGCCCCC AAAGCACTAT	900
	GCTGGTCATG AACTGCTTCA AAATGTGGAG GTAATAAAAT GCAACTGTGT AAAAAAAAAA	960
40	AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AACNC	1015

45

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1076 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

55	GGCACGAGGG GAAAGCCATG CTCCAGGAC TCCTTCCTTG CAGCCTTAAA TCGGTCTGTA	60
	CGGAAAATTC CGCGCCTTAG AAACCCACGC TTGGGTGTAA CTTATTATTG TTCTTCCTGA	120
60	CCTACTTCCT GTTTATCACT TCCGGGTTCA TCATTTTGGC ATTTCGGTGA TCGGGTTGGA	180

ACTATTGAAG CCCGCTTTCA GGTTCTTTTC CCCATTTTCC CTTTGAAAGG AAGACTTCTG 240
 GCTTCTCCTA AATCTCCGTT CTCTGGGTAA GGGGAGTCCA AGCCTCTGTC ATGAGGAACG 300
 5 GAAATGCGAG GGCCTCGGGT GTTACTCTAA AATCCGCCCT CAGCTTGCAC GCCGGAAGCT 360
 GCGATTCCCTG CAGCGGAAGA GGCCTGATCT GGCCTTCGAC TCGCTATGTC CACTAACAAT 420
 10 ATGTCGGACC CACGGAGGCC GAACAAAGTG CTGAGGTACA AGCCCCCGCC GAGCGAATGT 480
 AACCCGGCCT TGGACGACCC GACGCCGAC TACATGAACC TGCTGGGCAT GATCTTCAGC 540
 ATGTGCGGCC TCATGCTTAA GCTGAAGTGG TGTGCTTGGG TCGCTGTCTA CTGCTCCTTC 600
 15 ATCAGCTTTG CCAACTCTCG GAGCTCGGAG GACACGAAGC AAATGATGAG TAGCTTCATG 660
 CTGTCCATCT CTGCCGTGGT GATGTCCTAT CTGCAGAAIC CTCAGCCCAT GACGCCCCCA 720
 TGGTGATACC AGCCTAGAAG GGTCACATTT TGGACCCTGT CTATCCACTA GGCCTGGGCT 780
 20 TTGGCTGCTA AACCTGCTGC CTTGAGCTGC CATCTGGAC TTCCCTGAAT GAGGCCGTCT 840
 CGGTGCCCCC AGCTGGATAG AGGGAACCTG GCCCTTTCCT AGGGAACACC CTAGGCTTAC 900
 25 CCCTCCTGCC TCCCTTCCCC TGCCTGCTGC TGGGGGAGAT GCTGTCCATG TTTCTAGGGG 960
 TATTCAATTTG CTTTCTCGTT GAAACCTGTT GTTAATAAAG TTTTCTACTC TGAAAAAANA 1020
 AAAAAAANA RAAACNCGN GGGGGGGCCC GGAACCAAT TCSCCGGATA GTGAGT 1076
 30

(2) INFORMATION FOR SEQ ID NO: 115:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

CCGCTGCTGA TAACTATGGC ATCCCCCGGG CCTGCAGGAA TTCGGCACGG AGCTACGGCG 60
 45 CCGCCTGGCT CTGCTGNCA CCTGCAGGCT CGTCGCGGGT GGAGCCCACC CAAGACATCA 120
 GCATCAGCGA CCAGCTGGGG GGCCAGGACG TGCCCGTGTT CCGGAACCTG TCCCTGCTGG 180
 50 TGGTGGGTGT CGGCGCCGTG TTCTCACTGC TATTCACCT GGGCACCCGG GAGAGGCGCC 240
 GGCCGCATGC GGASGAGCCA GGCGAGCACA CCCCCTGTT GGCCCTGCC ACGGCCGAGC 300
 CCCTGCTGCT CTGGAAGCAC TGGCTCCGGG AGCSGGCTTT CTACCAGGTG GGCATACTGT 360
 55 ACATGACCAC CAGGCTCATC GTGAACCTGT CCCAGACCTA CATGGCCATG TACCTCACCT 420
 ACTCGCTCCA CTGCCCCAAG AAGTTCATCG CGACCATTC CCTGGTGATG TACCTCAGCG 480
 60 GCTTCTTGTC CTCCTTCCTC ATGAAGCCCA TCAACAAGTG CATGGGAGG AACATGACCT 540

	ACTTCTCAGG CCTCCTGGTG ATCCTGGCCT TTGCCGCCTG GGTGGCGCTG GCGGAGGGAC	600
5	TGGGTGTGGC CGTGACGCA GCGGCTGTGC TGCTGGGTGC TGGCTGTGCC ACCATCCTCG	660
	TCACCTCGCT GGCCATGACG GCCGACCTCA TCGGTCCCCA CACGAACAGC GGAGCKTTCTG	720
	TGTACGGCTC CATGAGCTTC TTGGATAAGG TGGCCAATGG GCTGGCAGTC ATGGCCATCC	780
10	AGAGCCTGCA CCCTTGCCCC TCAGAGCTCT GCTGCAGGGC CTGCGTGAGC TTTTACCACT	840
	GGGCGATGGT GGCTGTGACG GGCGGCGTGG GCGTGCCGC TGCCCTGTGT CTCTGTAGCC	900
15	TCCTGCTGTG GCCGACCCGC CTGCGACGCT GATGAGACCT GCACGCANTG GCTCACAGCA	960
	GCACGATTTG TGACAGCCCG AGGCGGAGAA CACCGAACAC CCAGTGAAGG TGAGGGGATC	1020
	AGCACGGCGC GGCCACCCAC GCACCCACGC GCTGGAATGA GACTCAGCCA CAAGGAGGTG	1080
20	CGAAGCTCTG ACCCAGGCCA CAGTGCGGAT GCACCTTGAG GATGTCACGC TCAGTGAGAG	1140
	ACACCAGACA CAGAAGGGTA CGCTGTGATC CCACTTCTAT GAAATGTCCA GGACAGACCA	1200
25	ATCCACAGAA TCAGGGAGAG GATTCGTGGG TGCCGGGACT GGGGAGGGGG ACCTGGGGGT	1260
	GACTAGGTGA CATAATGGGG ACAGGGCTGC CTTCTGGGTG ATGAGAATGT TCTGGAATCA	1320
	GATGGGATGG CTGCACGGCG TGGTGAAGGT ACTGAACGCC ACCTCACTGT AAGACGGTAG	1380
30	ATTTTGTATT TTACCACAAT AAACAAAACA AAACAAAACC AAAAAAAAAA AAAAAAAAAA	1440
	AAAAAAAAAG AATTCGATAT CAAGCTTATC GATACCGTCG ACCTCGA	1487

35

(2) INFORMATION FOR SEQ ID NO: 116:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

	GGCACGAGTG CGCANGCGTG GGGCTCTCTC CTTGTCAGTC GGCGCCCGT GCGGGCTGGT	60
50	GGCTCTGTGG CAGCGGCGGC GGCAGGACTC CGGCACTATG AGCGGCTTCA GCACCGAGGA	120
	GCGCGCCGCG CTTCTCCCT GGAGTACCGA GTCTTCTCA AAAATGAGAA AGGACAATAT	180
	ATATCTCCAT TTCATGATAT TCCAATTTAT GCAGATAAGG ATGTGTTTCA CATGGTAGTT	240
55	GAAGTACCAC GCTGGTCTAA TGCAAAAATG GAGATTGCTA CAAAGGACCC TTTAAACCTT	300
	ATTAAACAAG ATGTGAAAAA AGGAAAACCT CGCTATGTTG CGAATTTGTT CCCGTATAAA	360
60	GGATATATCT GGAACATATG TGCCATCCCT CAGACTTGGG AAGACCCAGG GCACAATGAT	420

AAACATACTG GCTGTTGTGG TGACAATGAC CCAATTGATG TGTGTGAAAT TGGAAGCAAG 480
 GTATGTGCAA GAGGTGAAAT AATTGGCGTG AAAGTTCTAG GCATATTGGC TATGATTGAC 540
 5 GAAGGGGAAA CCGACTGGAA AGTCATTGCC ATTAATGTGG ATGATCCTGA TGCAGCCAAT 600
 TATAATGATA TCAATGATGT CAAACGGCTG AAACCTGGCT ACTTAGAAGC TACTGTGGAC 660
 10 TGGTTTAGAA GGTATAAGGT TCCTGATGGA AAACCAGAAA ATGAGTTTGC GTTTAATGCA 720
 GAATTTAAAG ATAAGGACTT TGCCATTGAT ATTATTAAAA GCACTCATGA CCATTGGAAA 780
 GCATTAGTGA CTAAGAAAAC GAATGGAAAA GGAATCAGTT GCATGAATAC AACTTTGTCT 840
 15 GAGAGCCCCCT TCAAGTGTGA TCCTGATGCT GCCAGAGCCA TTGTGGATGC TTTACCACCA 900
 CCCTGTGAAT CTGCCTGCAC AGTACCAACA GACGTGGATA AGTGGTTCCA TCACCAGAAA 960
 AACTAATGAG ATTTCTCTGG AATACAAGCT GATATTGCTA CATCGTGTTC ATCTGGATGT 1020
 20 ATTAGAAGTA AAAGTAGTAG CTTTTCAAAG CTTTAAATTT GTAGAACTCA TCTAACTAAA 1080
 GTAAATTCTG CTGTGACTAA TCCAATATAC TCAGAATGTT ATCCATCTAA AGCATTTTTC 1140
 25 ATATCTCAAC TAAGATAACT TTTAGCACAT GCTTAAATAT CAAAGCAGTT GTCATTGGA 1200
 AGTCACTTGT GAATAGATGT GCAAGGGGAG CACATATTGG ATGTATATGT TACCATATGT 1260
 TAGGAAATAA AATTATTTTG CTGAAAAAAA AAAAAAAAAA ACCTSGGGGG GGGSCCCGGT 1320
 30 CCCCATTGG CCCTTTGGGG GNGGTTTTTA 1350

35

(2) INFORMATION FOR SEQ ID NO: 117:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

50

CTCTTGCTAC CTTCCCGGCG CAGAGAACCC CGGCTGCTCA GCGCGCTCCG GGGTCATGGA 60
 GATCCCCGGG AGCCTGTGCA AGAAAGTCAA GCTGAGCAAT AACGCGCAGA ACTGGGGAAT 120
 GCGAGAGCA ACCAATGTCA CCTACCAAGC CCATCATGTC AGCAGGAACA AGAGAGGTCA 180
 GGTGGTGGGG ACCAGAGGTG GCTTTCGTGG TTGCACAGTT TGGCTAACAG GCTTGTCTGG 240
 AGCGGGAAAG ACTACTGTGA GCATGGCCTT GGAGGAGTAC CTGGTTTGTC ATGGTATTCC 300
 55 ATGCTACACT CTGGATGGTG ACAATATTCTG TCAAGGTCTC AATAAAAATC TTGGCTTTAG 360
 TCCTGAAGAC AGAGAAGAGA ATGTTGACG CATCGCAGAA GTTGCTAAAC TGTTTGCGA 420
 60 TGCTGGCTTA GTGTGCATCA CAAGTTTCAT ATCACCTTAC ACTCAGGATC GCAACAATGC 480

	AAGGCAAATT CATGAAGGTG CAAGTTTACC GTTMTTGTAA GTATTTGTTG ATGCTCCTCT	540
5	GCATGTTTGT GAACAGAGGG ATGTCAAAGG ACTCTACAAA AAAGCCCGGG CAGGAGAAAT	600
	TAAAGGTTTC ACTGGGATCG ATCTGAATA TGAAGGCCA GAGGCCCTG AGTTGGTGCT	660
	GAAAACAGAC TCCTGTGATG TAAATGACTG TGTCCAGCAA GTTGTGGAAC TTCTACAGGA	720
10	ACGGGATATT GTACCTGTGG ATGCATCTTA TGAAGTAAAA GAACTATATG TGCCAGAAAA	780
	TAAACTTCAT TTGGCAAAAA CAGATGCGGA AACATTACCA GCACTGAAAA TTAATAAAGT	840
15	GGATATGCAG TGGGTGCAGG TTTTGGCAGA AGGTTGGGCA ACCCCATTGA ATGGCTTTAT	900
	GAGAGAGAGG GAGTACTTGC AGTGCCTTCA TTTTGATTGT CTTCTGGATG GAGGTGTCAT	960
	TAACCTGTCA GTACCTATAG TTCTGACTGC GACTCATGAA GATAAAGAGA GGCTGGACGG	1020
20	CTGTACAGCA TTTGCTCTGA TGTATGAGGG CCGCCGTGTG GCCATTCTTC GCAATCCAGA	1080
	GTTTTTTGAG CACAGGAAAG AGGAGCGCTG TGCCAGACAG TGGGGAACGA CATGCAAGAA	1140
25	CCACCCCTAT ATTAAGATGG TGATGGAACA AGGAGATTGG CTGATTGGAG GAGATCTTCA	1200
	AGTCTTGGAT CGAGTTTATT GGAATGATGG TCTTGATCAG TATCGTCTTA CTCCTACTGA	1260
	GCTAAAGCAG AAATTTAAAG ATATGAATGC TGATGCTGTC TTTGCATTTT AACTACGCAA	1320
30	CCCAGTGCAC AATGGACATG CCCTGTTAAT GCAGGATACC CATAAGCAAC TTCTAGAGAG	1380
	GGGCTACCGG CGCCCTGTCC TCCTCTCCA CCCTCTGGGT GGCTGGACAA AGGATGACGA	1440
35	TGTTCTTTG ATGTGGCGTA TGAAGCAGCA TGCTGCAGTG TTGAGGAAG GAGTTCTGAA	1500
	TCCTGAGACG ACAGTGGTGG CCATCTTCCC ATCTCCCATG ATGTATGCTG GACCAACTGA	1560
	GGTCCAGTGG CATTGCAGAG CACGGATGGT TGCAGGAGCC AACTTTTACA TTGTTGGACG	1620
40	AGACCCTGCT GGCATGCCTC ATCCAGAAAC AGGGAAGGAT CTTTATGAGC CAAGTCATGG	1680
	TGCCAAAGTG CTGACGATGG CCCCTGGTTT AATCACTTTG GAAATAGTTC CCTTTCGAGT	1740
45	TGCAGCTTAC AACAAGAAAA AGAAGCGTAT GGACTACTAT GACTCTGAAC ACCATGAAGA	1800
	CTTTGAATTT ATTTTCAGGAA CACGAATGCG CAAACTTGCT CGAGAAGGCC AGAAACCACC	1860
	TGAAGGTTTC ATGGCTCCCA AGGCTTGGAC CGTGCTGACA GAATACTACA AATCCTTGGA	1920
50	GAAAGCTTAG GCTGTTAACC CAGTCACTCC ACCTTTGACA CATTACTAGT AACAAGAGGG	1980
	GACCACATAG TCTCTGTTGG CATTTCTTTG TGGTGTCTGT CTGGACATGC TTCTAAAAA	2040
55	CAGACCATTT TCCTTAACTT GCATCAGTTT TGGTCTGCCT TATGAGTTCT GTTTTGAACA	2100
	AGTGTAACAC ACTGATGGTT TTAATGTATC TTTTCCACTT ATTATAGTTA TATTCTTACA	2160
	ATACAAATTT AAAATGTGCT TTTTATATTA TATTTATGCT TCTGTGTCAT GATTTTPTCA	2220
60	AGCTGTTATA TTAGTTGTAA CCAGTAGTAT TCACATPAAA TCTTGCTTTT TTTCCCCTTA	2280

AAAAAAGAAA AAAATTACCA AACAATAAAC TTGGCTAGAC CTTGTTTTGA GGATTTTACA 2340
 AGACCTTTGT AGCGATTAGA TTTTTTTTCT ACATTGAAAA TAGAACTGC TTCCTTCTT 2400
 5 CTTTCCAGTC' AGCTATTGGT CTTTCCAGCT GTTATAATCT AAAGTATTCT TATGATCTGT 2460
 GTAAGCTCTG AATGAAC'TC TTTACTCAAT AAAATTAAAT TTTTGGCTTC TTAAAAAAA 2520
 10 AAAAAAA 2527

15 (2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1098 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

25 CGCATCACAG ACAACCCAGA AGGAAAATGG TTGGGCAGAA CAGCAAGGGG TTCATATGGC 60
 TATATTAAAA CAACTGCTGT AGAGATNNC TATGATTCTT TGAACTGAA AAAAGACTCT 120
 CTTGGTGCCC CTTCAAGACC TATTGAAGAT GACCAAGAAG TATATGATGA TGTTGCAGAG 180
 30 CAGGATGATA TTAGCAGCCA CAGTCAGAGT GGAAGTGGAG GGATATTCCC TCCACCACCA 240
 GATGATGACA TTTATGATGG GATTGAAGAG GAAGATGCTG ATGATGGTTT CCCTGCTCCT 300
 35 CCTAAACAAT TGGACATGGG AGATGAAGTT TACGATGATG TGGATACCTC TGATTTCCCT 360
 GTTTCATCAG CAGAGATGAG TCAAGGAACT AATGTTGGAA AAGCTAAGAC AGAAGAAAAG 420
 GACCTTAAGA AGCTAAAAAA GCAGRAAAAA GAARAAAAAG ACTTCAGGAA AAAATTTAAA 480
 40 TATGATGGTG AAATTAGAGT CCTATATTCA ACTAAAGTTA CAACTTCCAT AACTTCTAAA 540
 AAGTGGGGAA CCAGAGATCT ACAGGTAAAA CCTGGTGAAT CTCTAGAAGT TATACAAACC 600
 45 ACAGATGACA CAAAAGTTCT CTGCAGAAAT GAAGAAGGGA AATATGGTTA TGCCTTCGG 660
 AGTTACCTAG CGGACAATGA TGGAGAGATC TATGATGATA TIGCTGATGG CTGCATCTAT 720
 GACAATGACT AGCACTCAAC TTTGGTCATT CTGCTGTGTT CATTAGGTGC CAATGTGAAG 780
 50 TCTGGATTTT AATTGGCATG TTATTGGGTA TCMAGAAAAT TAATGCACAR AACCCTTAT 840
 TATCATTTGT TATGAAATCC CAATTATCTT TACAAAGTGT TTAAAGTTTG AACATAGAAA 900
 55 ATAATCTCTC TGCTTAATTG TTATCTCAGA AGACTACATT AGTGAGATGT AAGAATTATT 960
 AAATATTCCA TTTCCGCTTT GGCTACAATT ATGAAGAAGT TGAAGGTACT TCTTTTAGAC 1020
 CACCAGTAAA TAATCCTCCT TCAAAAAATA AAAATAAAAA AAAAAAAAAA AACTCGAGG 1080
 60

GGGGGCCCCG TACCCAAT

1098

5

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 1679 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TCGACCCACG CGTCCGGCGA GATCCCTACC GCAGTAGCCG CCTCTGCCGC CGCGGAGCTT	60
CCCGAACCTC TTCAGCCGCC CGGAGCCGCT CCCGGAGCCC GGCCGTAGAG GCTGCAATCG	120
20 CAGCCGGGAG CCCGCAGCCC GCGCCCCGAG CCCGCCGCCG CCCTTCGAGG GCGCCCCAGG	180
CCGCGCCATG GTGAAGGTGA CGTCAACTC CGCTCTGGCC CAGAAGGAGG CCAAGAAGGA	240
CGAGCCCAAG AGCGGCGAGG AGGCGCTCAT CATCCCCCCC GACGCCGTCG CGGTGGACTG	300
25 CAAGGACCCA GATGATGTGG TACCAGTTGG CCAAAGAAGA GCCTGGTGTT GGTGCATGTG	360
CTTTGGACTA GCATTTATGC TTGCAGGTGT TATTCTAGGA GGAGCATACT TGTACAAATA	420
30 TTTTGCACTT CAACCAGATG ACGTGTACTA CTGTGGAATA AAGTACATCA AAGATGATGT	480
CATCTPAAAT GAGCCCTCTG CAGATGCCCC AGCTGCTCTC TACCAGACAA TTGAAGAAAA	540
35 TATTAATAATC TTTGAAGAAG AAGAAGTTGA ATTTATCAGT GTGCCTGTCC CAGAGTTTGC	600
AGATAGTGAT CCTGCCAACA TTGTTTCATGA CTTTAACAAG AAACCTACAG CCTATTTAGA	660
TCTTAACCTG GATAAGTGCT ATGTGATCCC TCTGAACACT TCCATTGTTA TGCCACCCAG	720
40 AAACCTACTG GAGTTACTTA TTAACATCAA GGCTGGAACC TATTTGCCTC AGTCCTATCT	780
GATTCATGAG CACATGGTTA TTAGTATCG CATGAAAAC ATTGATCACC TGGGTTTCTT	840
45 TATTTATCGA CTGTGTCATG ACAAGGAAAC TTACAAACTG CAACGCAGAG AAACATTTAA	900
AGGTATTCAG AAACGTGAAG CCAGCAATTG TTTTCGAATT CGGCATTTTG AAAACAAATT	960
TGCCGTGGAA ACTTTAATTT GTTCTTGAAC AGTCAAGAAA AACATTATTG AGGAAAATTA	1020
50 ATATCACAGC ATAACCCAC CCTTACATT TTGTGCAGTG ATTATTTTTT AAAGTCTTCT	1080
TTCATGTAAG TAGCAAACAG GGCTTTACTA TCTTTTCATC TCATTAATTC AATTAAACC	1140
55 ATTACCTTAA AATTTTTTTC TTTCGAAGTG TGGTGTCTTT TATATTTGAA TTAGTAACTG	1200
TATGAAGTCA TAGATAATAG TACATGTCAC CTTAGGTAGT AGGAAGAATT ACAATTTCTT	1260
TAAATCATTT ATCTGGATTT TTATGTTTTA TTAGCATTTT CAAGAAGACG GATTATCTAG	1320
60 AGAATAATCA TATATATGCA TACGTAAAAA TGGACCACAG TGAATTATTT GTAGTTGTTA	1380

GTTGCCCTGC TACCTAGTTT GTTAGTGCAT TTGAGCACAC ATTTTAATTT TCCTCTAATT 1440
 AAAATGTGCA GTATTTTCAG TGTCAAATAT ATTTAACTAT TTAGAGAATG ATTTCCACCT 1500
 5 TTATGTTTTA ATATCCTAGG CATCTGCTGT AATAATATTT TAGAAAATGT TTGGAATTTA 1560
 AGAAATAACT TGTGTTACTA ATTTGTATAA CCCATATCTG TGCAATGGAA TATAAATATC 1620
 10 ACAAAGTTGT TTAAMWAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAAN 1679

15 (2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1308 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

25 TTGGCANCNG GGAGAGGGAA AGAGGAGGAA ATGGGGTTTG AGGACCATGG CTTACCTTTC 60
 CTGCCTTTGA CCCATCACAC CCCATTTCCCT CCTCTTTCCC TCTCCCCGCT GCCAAAAAAA 120
 AAAAAAAGG AAACGTTTAT CATGAATCAA CAGGGTTTCA GTCCTTATCA AAGAGAGATG 180
 30 TGGAAAGAGC TAAAGAAACC ACCCTTTGTT CCCAACTCCA CTTTACCCAT ATTTTATGCA 240
 ACACAAACAC TGTCCCTTTG GGTCCCTTTC TTACAGATGG ACCTCTTGAG AAGAATTATC 300
 35 GTATTCCACG TTTTGTAGCC TCAGGTTACC AAGATAAATA TATGTATATA TAACCTTTAT 360
 TATTGCTATA TCTTTGTGGA TAATACATTC AGGTGGTGCT GGGTGATTTA TTATAATCTG 420
 AACCTAGGTA TATCCTTTGG TCTTCCACAG TCATGTTGAG GTGGGCTCCC TGGTATGGTA 480
 40 AAAAGCCAGG TATAATGTAA CTTACCCCCA GCCTTTGTAC TAAGCTCTTG ATAGTGATA 540
 TACTCTTTTA AGTTTAGCCC CAATATAGGG TAATGGAAAT TTCCTGCCCT CTGGGTTCCT 600
 45 CATTTTTACT ATTAAGAAGA CCAGTGATAA TTTAATAATG CCACCAACTC TGGCTTAGTT 660
 AAGTGAGAGT GTGAAGTGTG TGGCAAGAGA GCCTCACACC TCACTAGGTG CAGAGAGCCC 720
 AGGCCTTATG TTAAATCAT GCACTTGAAA AGCAAACCTT AATCTGCAA GACAGCAGCA 780
 50 AGCATTATAC GGTCACTTG AATGATCCCT TTGAAATTTT TTTTGTGTTT GTTTGTTTAA 840
 ATCAAGCCTG AGGCTGGTGA ACAGTAGCTA CACACCCATA TTGTGTGTTT TGTGAATGCT 900
 55 AGCTCTCTTG AATTTGGATA TTGGTTATTT TTTATAGAGT GTAAACCAAG TTTTATATTC 960
 TGCAATGCGA ACAGGTACCT ATCTGTTTCT AAATAAACT GTTTACATTC ATTATGGGGT 1020
 ATGTATGACC TTCATTTTCC AAGAAATAGA ACTCTAGCTT AGAATTATGG ATGCTCTAAA 1080
 60

	ATGTCAGAAT GGGAACTCTC CTCGAAGTTC TCCCAAACCTC AGAGACAGCA CTGCCTTCTC	1140
	CTAAATGATT ATTCTTTTCT CCCTGTTTTC TGGTATTTTC TAGGCATCCT TCTCACCACA	1200
5	GCCATAACCC TTTTTFACCT CCATTAGGCC GTATAACTGG NGGGACNGCT GGTCCGTATA	1260
	TAATACTGGT WCCAACAMAG GGGTTCTGGA TGTACACMAG GTTATCTT	1308
10		
	(2) INFORMATION FOR SEQ ID NO: 121:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1411 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:	
	GGCACAGGAG CGACCCGGGA GAAGGAGGGC CAMGAKGCGG AAGCGGAGGA GTCTCCAGGA	60
25	GACCCGGGGA CAGCATCGCC CAGGCCCTTG TTTGCAGGCC TTTCAGATAT ATCCATCTCA	120
	CAAGACATCC CCGTAGAAGG AGAAATCACC ATTCTATGA GATCTCGCAT CCGGGAGTTT	180
	GACAGCTCCA CATTAATGA ATCTGTTCGC AATACCATCA TCGGTGATCT AAAAGCTGTT	240
30	GGGAAAAAAT TCATGCATGT TTTGTACCCA AGGAAAAGTA ATACTCTTTT GAGAGATTGG	300
	GATTTGTGGG GCCCTTTGAT CCTTTGTGTG ACACTCGCAT TAATGCTGCA AAGAGACTCT	360
35	GCAGATAGTG AAAAAGATGG AGGGCCCCAA TTTGCAGAGG TGTGTGTCAT TGTCTGGTTT	420
	GGTGCAGTTA CCATCACCTT CAACTCAAAA CTCTTGGAG GGAACATATC TTTTTCAG	480
	AGCCTCTGTG TGCTGGGTTA CTGTATACTT CCCTTGACAG TAGCAATGCT GATTTGCCGG	540
40	CTGGTACTTT TGGCTGATCC AGGACCTGTA AACTTCATGG TTCGGCTTTT TGTGGTGATT	600
	GTGATGTTTG CCTGGTCTAT AGTTGCTCC ACAGCTTTCC TTGCTGATAG CCAGCCTCCA	660
45	AACCGCAGAG CCCTAGCTGT TTATCTGTT TTCCTGTTT ACTTTGTCAT CAGTTGGATG	720
	ATTCTCACCT TTAATCCTCA GTAAATCAGG AATGGGAAAT TAAAAACCAG TGAATTGAAA	780
	GCACATCTGA AAGATGCAAT TCACCATGGA GCTTTGTCTC TGGCCCTTAT TTGTCTAATT	840
50	TTGGAGGTAT TTGATAACTG AGTAGGTGAG GAGATTAAAA GGGAGCCATA TAGCACTGTC	900
	ACCCCTTATT TGAGGAACCT ATGTTTGAAA GGCTGTTCTT TTCTCTCTTA ATGTCATTTT	960
55	TTTAAAAATA CATGTGCATA CTACACACAG TATATAATGC CTCCTTAAGG CATGATGGAG	1020
	TCACCGTGGT CCATTTGGGT GACAACCACT GACTTGGGAA GCACATAGAT ACATCTTACA	1080
	AGTTGAATAG AGTTGATAAC TATTTTCAGT TTTGAGAATA CCAGTTCAGG TGCAGCTCTT	1140
60	AAACACATTG CCTTATGACT ATTAGAATAT GCCTCTCTTT TCATAAATAA AAATACATGG	1200

5 TCTATATCCA TTTTCTTTTA TTTCTCTCTC TTAAGCTTAA AAAGGCAATG AGAGAGGTTA 1260
GGAGTGGGTT CATAACCGGA GAATGAGAAA ACATGCATTA ACCAATATTC AGATTTTGAT 1320
CAGGGGAAAT TCTAYACTTG TTGCAAAAAA AAAAAAAAAA AACTCGAGG GGGGCCCCGT 1380
ACCCAATCGC NGTATATGAT CGNAAACAAT C 1411

10

(2) INFORMATION FOR SEQ ID NO: 122:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

GCTTTGGCTT TTTTGGCGG ACTGGGGCGC CCTCCGAAG CGTTTCCAAC TTCCAGAAG 60
25 TTTCTCGGA CGGCAGGAG GGGGTGGGA CTGCCATATA TAGATCCCG GAGCAGGGGA 120
GCGGGCTAAG AGTAGAATCG TGTCGGGCT CGAGAGCGAG AGTCACGTCC CGGCGCTAGC 180
CAGCCCAGC CAGGCCACC GTGTGCACG CAAACCACTT CCTGGCCATG CGCTCCCTCC 240
30 TGCTTCTCAG CGCCTTCTGC CTCCTGGAGG CGGCCCTGGC CGCCGAGGTG AAGAAACCTG 300
CAGCCGAGC AGCTCCTGGC ACTGCGGAGA AGTTGAGCCC CAAGGCGGCC ACGCTTGCCG 360
35 AGCGCANGCC GGCTGGCCT TCAGCTTGTA CCAGGCCATG GCCAAGGACC AGGCAGTGGA 420
GAACATCTG GTGTCACCCG TGGTGGTGGC CTCGTCGCTG GGGCTCGTGT CGCTGGGCGG 480
CAAGGCGACC ACGGCGTCGC AGGCCAAGGC AGTGCTGAGC GCCGAGCAGC TGCGCGACGA 540
40 GGAGGTGCAC GCCGGCCTGG GCGAGCTGCT GCGCTCACTC AGCAACTCGA CGGCGCGCAA 600
CGTGACCTGG AAGCTGGGCA GCCGACTGTA CGGACCCAGC TCAGTGAGCT TCGCTGATGA 660
45 C'TCGTGCGC ACAGCAAGCA GCACTACAAC TGCGAGCACT CCAAGATCAA CTTCCGCGAC 720
AAGCGCAGNG CGCTGCAGTC CATCAACGAG TGGGCCGCGC AGACCACCGA CGGCAAGCTG 780
CCCCAGGTCA CCAAGGACGT GGAGCGCACG GACGGCGCCC TGCTAGTCAA CGCCATGTTT 840
50 TTCAAGCCAC ACTGGGATGA GAAATTCCAC CACAAGATGG TGGACAACCG TGGCTTCATG 900
GTGACTCGGT CCTATACYGT GGGTGTCTATG ATGATGCACC GGACAGGCCT CTACAACTAC 960
55 TACGACGACG AGAAGGAAA GCTGCAAATC GTGGAGATGC CCCTGGCCCA CAAGCTCTCC 1020
AGCCTCATCA TCCTCATGCC CCATCAGTG GAGCCTCTCG AGCGCCTTGA AAAGCTGCTA 1080
ACCAAAGAGC AGCTGAAGAT CTGGATGGGG AAGATGCAGA AGAAGGCTGT TGCCATCTCC 1140
60

	TTGCCCAAGG GTGTGGTGGA GGTGACCCAT GACCTGCAGA AACACCTGGC TGGGCTGGGC	1200
	CTGACTGAGG CCATTGACAA GAACAAGGCC GACTTTRTCAC GCATGTCAGG CAAGAAGGAC	1260
5	CTGTACCTGG CCAGCGTGTT CCACGCCACC GCCTTTGAGT TGGACACAGA TGGCAACCCC	1320
	TTTGACCAGG ACATCTACGG GCGCGAGGAG CTGCGCANCC CAAGCTGTTC TACGCCGACC	1380
10	ACCCCTTCAT CTTCTAGTG CGGGACACCC AAAGCGGCTC CCTGCTATTC ATTGGGCGCC	1440
	TGGTCCGGCC TAAGGGTGAC AAGATGCGAG ACGAGTTATA GGGCCTCAGG GTGCACACAG	1500
	GATGGCAGGA GGCATCCAAA GGCTCCTGAG ACACATGGGT GCTATTGGGG TTGGGGGGGA	1560
15	GGTGAGGTAC CAGCCTTGGA TACTCCATGG GGTGGGGGTG GAAAARCAGA CCGGGGTTCC	1620
	CGTGTGCTG AGCGGACCTT CCCAGCTAGA ATTCACCTCA CTTGGACATG GGCCCCAGAT	1680
20	ACCATGATGC TGAGCCCGGA AACTCCACAT CCTGTGGGAC CTGGGCCATA GTCATTCTGC	1740
	CTGCCCTGAA AGTCCCAGAT CAAGCCTGCC TCAATCAGTA TTCATATTTA TAGCCAGGTA	1800
	CCTTCTCACC TGTGAGACCA AATTGAGCTA GGGGGTTCAG CCAGCCCTCT TCTGACACTA	1860
25	AAACACCTCA GCTGCCTCCC CAGCTCTATC CCAACCTCTC CCAACTATAA AACTAGGTGC	1920
	TGCAGCCCTT GGGACCAGGC ACCCCCAGAA TGACCTGGCC GCAGTGAGGC GGATTGAGAA	1980
30	GGAGCTCCCA GGAGGGGCTT CTGGGCAGAC TCTGGTCAAG AAGCATCGTG TCTGGCGTTG	2040
	TGGGGATGAA CTTTGTGTTT TGTTTCTTCC TTTTGTAGTT CTTCAAAGAT AGGGAGGGAA	2100
	GGGGGAACAT GAGCCTTTGT TGCTATCAAT CCAAGAACTT ATTTGTACAT TTTTTTTTTC	2160
35	AATAAACTT TTCCAATGAC AAAAAAAAAA AAAAAAAAAA AAAAAGGGGS GGGCCGCTCC	2220
	TAGAGGGATC CCTCCGANGG NGCCAATCG AAAATN	2256

40

(2) INFORMATION FOR SEQ ID NO: 123:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 829 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

	ATGCGCTCCC TCCTGCTTCT CAGCGCCTTC TGCCTCCTGG AGGCGGCCCT GGCCGCCGAG	60
55	GTGAAGAAAC CTGCAGCCGC AGCAGCTCCT GGCAC TGCGG AGAAGTTGAG CCCCAAGGCG	120
	GCCACGCTTG CCGAGCGCAA GCGGCCTGGC CTTGAGCTTG TACCAGGCCA TGGCCAAGGA	180
	CCAGGCAGTG GAGAACATCC TGGTGTACCC CGTGGTGGTG GCCTCGTCGC TGGGGCTCGT	240
60	GTCGCTGGGC GGCAAGGCGA CCACGGCGTC GCAGGCCAAG GCAGTGCTGA GCGCCGAGCA	300

5 GCTGCGCGAC GAGGAGGTGC ACGCCGGCCT GGGCGAGCTG CTGCGCTCAC TCAGCAACTC 360
 CACGGCGCGC AACGTGACCT GGAAGCTGGG CAGCCGACTG TACGGACCCA GCTCAGTGAG 420
 CTTCGCTGAT GACTTCGTGC GCAGCAGCAA GCAGCACTAC AACTGCGAGC ACTCCAAGAT 480
 CAACTTCCGC GACAAGCGCA GCGCGCTGCA GTCCATCAAC GAGTGGGCCG CGCAGACCAC 540
 10 CGACGGCAAG CTGCCCCGAGG TCACCAAGGA CGTGGAGCGC ACGGACGGCG CCCTGTTAGT 600
 CAACGCCATG TTCTTCAAGC CAACTGCGGA TGAGAAATTC CACCACAAGA TGGTGGACAA 660
 CCGTGGCTTC ATGGTGACTC GGTCTTATAC CGTGGGTGTC ATGATGATGC ACCGGACAGG 720
 15 CCTCTACAAC TACTACGACG ACGAGAAGGA AAAGCTGCAA ATCGTGGAGA TGCCCTGGC 780
 CCACAAGCTC TCCAGCCTCA TCATCCTCAT GCCCCATCAC GTGGAGCCT 829

20

(2) INFORMATION FOR SEQ ID NO: 124:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

CCTCCGGAAG CGTTTCCAAC TTTCAGAAG TTTCTCGGGA CGGGCAGGAG GGGGTGGGGA 60
 35 CTGCCATATA TAGATCCCGG GAGCAGGGGA GCGGGCTAAG AGTAGAATCG TGTCGCGGCT 120
 CGAGAGCGAG AGTCACGTCC CGGCGCTAGC CAGCCCGACC CAGGCCACCC GTGGTGCACG 180
 CAAACCACTT CCTGGCCATG CGCTCCCTCC TGCTTCTCAG CGCCTTCTGC CTCTGGAGG 240
 40 CGGCCCTGGC CGCCGAGGTG AAGAAACCTG CAGCCGACG AGCTCCTGGC ACTGCGGAGA 300
 AGTTGAGCCC CAAGGCGGCC ACGCTTGCCG AGCGCAGNCG GCCTGGCCTT CAGCTTGATC 360
 45 CAGGCCATGG CCAAGGACCA GGCAGTGGAG AACATCCTGG TGTCACCCGT GGTGGTGGCC 420
 TCGTCGCTGG GGCTCGTGTC GCTGGGCGGC AAGGCGACCA CGGCGTCGCA GGCCAAGGCA 480
 GTGCTGAGCG CCGAGCAGCT GCGCGACGAG GAGGTGCACG CCGGCCTGGG CGAGCTGCTG 540
 50 CGCTCACTCA GCAACTCSAC GGCGCGCAAC GTGACCTGGA AGCTGGGCAG CCGACTGTAC 600
 GGACCCAGCT CAGTGAGCTT CGCTGATGAC TTCGTGCGCA CAGCAAGCAG CACTACAAC 660
 55 GCGAGCACTC CAAGATCAAC TTCCGCGACA AGCGCACGCG CTGCAGTCCA TCAACGAGTG 720
 GGCCGCGCAG ACCACCGACG GCAAGCTGCC CGAGGTCACC AAGGACGTGG AGCGCACGGA 780
 CGGCGCCCTG YTAGTCAACG CCATGTTCTT CAAGCCACAC TGGGATGAGA AATTCCACCA 840
 60

	CAAGATGGTG GACAACCGTG GCTTCATGGT GACTCGGTCC TATACYGTGG GTGTCATGAT	900
	GATGCACCGG ACAGGCCTCT ACAACTACTA CGACGACGAG AAGGAAAAGC TGCAAATCGT	960
5	GGAGATGCCC CTGGCCCACA AGCTCTCCAG CCTCATCATC CTCATGCCCC ATCACGTGGA	1020
	GCCTCTCGAG CGCCTTGAAA AGCTGCTAAC CAAAGAGCAG CTGAAGATCT GGATGGGGAA	1080
10	GATGCAGAAG AAGGCTGTTG CCATCTCCTT GCCCAAGGGT GTGGTGGAGG TGACCCATGA	1140
	CCTGCAGAAA CACCTGGCTG GGCTGGGCCT GACTGAGGCC ATTGACAAGA ACAAGGCCGA	1200
	CTTRTCACGC ATGTCAGGCA AGAAGGACCT GTACCTGGCC AGCGTGTTCC ACGCCACCGC	1260
15	CTTTGAGTTG GACACAGATG GCAACCCCTT TGACCAGGAC ATCTACGGGC GCGAGGAGCT	1320
	GCGCASCCEA AGCTGTTCTA CGCCGACCAC CCCTTCATCT TCCTAGTGCG GGACACCCAA	1380
20	AGCGGCTCCC TGCTATTCTA TGGGCGCCTG GTCCGGCCTA AGGGTGACAA GATGCGAGAC	1440
	GAGTTATAGG GCCTCAGGGT GCACACAGGA TGGCAGGAGG CATCCAAAAG CTCCTGAGAC	1500
	ACATGGGTGC TATTGGGGTT GGGGGGAGG TGAGGTACCA GCCTTGATA CTCCATGGGG	1560
25	TGGGGGTGGA AAARCAGACC GGGGTTCCCG TGTGCCTGAG CGGACCTTCC CAGCTAGAAT	1620
	TCACTCCACT TGGACATGGG CCCCAGATAC CATGATGCTG AGCCCCGAAA CTCCACATCC	1680
30	TGTGGGACCT GGGCCATAGT CATCTGCCT GCCCTGAAAG TCCCAGATCA AGCCTGCCTC	1740
	AATCAGTATT CATATTTATA GCCAGGTACC TTCTCACCTG TGAGACCAA TTGAGCTAGG	1800
	GGGGTCAGCC AGCCCTCTTC TGACACTAAA ACACCTCAGC TGCTCCCCA GCTCTATCCC	1860
35	AACCTCTCCC AACTATAAAA CTAGGTGCTG CAGCCCCTGG GACCAGGCAC CCCCAGAATG	1920
	ACCTGGCCGC AGTGAGGCGG ATTGAGAAGG AGCTCCAGG AGGGGCTTCT GGGCAGACTC	1980
40	TGGTCAAGAA GCATCGTGTG TGGCGTTGTG GGGATGAACT TTTTGTPTTG TTTCTCCTT	2040
	TTTTAGTTCT TCAAAGATAG GGAGGGAAGG GGAACATGA GCCTTTGTG CTATCAATCC	2100
	AAGAACTTAT TTGTACATTT TTTTTTCAA TAAACTTTT CCAATGACAA AAAAAAAAAA	2160
45	AAAAAAAAA MWMGGGSGG GCCGCTCCTA GAGGGATCCC TCCGANGNG CCAATCGAA	2220
	AAT	2223

50

(2) INFORMATION FOR SEQ ID NO: 125:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

60

Met Lys Lys Gln Ser Lys Arg Cys Leu Trp Lys Pro Pro Gly Ser Leu

275

1 5 10 15
 Arg Arg Leu Trp Trp Met Arg Ala Leu Leu Ile Leu Lys Tyr Ile
 20 25 30
 5

(2) INFORMATION FOR SEQ ID NO: 126:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

15 Met Lys Lys Ser Leu Glu Asn Leu Asn Arg Leu Gln Val Met Leu Leu
 1 5 10 15
 20 His Leu Thr Ala Ala Phe Leu Gln Arg Ala His Xaa Ile Leu Thr Thr
 20 25 30
 Arg Met Ser Leu Gly Phe Gln Ser Pro His Leu Thr Met
 35 40 45

25

(2) INFORMATION FOR SEQ ID NO: 127:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

35 Met His Asn Gln Arg Gln Val Phe Leu Phe His Leu Phe Ser Asn Tyr
 1 5 10 15
 Leu Leu Ser Ile Asn Ser Val Pro Gly Thr Leu Leu Ala Ala Thr Tyr
 20 25 30
 40 Cys Leu Asn Met Thr Tyr Gly
 35

45

(2) INFORMATION FOR SEQ ID NO: 128:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

55 Met Arg Lys Lys Phe Leu Leu Ala Gln Val Phe Leu Ser Leu Ser Val
 1 5 10 15
 Met Pro Ser Met Pro Val Thr
 20

60

(2) INFORMATION FOR SEQ ID NO: 129:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

10 Met Val Leu Leu Cys Leu Leu Leu Val Pro Leu Leu Leu Ser Leu Phe
 1 5 10 15
 Val Leu Gly Leu Phe Leu Trp Phe Leu Lys Arg Glu Arg Gln Glu Glu
 20 25 30
 15 Tyr Ile Glu Glu Lys Lys Arg Val Asp Ile Cys Arg Glu Thr Pro Asn
 35 40 45
 20 Ile Cys Pro His Ser Gly Glu Asn Thr Glu Tyr Asp Thr Ile Pro His
 50 55 60
 Thr Asn Arg Thr Ile Leu Lys Glu Asp Pro Ala Asn Thr Val Tyr Ser
 65 70 75 80
 25 Thr Val Glu Ile Pro Lys Lys Met Glu Asn Pro His Ser Leu Leu Thr
 85 90 95
 Met Pro Asp Thr Pro Arg Leu Phe Ala Tyr Glu Asn Val Ile
 100 105 110
 30

(2) INFORMATION FOR SEQ ID NO: 130:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

40 Met Leu Leu Leu Phe Ile Tyr Phe Tyr Ser His Pro Ala Pro Val Pro
 1 5 10 15
 45 Ala Gly Ala Thr Ser Lys Pro Arg Tyr Arg Val Ile Thr Cys Gly Pro
 20 25 30
 Ala Ser Val Phe Ser Thr Ser Phe Ser His Ser Pro Pro Ala Arg Cys
 35 40 45
 50 Leu Gly Arg Leu Glu Gln Met Phe His Phe Gly Leu Ala Ser Gly
 50 55 60

55 (2) INFORMATION FOR SEQ ID NO: 131:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Met Pro Phe Pro Ile Ser Ile Leu Gln Leu Cys Leu Gln Ile Ser Asn
 1 5 10 15
 5 Leu Ser Phe Cys Leu Gln Lys Ile Tyr Lys Ile Pro Phe Val
 20 25 30

10

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Met Ala Ala Ala Cys Arg Ser Val Lys Gly Leu Val Ala Val Ile Thr
 20 1 5 10 15
 Gly Gly Ala Ser Gly Leu Gly Leu Ala Thr Ala Asp Asp Leu Trp Gly
 20 25 30
 25 Arg Glu Pro Leu Leu Cys Phe Trp Thr Cys Pro Thr Arg Val Gly Arg
 35 40 45
 Pro Lys Pro Arg Ser
 50

30

(2) INFORMATION FOR SEQ ID NO: 133:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

40

Met Leu Leu Val Tyr Asp Leu Tyr Leu Xaa Pro Lys Leu Trp Ala Leu
 1 5 10 15
 45 Ala Thr Pro Gln Lys Asn Gly Lys Gly Ala Arg Xaa Gly Asp Gly Thr
 20 25 30
 Pro Ala Gln Ala Phe Trp Asp Phe Trp Ser His Leu Ile Ser Ala Asp
 35 40 45
 50 Pro Gln Thr Trp Glu Arg Ala Ala Pro
 50 55

55

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 amino acids

(B) TYPE: amino acid

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

5 Met Arg Leu Ser Ala Leu Leu Ala Leu Ala Ser Lys Val Thr Leu Pro
 1 5 10 15
 Pro His Tyr Arg Tyr Gly Met Ser Pro Pro Gly Ser Val Ala Asp Lys
 20 25 30
 10 Arg Lys Asn Pro Pro Trp Ile Arg Arg Arg Pro Val Val Val Glu Pro
 35 40 45
 Ile Ser Asp Glu Asp Trp Tyr Leu Phe Cys Gly Asp Thr Val Glu Ile
 50 55 60
 15 Leu Glu Gly Lys Asp Ala Gly Lys Gln Gly Lys Val Val Gln Val Ile
 65 70 75 80
 Arg Gln Arg Asn Trp Val Val Val Gly Gly Leu Asn Thr His Tyr Arg
 85 90 95
 20 Tyr Ile Gly Lys Thr Met Asp Tyr Arg Gly Thr Met Ile Pro Ser Glu
 100 105 110
 Ala Pro Leu Leu His Arg Gln Val Lys Leu Val Asp Pro Met Asp Arg
 115 120 125
 Lys Pro Thr Glu Ile Glu Trp Arg Phe Thr Glu Ala Gly Glu Arg Val
 130 135 140
 30 Arg Val Ser Thr Arg Ser Gly Arg Ile Ile Pro Lys Pro Glu Phe Pro
 145 150 155 160
 Arg Ala Asp Gly Ile Val Pro Glu Thr Trp Ile Asp Gly Pro Lys Asp
 165 170 175
 35 Thr Ser Val Glu Asp Ala Leu Glu Arg Thr Tyr Val Pro Cys Leu Lys
 180 185 190
 40 Thr Leu Gln Glu Glu Val Met Glu Ala Met Gly Ile Lys Glu Thr Arg
 195 200 205
 Lys Tyr Lys Lys Val Tyr Trp Tyr
 210 215

45

(2) INFORMATION FOR SEQ ID NO: 135:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

55 Met Ser Leu Arg Gln Lys Ser Ser Phe Arg Leu Met Val Met Ser Leu
 1 5 10 15
 Thr Ile Leu Lys Leu Ser Lys Thr Thr Val Leu Cys Leu Arg Cys Leu
 20 25 30

60

279

His Ser Leu Lys Leu Thr Trp Arg Asp Gly Ala Arg Cys Ile Asn Ala
 35 40 45

Glu

5

(2) INFORMATION FOR SEQ ID NO: 136:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

Met Ser Gly Ser Phe Ile Leu Cys Leu Ala Leu Val Thr Arg Trp Ser
 1 5 10 15

20

Pro Gln Ala Ser Ser Val Pro Leu Ala Val Tyr Glu Ser Lys Thr Arg
 20 25 30

Lys Ser Tyr Arg Ser Gln Arg Asp Arg Asp Gly Lys Asp Arg Ser Gln
 35 40 45

25

Gly Met Gly Leu Ser Leu Leu Val Glu Thr Arg Lys Leu Leu Leu Ser
 50 55 60

Ala Asn Gln Gly
 65

30

(2) INFORMATION FOR SEQ ID NO: 137:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

Met Cys Phe Arg Phe Phe Leu Phe Cys Ser Arg Ile Leu Leu Lys Leu
 1 5 10 15

45

Phe Phe Leu Leu Phe Pro Ala Ser Ala Phe Pro Leu Ser Thr Arg Ser
 20 25 30

Ser Leu Ser Val Asn Glu His Val Val Val Ser Pro Arg Ser Thr Val
 35 40 45

50

Ser Ile Ser Arg
 50

55

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 541 amino acids

60

(B) TYPE: amino acid

280

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

5 Met Val Arg Thr Asp Gly His Thr Leu Ser Glu Lys Arg Asn Tyr Gln
 1 5 10 15
 Val Thr Asn Ser Met Phe Gly Ala Ser Arg Lys Lys Phe Val Glu Gly
 20 25 30
 10 Val Asp Ser Asp Tyr His Asp Glu Asn Met Tyr Tyr Ser Gln Ser Ser
 35 40 45
 Met Phe Pro His Arg Ser Glu Lys Asp Met Leu Ala Ser Pro Ser Thr
 50 55 60
 15 Ser Gly Gln Leu Ser Gln Phe Gly Ala Ser Leu Tyr Gly Gln Gln Ser
 65 70 75 80
 Ala Leu Gly Leu Pro Met Arg Gly Met Ser Asn Asn Thr Pro Gln Leu
 85 90 95
 20 Asn Arg Ser Leu Ser Gln Gly Thr Gln Leu Pro Ser His Val Thr Pro
 100 105 110
 25 Thr Thr Gly Val Pro Thr Met Ser Leu His Thr Pro Pro Ser Pro Ser
 115 120 125
 Arg Gly Ile Leu Pro Met Asn Pro Xaa Asn Met Met Asn His Ser Gln
 130 135 140
 30 Val Gly Gln Gly Ile Gly Ile Pro Ser Arg Thr Asn Ser Met Ser Ser
 145 150 155 160
 Ser Gly Leu Gly Ser Pro Asn Arg Ser Ser Pro Ser Ile Ile Cys Met
 165 170 175
 Pro Lys Gln Gln Pro Ser Arg Gln Pro Phe Thr Val Asn Ser Met Ser
 180 185 190
 40 Gly Phe Gly Met Asn Arg Asn Gln Ala Phe Gly Met Asn Asn Ser Leu
 195 200 205
 Ser Ser Asn Ile Phe Asn Gly Thr Asp Gly Ser Glu Asn Val Thr Gly
 210 215 220
 45 Leu Asp Leu Ser Asp Phe Pro Ala Leu Ala Asp Arg Asn Arg Arg Glu
 225 230 235 240
 Gly Ser Gly Asn Pro Thr Pro Leu Ile Asn Pro Leu Ala Gly Arg Ala
 245 250 255
 50 Pro Tyr Val Gly Met Val Thr Lys Pro Ala Asn Glu Gln Ser Gln Asp
 260 265 270
 55 Phe Ser Ile His Asn Glu Asp Phe Pro Ala Leu Pro Gly Ser Ser Tyr
 275 280 285
 Lys Asp Pro Thr Ser Ser Asn Asp Asp Ser Lys Ser Asn Leu Asn Thr
 290 295 300
 60

281

Ser Gly Lys Thr Thr Ser Ser Thr Asp Gly Pro Lys Phe Pro Gly Asp
 305 310 315 320
 5 Lys Ser Ser Thr Thr Gln Asn Asn Asn Gln Gln Lys Lys Gly Ile Gln
 325 330 335
 Val Leu Pro Asp Gly Arg Val Thr Asn Ile Pro Gln Gly Met Val Thr
 340 345 350
 10 Asp Gln Phe Gly Met Ile Gly Leu Leu Thr Phe Ile Arg Ala Ala Glu
 355 360 365
 Thr Asp Pro Gly Met Val His Leu Ala Leu Gly Ser Asp Leu Thr Thr
 370 375 380
 15 Leu Gly Leu Asn Leu Asn Ser Pro Glu Asn Leu Tyr Pro Lys Phe Ala
 385 390 395 400
 Ser Pro Trp Ala Ser Ser Pro Cys Arg Pro Gln Asp Ile Asp Phe His
 405 410 415
 20 Val Pro Ser Glu Tyr Leu Thr Asn Ile His Ile Arg Asp Lys Leu Ala
 420 425 430
 25 Ala Ile Lys Leu Gly Arg Tyr Gly Glu Asp Leu Leu Phe Tyr Leu Tyr
 435 440 445
 Tyr Met Asn Gly Gly Asp Val Leu Gln Leu Leu Ala Ala Val Glu Leu
 450 455 460
 30 Phe Asn Arg Asp Trp Arg Tyr His Lys Glu Glu Arg Val Trp Ile Thr
 465 470 475 480
 Arg Ala Pro Gly Met Glu Pro Thr Met Lys Thr Asn Thr Tyr Glu Arg
 485 490 495
 35 Gly Thr Tyr Tyr Phe Phe Asp Cys Leu Asn Trp Arg Lys Val Ala Lys
 500 505 510
 40 Glu Phe His Leu Glu Tyr Asp Lys Leu Glu Glu Arg Pro His Leu Pro
 515 520 525
 Ser Thr Phe Asn Tyr Asn Pro Ala Gln Gln Ala Phe Xaa
 530 535 540
 45

(2) INFORMATION FOR SEQ ID NO: 139:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

55

Met Ile Cys Pro Gln Cys Pro Leu Ser Leu Leu Cys Leu Ile Ser Ser
 1 5 10 15

60

Leu Cys Ser Leu Val Ile Gln Ile Ser Leu Lys Thr Ile Arg Asp Ile
 20 25 30

Thr Leu Leu Asn Met Val Gly Ile Lys Phe Ser Ile Ser Leu Ser Asn
 35 40 45

5 Lys Ile Asn Ile Asn Ser Arg Thr Trp Xaa
 50 55

10 (2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

Met Thr Leu Arg Pro Ser Leu Leu Pro Leu His Leu Leu Leu Leu
 1 5 10 15

20 Leu Leu Ser Ala Ala Val Cys Arg Ala Glu Ala Gly Leu Glu Thr Glu
 20 25 30

25 Ser Pro Val Arg Thr Leu Gln Val Glu Thr Leu Val Glu Pro Pro Glu
 35 40 45

Pro Cys Ala Glu Pro Ala Ala Phe Gly Asp Thr Leu His Ile His Tyr
 50 55 60

30 Thr Gly Ser Leu Val Asp Gly Arg Ile Ile Asp Thr Ser Leu Thr Arg
 65 70 75 80

35 Asp Pro Leu Val Ile Glu Leu Gly Gln Lys Gln Val Ile Pro Gly Leu
 85 90 95

Glu Gln Ser Leu Leu Asp Met Cys Val Gly Glu Lys Arg Arg Ala Ile
 100 105 110

40 Ile Pro Ser His Leu Ala Tyr Gly Lys Arg Gly Phe Pro Pro Ser Val
 115 120 125

Pro Ala Asp Ala Val Val Gln Tyr Asp Val Glu Leu Ile Ala Leu Ile
 130 135 140

45 Arg Ala Asn Tyr Trp Leu Lys Leu Val Lys Gly Ile Leu Pro Leu Val
 145 150 155 160

Gly Met Ala Met Val Pro Ala Leu Leu Gly Leu Ile Gly Tyr His Leu
 165 170 175

50 Tyr Arg Lys Ala Asn Arg Pro Lys Val Ser Lys Lys Lys Leu Lys Glu
 180 185 190

55 Glu Lys Arg Asn Lys Ser Lys Lys Lys Xaa
 195 200

60 (2) INFORMATION FOR SEQ ID NO: 141:

283

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

Met Phe Leu Arg Leu Tyr Leu Ile Ala Arg Val Met Leu Leu His Ser
 1 5 10 15

10 Lys Leu Phe Thr Asp Ala Ser Ser Arg Ser Ile Gly Ala Leu Asn Lys
 20 25 30

Ile Asn Phe Asn Thr Arg Phe Val Met Lys Thr Leu Met Thr Ile Cys
 35 40 45

15 Pro Gly Thr Val Leu Leu Val Phe Ser Ile Ser Leu Trp Ile Ile Ala
 50 55 60

Ala Trp Thr Val Arg Val Cys Glu Ser Pro Glu Ser Pro Ala Gln Pro
 20 65 70 75 80

Ser Gly Ser Ser Leu Pro Ala Trp Tyr His Asp Gln Gln Asp Val Thr
 85 90 95

25 Ser Asn Phe Leu Gly Ala Met Trp Leu Ile Ser Ile Thr Phe Leu Ser
 100 105 110

Ile Gly Tyr Gly Asp Met Val Pro His Thr Tyr Cys Gly Lys Gly Val
 115 120 125

30 Cys Leu Leu Thr Gly Ile Met Gly Ala Gly Cys Thr Ala Leu Val Val
 130 135 140

Ala Val Val Ala Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His Val
 35 145 150 155 160

His Asn Phe Met Met Asp Thr Gln Leu Thr Lys Arg Ile Lys Asn Ala
 165 170 175

40 Ala Ala Asn Val Leu Arg Glu Thr Trp Leu Ile Tyr Lys His Thr Lys
 180 185 190

Leu Leu Lys Lys Ile Asp His Ala Lys Val Arg Lys His Gln Arg Lys
 195 200 205

45 Phe Leu Pro Ser Tyr Pro Pro Val Xaa
 210 215

50

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

55

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

60 Met Ser Asn Thr Thr Val Pro Asn Ala Pro Gln Ala Asn Ser Asp Ser
 1 5 10 15

Met Val Gly Tyr Val Leu Gly Pro Phe Phe Leu Ile Thr Leu Val Gly
 20 25 30
 5 Val Val Val Ala Val Val Met Tyr Val Gln Lys Lys Lys Arg Val Asp
 35 40 45
 Arg Leu Arg His His Leu Leu Pro Met Tyr Ser Tyr Asp Pro Ala Glu
 50 55 60
 10 Glu Leu His Glu Ala Glu Gln Glu Leu Leu Ser Asp Met Gly Asp Pro
 65 70 75 80
 Lys Val Val His Gly Trp Gln Ser Gly Tyr Gln His Lys Arg Met Pro
 85 90 95
 Leu Leu Asp Val Lys Thr
 100

20

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 112 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

30 Met Arg Glu Cys Gln Glu Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe
 1 5 10 15
 Ser Leu Val Ser Met Leu Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr
 20 25 30
 35 Leu Ala Ala Asn Ser Arg Phe Gly Ser Leu Pro Lys Val Ala Leu Ala
 35 40 45
 40 Gly Leu Leu Gly Phe Gly Leu Gly Lys Val Ser Tyr Ile Gly Val Cys
 50 55 60
 Gln Ser Lys Phe His Phe Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe
 65 70 75 80
 45 Gly Pro Gln His Asn Arg His Cys Leu Leu Thr Cys Glu Glu Cys Lys
 85 90 95
 Ile Lys His Gly Leu Ser Glu Lys Gly Asp Ser Gln Pro Ser Ala Ser
 100 105 110

50

55

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:
 60 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid

285

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

5 Met Lys Asn Asp Arg Asn Gln Gly Phe Ser Leu Leu Gln Leu Ile Asp
 1 5 10 15
 Trp Asn Lys Pro
 20

10

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

20 Met Gly Thr Gln Pro Pro Val Val Ala Gly Phe Thr Ile Pro Met Leu
 1 5 10 15
 Gly Tyr Thr Val Arg Val Leu Thr Phe His Leu Ser Cys Ser
 20 25 30

25

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

35

Met Lys Ile Pro Val Leu Pro Ala Val Val Leu Leu Ser Leu Leu Val
 1 5 10 15

40

Leu His Ser Ala Gln Gly Ala Thr Leu Gly Gly Pro Glu Glu Glu Ser
 20 25 30

Thr Ile Glu Asn Tyr Ala Ser Arg Pro Glu Ala Phe Asn Thr Pro Phe
 35 40 45

45

Leu Asn Ile Asp Lys Leu Arg Ser Ala Phe Lys Ala Asp Glu Phe Leu
 50 55 60

Asn Trp His Ala Leu Phe Glu Ser Ile Lys Arg Lys Leu Pro Phe Leu
 65 70 75 80

50

Asn Trp Asp Ala Phe Pro Lys Leu Lys Gly Leu Arg Ser Ala Thr Pro
 85 90 95

55

Asp Ala Gln

60

(2) INFORMATION FOR SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:
- Met Val Trp Gly Leu Leu Leu Gly
 1 5
- 10
- (2) INFORMATION FOR SEQ ID NO: 148:
- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:
- Met Leu Pro Leu Leu Ser Leu Leu Phe Leu Phe Phe Ser Thr Val Ser
 1 5 10 15
- Ser Phe Cys Gly Met Pro Leu Arg Ala His Thr Arg Ala Xaa Ala His
 20 25 30
- 25 Thr Arg Thr Phe Ala Ser Arg
 35
- 30
- (2) INFORMATION FOR SEQ ID NO: 149:
- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:
- Met Ile Cys Glu Thr Lys Ala Arg Lys Ser Ser Gly Gln Pro Gly Arg
 1 5 10 15
- Leu Pro Pro Pro Thr Leu Ala Pro Pro Gln Pro Pro Leu Pro Glu Thr
 20 25 30
- 45 Ile Glu Arg Pro Val Gly Thr Gly Ala Met Val Ala Arg Ser Ser Asp
 35 40 45
- Leu Pro Tyr Leu Ile Val Gly Val Val Leu Gly Ser Ile Val Leu Ile
 50 55 60
- 50 Ile Val Thr Phe Ile Pro Phe Cys Leu Trp Arg Ala Trp Ser Lys Gln
 65 70 75 80
- 55 Lys His Thr Thr Asp Leu Gly Phe Pro Arg Ser Ala Leu Pro Pro Ser
 85 90 95
- Cys Pro Tyr Thr Met Val Pro Leu Gly Gly Leu Pro Gly His Gln Ala
 100 105 110
- 60 Val Asp Ser Pro Thr Ser Val Ala Ser Val Asp Gly Pro Val Leu Met

115 120 125

Gly Ser Thr
130

5

(2) INFORMATION FOR SEQ ID NO: 150:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

15 Met Gly Ala Pro Ser Leu Thr Met Leu Leu Leu Lys Val Gln Pro
 1 5 10 15

20 Arg Arg Thr Gln Ala Phe Asp Ala His Trp Val Gly Leu Pro Leu Leu
 20 25 30

25

(2) INFORMATION FOR SEQ ID NO: 151:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

35 Met Cys Leu Ile Phe Leu Leu Leu Leu Leu Ser Phe Ser
 1 5 10

40 (2) INFORMATION FOR SEQ ID NO: 152:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

50 His Pro His Gln Asp Ser Gln Pro
 1 5

(2) INFORMATION FOR SEQ ID NO: 153:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

60

288

Met Asn Thr Ser Tyr Ile Leu Arg Leu Thr Val Val Val Ser Val Val
 1 5 10 15

Ile Tyr Leu Ala Ile His Pro Leu Leu Ser Phe Ser Leu Glu Ser Pro
 5 20 25 30

Leu Leu Val Pro Trp Arg Asp Cys Cys Gln Asn Ile Trp Lys Ser Gly
 35 40 45

10 Ser Val Trp Tyr Lys Arg Trp Thr Leu Pro His Met Glu Val Cys Cys
 50 55 60

Gln Asp Leu His
 65

15

(2) INFORMATION FOR SEQ ID NO: 154:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

Met Leu Lys Ile Phe Lys Glu Trp Glu Asn Leu Asn Leu Ile Leu Thr
 1 5 10 15

Ser Ile Arg Ile Leu Glu Arg Gln Asn Met
 30 20 25

(2) INFORMATION FOR SEQ ID NO: 155:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 195 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

Met Asp Cys Glu Val Asn Asn Gly Ser Ser Leu Arg Asp Glu Cys Ile
 1 5 10 15

45 Thr Asn Leu Leu Val Phe Gly Phe Leu Gln Ser Cys Ser Asp Asn Ser
 20 25 30

Phe Arg Arg Glu Leu Asp Ala Leu Gly His Glu Leu Pro Val Leu Ala
 35 40 45

50 Pro Gln Trp Glu Gly Tyr Asp Glu Leu Gln Thr Asp Gly Asn Arg Ser
 50 55 60

55 Ser His Ser Arg Leu Gly Arg Ile Glu Ala Asp Ser Glu Ser Gln Glu
 65 70 75 80

Asp Ile Ile Arg Asn Ile Ala Arg His Leu Ala Gln Val Gly Asp Ser
 85 90 95

60 Met Asp Arg Ser Ile Pro Pro Gly Leu Val Asn Gly Leu Ala Leu Gln

100 105 110

Leu Arg Asn Thr Ser Arg Ser Glu Glu Asp Arg Asn Arg Asp Leu Ala
 115 120 125

5 Thr Ala Leu Glu Gln Leu Leu Gln Ala Tyr Pro Arg Asp Met Glu Lys
 130 135 140

10 Glu Lys Thr Met Leu Val Leu Ala Leu Leu Leu Ala Lys Lys Val Ala
 145 150 155 160

Ser His Thr Pro Ser Leu Leu Arg Asp Val Phe His Thr Thr Val Asn
 165 170 175

15 Phe Ile Asn Gln Asn Leu Arg Thr Tyr Val Arg Ser Leu Ala Arg Asn
 180 185 190

Gly Met Asp
 195

20

(2) INFORMATION FOR SEQ ID NO: 156:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 91 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

30 Met Ser Leu Ser Leu Val Ser Val Ser Val Gly Pro Ser Thr Leu Ala
 1 5 10 15

35 Cys Ser Phe Leu Arg Pro Lys Ala Arg Pro Ser Lys Arg Ser Pro Arg
 20 25 30

Asn Tyr Thr Asp Ser Thr Ser Pro Gly Gly Pro Arg Ala Pro Arg Gly
 35 40 45

40 Gly Ala Trp Arg Leu Ser Ser Gln Gln Asn Ser Ser Pro Lys Gly Val
 50 55 60

Ala Val Ala Lys Ala Ser Tyr Arg Pro Val Leu Cys Phe Leu Pro Gly
 65 70 75 80

45 Pro Trp Ser Ser Xaa Pro Xaa Ala Phe Leu Ile
 85 90

50

(2) INFORMATION FOR SEQ ID NO: 157:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

60 Met Gly Thr Leu Ser Ala Glu Cys Ser Gly Pro Ala Thr Leu Gly Leu
 1 5 10 15

290

Cys Leu Val Val Pro Trp Asn Ser Ser Gly Leu Ser Gln Pro Pro
 20 25 30

5

(2) INFORMATION FOR SEQ ID NO: 158:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

15

Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile Phe Leu
 1 5 10 15

Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr Tyr Pro
 20 25 30

20

Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu Thr Thr Ala
 35 40 45

25

Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr Ala Thr Thr Ala
 50 55 60

Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val Leu Pro Lys Trp Val
 65 70 75 80

30

Gly Asp Leu Pro Asn Gly Arg Val Cys Pro Xaa
 85 90

35

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser Asn Thr
 1 5 10 15

45

Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala
 20 25 30

50

Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe
 35 40 45

Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His Leu Ile
 50 55 60

55

Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Trp Asp Trp Ala
 65 70 75 80

Glu Ala Gly Ala Ser Leu Tyr Ser Pro
 85

60

(2) INFORMATION FOR SEQ ID NO: 160:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

10

Met Ser Ser Ala Ala Ala Asp His Trp Ala Trp Leu Leu Val Leu Ser
1 5 10 15

15

Phe Val Phe Gly Cys Asn Val Leu Arg Ile Leu Leu Pro Ser Phe Ser
20 25 30

Ser Phe Met Ser Arg Val Leu Gln Lys Asp Ala Glu Gln Glu Ser Gln
35 40 45

20

Met Arg Ala Glu Ile Gln Asp Met Lys Gln Glu Leu Ser Thr Val Asn
50 55 60

Met Met Asp Glu Phe Ala Arg Tyr Ala Arg Leu Glu Arg Lys Ile Asn
65 70 75 80

25

Lys Met Thr Asp Lys Leu Lys Thr His Val Lys Ala Arg Thr Ala Gln
85 90 95

30

Leu Ala Lys Ile Lys Trp Val Ile Ser Val Ala Phe Tyr Val Leu Gln
100 105 110

Ala Ala Leu Met Ile Ser Leu Ile Trp Lys Tyr Tyr Ser Val Pro Val
115 120 125

35

Ala Val Val Pro Ser Lys Trp Ile Thr Pro Leu Asp Arg Leu Val Ala
130 135 140

Phe Pro Thr Arg Val Ala Gly Gly Val Gly Ile Thr Cys Trp Ile Leu
145 150 155 160

40

Val Cys Asn Lys Val Val Ala Ile Val Leu His Pro Phe Ser
165 170

45

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

50

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

55

Met Gly Lys Leu Ile Asn Ile Val Ile Arg Lys Pro Leu Leu Leu Leu
1 5 10 15

Leu Val Gln Cys Glu Asn Cys Cys Arg Lys Asn Met Leu Tyr Asn Ile
20 25 30

60

Phe Leu Asn Ile His Asn Ile His Lys Phe Ser Asn His

35

40

45

5 (2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Met Val Ala Ser Thr Leu Val Thr Asn Leu Phe Gly Val Ala Phe Ala
1 5 10 15

15

Thr Thr Ala Ala Thr Arg Ala
20

20

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

Met Leu Met Ala Pro Val Val Cys Leu Ser Phe Ser Pro Cys Pro Ala
1 5 10 15

30

Asp Thr Ser Leu Thr Gly Asp Gly Leu Lys Ala Gly Leu Glu Arg Gly
20 25 30

35

Xaa Ala Leu Val Thr Leu Phe Asp Ser Val Thr His Phe Leu Ala His
35 40 45

Thr Leu Phe Glu Leu Leu Asp Phe Gln Leu Ala Phe Leu Arg Ser Gly
50 55 60

40

Lys Gln Thr Ala Pro His
65 70

45

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Met Leu Leu Leu Leu Leu Leu Gly Ser Gly Gln Gly Pro Gln Gln
1 5 10 15

55

Val Gly Ala Gly Gln Thr Phe Glu Tyr Leu Lys Arg Glu His Ser Leu
20 25 30

60

Ser Lys Pro Tyr Gln Gly Val Gly Thr Gly Ser Ser Ser Leu Trp Asn

293

	35	40	45
	Leu Met Gly Asn Ala Met Val Met Thr Gln Tyr Ile Arg Leu Thr Pro		
	50	55	60
5	Asp Met Gln Ser Lys Gln Gly Ala Leu Trp Asn Arg Val Pro Cys Phe		
	65	70	75 80
10	Leu Arg Asp Trp Glu Leu Gln Val His Phe Lys Ile His Gly Gln Gly		
	85	90	95
	Lys Lys Asn Leu His Gly Asp Gly Leu Ala Ile Trp Tyr Thr Arg Asn		
	100	105	110
15	Arg Met Gln Pro Gly Pro Val Phe Gly Asn Met Asp Lys Phe Val Gly		
	115	120	125
	Leu Gly Val Phe Val Asp Thr Tyr Pro Asn Glu Glu Lys Gln Gln Glu		
	130	135	140
20	Arg Val Phe Pro Tyr Ile Ser Ala Met Val Asn Asn Gly Ser Leu Ser		
	145	150	155 160
	Tyr Asp His Glu Arg Asp Gly Arg Pro Thr Glu Leu Gly Gly Cys Thr		
25	165	170	175
	Ala Ile Val Arg Asn Leu His Tyr Asp Thr Phe Leu Val Ile Arg Tyr		
	180	185	190
30	Val Lys Arg His Leu Thr Ile Met Met Asp Ile Asp Gly Lys His Glu		
	195	200	205
	Trp Arg Asp Cys Ile Glu Val Pro Gly Val Arg Leu Pro Arg Gly Tyr		
	210	215	220
35	Tyr Phe Gly Thr Ser Ser Ile Thr Gly Asp Leu Ser Asp Asn His Asp		
	225	230	235 240
	Val Ile Ser Leu Lys Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu		
40	245	250	255
	Glu Glu Lys Leu His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met		
	260	265	270
45	Lys Leu Pro Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala		
	275	280	285
	Leu Phe Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile		
	290	295	300
50	Val Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys		
	305	310	315 320
55	Arg Phe Tyr		

(2) INFORMATION FOR SEQ ID NO: 165:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

Met Pro Ser Glu Tyr Thr Tyr Val Lys Leu Arg Ser Asp Cys Ser Arg
 1 5 10 15
 10 Pro Ser Leu Gln Trp Tyr Thr Arg Ala Gln Ser Lys Met Arg Arg Pro
 20 25 30
 Ser Leu Leu Leu Lys Asp Ile Leu Lys Cys Thr Leu Leu Val Phe Gly
 35 40 45
 15 Val Trp Ile Leu Tyr Ile Leu Lys Leu Asn Tyr Thr Thr Glu Glu Cys
 50 55 60
 20 Asp Met Lys Lys Met His Tyr Val Asp Pro Asp His Val Lys Arg Ala
 65 70 75 80
 Gln Lys Tyr Ala Gln Gln Val Leu Gln Lys Glu Cys Arg Pro Lys Phe
 85 90 95
 25 Ala Lys Thr Ser Met Ala Leu Leu Phe Glu His Arg Tyr Ser Val Asp
 100 105 110
 Leu Leu Pro Phe Val Gln Lys Xaa Pro Lys Asp Ser Glu Ala Glu Ser
 115 120 125
 30 Lys Tyr Asp Pro Pro Phe Gly Phe Arg Lys Phe Ser Ser Lys Val Gln
 130 135 140
 35 Thr Leu Leu Glu Leu Leu Pro Glu His Asp Leu Pro Glu His Leu Lys
 145 150 155 160
 Ala Lys Thr Cys Arg Arg Cys Val Val Ile Gly Ser Gly Gly Ile Leu
 165 170 175
 40 His Gly Leu Glu Leu Gly His Thr Leu Asn Gln Phe Asp Val Val Ile
 180 185 190
 Arg Leu Asn Ser Ala Pro Val Glu Gly Tyr Ser Glu His Val Gly Asn
 195 200 205
 45 Lys Thr Thr Ile Arg Met Thr Tyr Pro Glu Gly Ala Pro Leu Ser Asp
 210 215 220
 50 Leu Glu Tyr Tyr Ser Asn Asp Leu Phe Val Ala Val Leu Phe Lys Ser
 225 230 235 240
 Val Asp Phe Asn Trp Leu Gln Ala Met Val Lys Lys Glu Thr Leu Pro
 245 250 255
 55 Phe Trp Val Arg Leu Phe Phe Trp Lys Gln Val Ala Glu Lys Ile Pro
 260 265 270
 60 Leu Gln Pro Lys His Phe Arg Ile Leu Asn Pro Val Ile Ile Lys Glu
 275 280 285

295

Thr Ala Phe Xaa His Pro Ser Val Leu Arg Ala Ser Val Lys Val Leu
 290 295 300

5 Gly Ala Glu Ile Arg Thr Ser Pro Gln Ser Val Ser Leu Pro Leu Ser
 305 310 315 320

Xaa

10

(2) INFORMATION FOR SEQ ID NO: 166:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

20 Met Thr Leu Asp Val Gln Thr Val Val Val Phe Ala Val Ile Val Val
 1 5 10 15

Leu Leu Leu Val Asn Val Ile Leu Met Phe Phe Leu Gly Thr Arg
 20 25 30

25

(2) INFORMATION FOR SEQ ID NO: 167:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

35 Met Leu Pro Leu Leu Phe Cys Ala Phe Cys Leu His Lys Leu Gly Pro
 1 5 10 15

40 Leu Leu Phe Leu Tyr Asp Val Leu Met Xaa His Glu Ala Val Met Arg
 20 25 30

Thr His Gln Ile Gln Leu Pro Asp Pro Glu Phe Pro Ser Gln Gln Asn
 35 40 45

45 Gln Val Leu Asn Lys Thr Leu Phe Asn Lys Leu Lys Lys Lys Lys
 50 55 60

Lys Lys Lys Xaa Xaa Xaa Lys Lys
 65 70

50

(2) INFORMATION FOR SEQ ID NO: 168:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 282 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

60

296

Met Ala Ser Arg Gly Arg Arg Pro Glu His Gly Gly Pro Pro Glu Leu
 1 5 10 15
 5 Phe Tyr Asp Glu Thr Glu Ala Arg Lys Tyr Val Arg Asn Ser Arg Met
 20 25 30
 Ile Asp Ile Gln Thr Arg Met Ala Gly Arg Ala Leu Glu Leu Leu Tyr
 35 40 45
 10 Leu Pro Glu Asn Lys Pro Cys Tyr Leu Leu Asp Ile Gly Cys Gly Thr
 50 55 60
 Gly Leu Ser Gly Ser Tyr Leu Ser Asp Glu Gly His Tyr Trp Val Gly
 65 70 75 80
 15 Leu Asp Ile Ser Pro Ala Met Leu Asp Glu Ala Val Asp Arg Glu Ile
 85 90 95
 20 Glu Gly Asp Leu Leu Leu Gly Asp Met Gly Gln Gly Ile Pro Phe Lys
 100 105 110
 Pro Gly Thr Phe Asp Gly Cys Ile Ser Ile Ser Ala Val Gln Trp Leu
 115 120 125
 25 Cys Asn Ala Asn Lys Lys Ser Glu Asn Pro Ala Lys Arg Leu Tyr Cys
 130 135 140
 Phe Phe Ala Ser Leu Phe Ser Val Leu Val Arg Gly Ser Arg Ala Val
 145 150 155 160
 30 Leu Gln Leu Tyr Pro Glu Asn Ser Glu Gln Leu Glu Leu Ile Thr Thr
 165 170 175
 35 Gln Ala Thr Lys Ala Gly Phe Ser Gly Gly Met Val Val Asp Tyr Pro
 180 185 190
 Asn Ser Ala Lys Ala Lys Lys Phe Tyr Leu Cys Leu Phe Ser Gly Pro
 195 200 205
 40 Ser Thr Phe Ile Pro Glu Gly Leu Ser Glu Asn Gln Asp Glu Val Glu
 210 215 220
 Pro Arg Glu Ser Val Phe Thr Asn Glu Arg Phe Pro Leu Arg Met Ser
 225 230 235 240
 45 Arg Arg Gly Met Val Arg Lys Ser Arg Ala Trp Val Leu Glu Lys Lys
 245 250 255
 50 Glu Arg His Arg Arg Gln Gly Arg Glu Val Arg Pro Asp Thr Gln Tyr
 260 265 270
 Thr Gly Arg Lys Arg Lys Pro Arg Phe Xaa
 275 280

55

(2) INFORMATION FOR SEQ ID NO: 169:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

5 Met Leu Gly Lys Thr Lys Phe Gln Ser Tyr Lys Ser Phe Ser Arg Lys
 1 5 10 15

Leu Met Val Cys Pro Ser Thr
 20

10

(2) INFORMATION FOR SEQ ID NO: 170:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

20

Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His Gly
 1 5 10 15

25

Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly Arg
 20 25 30

Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala His
 35 40 45

30

Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val Ala
 50 55 60

Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu Gly
 65 70 75 80

35

Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp Val
 85 90 95

40

Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg His
 100 105 110

Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp Arg
 115 120 125

45

Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly His
 130 135 140

Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr Tyr
 145 150 155 160

50

Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp Gln
 165 170 175

55

Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu His
 180 185 190

Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr Leu
 195 200 205

60

Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu Tyr

298

210 215 220

Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala Trp
 225 230 235 240

5 Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn Lys
 245 250 255

Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro Pro
 10 260 265 270

Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu Ser
 275 280 285

15 Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Xaa Ile Leu Gly Asn
 290 295 300

Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp Leu
 20 305 310 315 320

Thr Arg His His Asp Glu Leu Xaa
 325

25

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

35 Met Cys Trp Leu Arg Ala Trp Xaa Gln Ile Xaa Leu Pro Val Phe Xaa
 1 5 10 15

Ser Xaa Phe Leu Ile Gln Leu Leu Ile Ser Phe Ser Glu Asn Gly Phe
 20 25 30

40 Ile His Ser Pro Arg Asn Asn Gln Lys Pro Arg Asp Gly Asn Xaa Glu
 35 40 45

Glu Cys Ala Val Lys Lys Ser Cys Gln Leu Cys Thr Glu Asp Lys Lys
 45 50 55 60

Tyr Met Met Asn Arg
 65

50

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 160 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

60 Met Trp Leu Phe Ile Leu Leu Ser Leu Ala Leu Ile Ser Asp Ala Met
 1 5 10 15

Val Met Asp Glu Lys Val Lys Arg Ser Phe Val Leu Asp Thr Ala Ser
 20 25 30

5 Ala Ile Cys Asn Tyr Asn Ala His Tyr Lys Asn His Pro Lys Tyr Trp
 35 40 45

Cys Arg Gly Tyr Phe Arg Asp Tyr Cys Asn Ile Ile Ala Phe Ser Pro
 50 55 60

10 Asn Ser Thr Asn His Val Ala Leu Lys Asp Thr Gly Asn Gln Leu Ile
 65 70 75 80

Val Thr Met Ser Cys Leu Asn Lys Glu Asp Thr Gly Trp Tyr Trp Cys
 85 90 95

15 Gly Ile Gln Arg Asp Phe Ala Arg Asp Asp Met Asp Phe Thr Glu Leu
 100 105 110

20 Ile Val Thr Asp Asp Lys Gly Thr Trp Pro Met Thr Leu Val Trp Glu
 115 120 125

Arg Leu Ser Gly Thr Lys Pro Glu Ala Ala Arg Leu Pro Lys Leu Ser
 130 135 140

25 Ala Arg Leu Thr Ala Pro Gly Arg Pro Phe Ser Ser Phe Ala Tyr Xaa
 145 150 155 160

30

- (2) INFORMATION FOR SEQ ID NO: 173:
- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

Met Ala Xaa His Phe Leu Leu Val Ala Leu Gln Ser Val Pro His Cys
 1 5 10 15

45 Pro His Leu Leu Glu Glu Glu His Lys Leu Cys Lys Val Ser His Phe
 20 25 30

Ser Gly Val Thr Leu Val Thr Ser Arg Gln Asp Ser Ser Ser Tyr Val
 35 40 45

50 Pro Val Gln Thr Leu Phe Ile His Leu Gly Pro Trp Ala Trp Asp Leu
 50 55 60

55 Xaa Pro Cys Thr Ala Glu Asp Pro Glu Ala Glu Arg Ser Leu Arg Leu
 65 70 75 80

Cys His Ser His Leu Ala Arg Xaa Asn Val Ser Pro Ser Gln Ala Ala
 85 90 95

60 Glu Gly Xaa Xaa Xaa Arg Gly Cys Gln His Arg Gly Ser Arg Glu Leu

300

100 105 110
 Thr Phe Leu Ser Ala Glu Asn Glu Ala Gly Ile
 115 120
 5

(2) INFORMATION FOR SEQ ID NO: 174:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

15 Met Lys Val Gly Ala Arg Ile Arg Val Lys Met Ser Val Asn Lys Ala
 1 5 10 15
 20 His Pro Val Val Ser Thr His Trp Arg Trp Pro Ala Glu Trp Pro Gln
 20 25 30
 Met Phe Leu His Leu Ala Gln Glu Pro Arg Thr Glu Val Lys Ser Arg
 35 40 45
 25 Pro Leu Gly Leu Ala Gly Phe Ile Arg Gln Asp Ser Lys Thr Arg Lys
 50 55 60
 Pro Leu Glu Gln Glu Thr Ile Met Ser Ala Ala Asp Thr Ala Leu Trp
 65 70 75 80
 30 Pro Tyr Gly His Gly Asn Arg Glu His Gln Glu Asn Glu Leu Gln Lys
 85 90 95
 Tyr Leu Gln Tyr Lys Asp Met His Leu Leu Asp Ser Gly Gln Ser Leu
 100 105 110
 35 Gly His Thr His Thr Leu Gln Gly Ser His Asn Leu Thr Ala Leu Asn
 115 120 125
 40 Ile

45 (2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 372 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

50 Met Ala Tyr His Ser Phe Leu Val Glu Pro Ile Ser Cys His Ala Trp
 1 5 10 15
 55 Asn Lys Asp Arg Thr Gln Ile Ala Ile Cys Pro Asn Asn His Glu Val
 20 25 30
 60 His Ile Tyr Glu Lys Ser Gly Ala Lys Trp Thr Lys Val His Glu Leu
 35 40 45

301

Lys Glu His Asn Gly Gln Val Thr Gly Ile Asp Trp Ala Pro Glu Ser
 50 55 60

5 Asn Arg Ile Val Thr Cys Gly Thr Asp Arg Asn Ala Tyr Val Trp Thr
 65 70 75 80

Leu Lys Gly Arg Thr Trp Lys Pro Thr Leu Val Ile Leu Arg Ile Asn
 85 90 95

10 Arg Ala Ala Arg Cys Val Arg Trp Ala Pro Asn Glu Asn Lys Phe Ala
 100 105 110

Val Gly Ser Gly Ser Arg Val Ile Ser Ile Cys Tyr Phe Glu Gln Glu
 115 120 125

15 Asn Asp Trp Trp Val Cys Lys His Ile Lys Lys Pro Ile Arg Ser Thr
 130 135 140

20 Val Leu Ser Leu Asp Trp His Pro Asn Asn Val Leu Leu Ala Ala Gly
 145 150 155 160

Ser Cys Asp Phe Lys Cys Arg Ile Phe Ser Ala Tyr Ile Lys Glu Val
 165 170 175

25 Glu Glu Arg Pro Ala Pro Thr Pro Trp Gly Ser Lys Met Pro Phe Gly
 180 185 190

Glu Leu Met Phe Glu Ser Ser Ser Ser Cys Gly Trp Val His Gly Val
 195 200 205

30 Cys Phe Ser Ala Ser Gly Ser Arg Val Ala Trp Val Ser His Asp Ser
 210 215 220

35 Thr Val Cys Leu Ala Asp Ala Asp Lys Lys Met Ala Val Ala Thr Leu
 225 230 235 240

Ala Ser Glu Thr Leu Pro Leu Leu Ala Leu Thr Phe Ile Thr Asp Asn
 245 250 255

40 Ser Leu Val Ala Ala Gly His Asp Cys Phe Pro Val Leu Phe Thr Tyr
 260 265 270

Asp Ala Ala Ala Gly Met Leu Ser Phe Gly Gly Arg Leu Asp Val Pro
 275 280 285

Lys Gln Ser Ser Gln Arg Gly Leu Thr Ala Arg Glu Arg Phe Gln Asn
 290 295 300

50 Leu Asp Lys Lys Ala Ser Ser Glu Gly Gly Thr Ala Ala Gly Ala Gly
 305 310 315 320

Leu Asp Ser Leu His Lys Asn Ser Val Ser Gln Ile Ser Val Leu Ser
 325 330 335

55 Gly Gly Lys Ala Lys Cys Ser Gln Phe Cys Thr Thr Gly Met Asp Gly
 340 345 350

Gly Met Ser Ile Trp Asp Val Lys Ser Leu Glu Ser Ala Leu Lys Asp
 355 360 365

60

Leu Lys Ile Lys
370

5

(2) INFORMATION FOR SEQ ID NO: 176:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

15

Met Trp Ser Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu
1 5 10 15

Leu Leu Ala Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala
20 25 30

20

Leu Glu Tyr Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro
35 40 45

25

Arg Thr Phe Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile
50 55 60

Met Ala Val Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala
65 70 75 80

30

Asp Leu Ser Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu
85 90 95

Tyr Ala Val Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln
100 105 110

35

Pro Tyr Phe Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr
115 120 125

40

Gly Pro Gln Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly
130 135 140

Val Trp Tyr Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn
145 150 155 160

45

Leu Glu Gly Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser
165 170 175

Gly Lys Gln Gly Ile Leu Leu Glu His Arg Glu Lys Glu Phe Gly Asp
180 185 190

50

Lys Val Asn Leu Leu Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro
195 200 205

55

Gln Thr Leu Ala Ser Glu Lys Lys
210 215

(2) INFORMATION FOR SEQ ID NO: 177:

60

303

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

Met Lys Pro Val Ser Arg Arg Thr Leu Asp Trp Ile Tyr Ser Val Leu
 1 5 10 15

10 Leu Leu Ala Ile Val Leu Ile Ser Trp Gly Cys Ile Ile Tyr Ala Ser
 20 25 30

Met Val Ser Ala Arg Arg Gln Leu Arg Lys Lys Tyr Pro Asp Lys Ile
 35 40 45

15 Phe Gly Thr Asn Glu Asn Leu
 50 55

20

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

25 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

30 Met Ala Ala Asn Thr Phe Val Leu Ile Met Gly Ile Pro Thr Ser Ala
 1 5 10 15

Asn Ala Xaa Arg Asp Leu Phe
 20

35

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

40 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

45 Met Ser Ile Cys His Arg Gly Thr Gly Ile Ala Leu Ser Ala Gly Val
 1 5 10 15

Ser Leu Phe Gly Met Ser Ala Leu Leu Leu Pro Gly Asn Phe Glu Ser
 20 25 30

50 Tyr Leu Glu Leu Val Lys Ser Leu Cys Leu Gly Pro Ala Leu Ile His
 35 40 45

Thr Ala Lys Phe Ala Leu Val Phe Pro Leu Met Tyr His Thr Trp Asn
 55 50 55 60

Gly Ile Arg His Leu Met Trp Asp Leu Gly Lys Gly Leu Lys Ile Pro
 65 70 75 80

60 Gln Leu Tyr Gln Ser Gly Val Val Val Leu Val Leu Thr Val Leu Ser

304

85 90 95
 Ser Met Gly Leu Ala Ala Met
 100

5

(2) INFORMATION FOR SEQ ID NO: 180:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

15

Met Thr Lys Ala Ser Ser Leu Trp Pro Leu Lys Thr Thr Cys Gln Ile
 1 5 10 15

20

Ser Gly Thr Val Phe Phe Phe Leu Phe Leu Phe Ser Cys Phe Leu Met
 20 25 30

Gln Ala Gln Cys Asp Lys Phe Val Gly Trp Asp Phe Phe Phe Phe Leu
 35 40 45

25

30

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

40

Met Arg Arg Ala Leu Ile Pro Pro Cys Arg Gly Gly Pro Ser Ala Ser
 1 5 10 15

Asp Xaa Cys Cys Ser Cys Ser Pro Ser Gly Phe Ser Ala Gly Arg Gly
 20 25 30

45

Arg Cys Pro Val Gln Gly Cys Leu Arg Pro His Arg Val Gln Leu Leu
 35 40 45

Arg Arg Trp Gly Pro Gly Ser Pro Ala Gly Gln Arg Leu Ser Lys Gly
 50 55 60

50

Phe Gln Leu Leu Arg Trp Trp Gly Pro Gly Ser Pro Ala Pro Glu Pro
 65 70 75 80

55

Arg Lys Gly Pro Phe Pro Pro Pro Asp Pro Pro Trp Pro Val Thr Leu
 85 90 95

60

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Met Leu Glu Thr Thr Lys His Val Gln Ile Ala Cys Met Leu Leu Leu
 1 5 10 15
 Thr Cys Gln Ile Phe Leu Pro Ser Ser Leu Ser Pro Ser Phe Ile His
 20 25 30
 Ser Leu Thr Asp Ser Phe Ile Pro Leu Lys Lys Leu Tyr Val Cys Phe
 35 40 45
 Val Gln Ser Thr Leu Leu Lys Ala Ala Gly Tyr Lys Ser Ile Ser Glu
 50 55 60
 Ala Leu Gly Phe Asp Xaa Leu Leu Cys Ser Ser Ala Arg Phe Val Trp
 65 70 75 80
 Ile Cys His Thr Tyr Ser Arg Pro Leu Val Thr Cys Ala Leu His
 85 90 95

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

Met Ser Val Ile Gly Gly Leu Leu Leu Val Val Ala Leu Gly Pro Gly
 1 5 10 15
 Gly Val Ser Met Asp Glu Lys Lys Lys Glu Trp
 20 25

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

Met Ser Gly Gly Leu Ser Phe Leu Leu Leu Val
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

306

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

5

Met Phe Ala Asp Phe Ile Val Val Thr Ala Thr Val Gln Arg Cys Pro
 1 5 10 15

10

Gly Ser Pro Pro Leu Ser Glu Ile Leu Trp Lys Asp Glu Pro Phe Ala
 20 25 30

Ile Ser Ser His Ala Gly Leu Pro Trp Leu Ser Ser Trp Pro Ala Pro
 35 40 45

15

Pro Trp Thr Trp Ser Trp Ile Ser Arg Arg Arg Glu His Gly Arg Gly
 50 55 60

Ser
 65

20

(2) INFORMATION FOR SEQ ID NO: 186:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

30

Met Val Glu Ser Val Met Pro Val Val Val Cys Thr Leu Ser Pro Gly
 1 5 10 15

35

Ile Asp Ser Ser Pro Ser
 20

(2) INFORMATION FOR SEQ ID NO: 187:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

Met Asp Val Leu Phe Val Ala Ile Phe Ala Val Pro Leu Ile Leu Gly
 1 5 10 15

50

Gln Glu Tyr Glu Asp Glu Glu Arg Leu Gly Glu Asp Glu Tyr Tyr Gln
 20 25 30

Val Val Tyr Tyr Tyr Thr Val Thr Pro Ser Tyr Asp Asp Phe Ser Ala
 35 40 45

55

Asp Phe Thr Ile Asp Tyr Ser Ile Phe Glu Ser Glu Asp Arg Leu Asn
 50 55 60

60

Arg Leu Asp Lys Asp Ile Thr Glu Ala Ile Glu Thr Thr Ile Ser Leu
 65 70 75 80

Glu Thr Ala Arg Ala Asp His Pro Lys Pro Val Thr Val Lys Pro Val
 85 90 95
 5 Thr Thr Glu Pro Gln Ser Pro Asp Leu Asn Asp Ala Val Ser Ser Leu
 100 105 110
 Arg Ser Pro Ile Pro Leu Leu Leu Ser Cys Ala Phe Val Gln Val Gly
 115 120 125
 10 Met Tyr Phe Met
 130

15

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 amino acids
 20 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

25 Met Pro Cys Gln Pro Gly Gln Val Pro Ser Cys Gln Cys Thr Phe Gly
 1 5 10 15
 Leu Leu Leu Met Leu Pro Ser Leu Pro Ser Pro Ala Ser Gln Pro Arg
 20 25 30
 30 Pro Phe Cys Ser Ser Met Glu Tyr Phe His Gly Cys Ala Ser Pro Ser
 35 40 45
 Gln Ala Ile Ile Gly Gly Phe Pro Phe Ala Ser Val Ala Leu Ala Asp
 50 55 60
 35 Ile Leu Cys Leu Gln
 65

40

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 45 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

50 Met Ser Leu Leu Ser Pro Ala Ile Pro Ala Leu Thr Leu Ile Phe Ile
 1 5 10 15
 Leu Met Phe Phe Ser Phe Pro Phe Arg Ala His Thr Val Val Thr Ile
 20 25 30
 55 Val Ala Ser Gly Phe Leu Gly Leu Ser Pro Leu Cys Gly
 35 40 45

60

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Met Ala Phe Gly Leu Gln Met Phe Ile Gln Arg Lys Phe Pro Tyr Pro
 1 5 10 15
 Leu Gln Trp Ser Leu Leu Val Ala Val Val Ala Gly Ser Val Val Ser
 20 25 30
 Tyr Gly Val Thr Arg Val Glu Ser Glu Lys Cys Asn Asn Leu Trp Leu
 35 40 45
 Phe Leu Glu Thr Gly Gln Leu Pro Lys Asp Arg Ser Thr Asp Gln Arg
 50 55 60
 Ser
 65

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

Met Asn Leu Leu Gly Met Ile Phe Ser Met Cys Gly Leu Met Leu Lys
 1 5 10 15
 Leu Lys Trp Cys Ala Trp Val Ala Val Tyr Cys Ser Phe Ile Ser Phe
 20 25 30
 Ala Asn Ser Arg Ser Ser Glu Asp Thr Lys Gln Met Met Ser Ser Phe
 35 40 45
 Met Xaa
 50

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Met Leu Leu Asn Val Ala Leu Val Ala Leu Val Leu Leu Gly Ala Tyr
 1 5 10 15
 Arg Leu Trp Val Arg Trp Gly Arg Arg Gly Leu Gly Ala Gly Ala Gly
 20 25 30

309

Ala Gly Glu Glu Ser Pro Ala Thr Ser Leu Pro Arg Met Lys Lys Arg
 35 40 45

5 Asp Phe Ser Leu Glu Gln Leu Arg Gln Tyr Asp Gly Ser Arg Asn Pro
 50 55 60

Arg Ile Leu Leu Ala Val Asn Gly Lys Val Phe Asp Val Thr Lys Gly
 65 70 75 80

10 Ser Lys Phe Tyr Gly Pro Ala Gly Pro Tyr Gly Ile Phe Ala Gly Arg
 85 90 95

Asp Ala Ser Arg Gly Leu Ala Thr Phe Cys Leu Asp Lys Asp Ala Leu
 100 105 110

15 Arg Asp Glu Tyr Asp Asp Leu Ser Asp Leu Asn Ala Val Gln Met Glu
 115 120 125

20 Ser Val Arg Glu Trp Glu Met Gln Phe Lys Glu Lys Tyr Asp Tyr Val
 130 135 140

Gly Arg Leu Leu Lys Pro Gly Glu Glu Pro Ser Glu Tyr Thr Asp Glu
 145 150 155 160

25 Glu Asp Thr Lys Asp His Asn Lys Gln Asp
 165 170

30 (2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

Met Thr Tyr Phe Ser Gly Leu Leu Val Ile Leu Ala Phe Ala Ala Trp
 1 5 10 15

40 Val Ala Leu Ala Glu Gly Leu Gly Val Ala Val Tyr Ala Ala Ala Val
 20 25 30

45 Leu Leu Gly Ala Gly Cys Ala Thr Ile Leu Val Thr Ser Leu Ala Met
 35 40 45

Thr Ala Asp Leu Ile Gly Pro His Thr Asn Ser Gly Leu Ser Cys Thr
 50 55 60

50 Ala Pro
 65

55 (2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

5 Met Ala Ala Gly Pro Ser Gly Cys Leu Val Pro Ala Phe Gly Leu Arg
 1 5 10 15
 Leu Leu Leu Ala Thr Val Leu Gln Ala Val Ser Ala Phe Gly Ala Glu
 20 25 30
 10 Phe Ser Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser Asn Leu Leu
 35 40 45
 Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu Gln Leu Asp
 50 55 60
 15 Pro Asp Cys Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe Glu Thr Lys
 65 70 75 80
 Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val Cys Gly
 85 90
 20

(2) INFORMATION FOR SEQ ID NO: 195:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 176 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

30 Met Arg Gly Ser His Leu Arg Leu Leu Pro Tyr Leu Val Ala Ala Asn
 1 5 10 15
 35 Pro Val Asn Tyr Gly Arg Pro Tyr Arg Leu Ser Cys Val Glu Ala Phe
 20 25 30
 Ala Ala Thr Phe Cys Ile Val Gly Phe Pro Asp Leu Ala Val Ile Leu
 35 40 45
 40 Leu Arg Lys Phe Lys Trp Gly Lys Gly Phe Leu Asp Leu Asn Arg Gln
 50 55 60
 Leu Leu Asp Lys Tyr Ala Ala Cys Gly Ser Pro Glu Glu Val Leu Gln
 65 70 75 80
 45 Ala Glu Gln Glu Phe Leu Ala Asn Ala Lys Glu Ser Pro Gln Glu Glu
 85 90 95
 50 Glu Ile Asp Pro Phe Asp Val Asp Ser Gly Arg Glu Phe Gly Asn Pro
 100 105 110
 Asn Arg Pro Val Ala Ser Thr Arg Leu Pro Ser Asp Thr Asp Asp Ser
 115 120 125
 55 Asp Ala Ser Glu Asp Pro Gly Pro Xaa Ala Glu Arg Gly Gly Ala Ser
 130 135 140
 Ser Ser Cys Cys Glu Glu Glu Gln Thr Gln Gly Arg Gly Ala Glu Ala
 145 150 155 160
 60

Arg Ala Pro Ala Glu Val Trp Lys Gly Ile Lys Lys Arg Gln Arg Asp
 165 170 175

5

10 (2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Met Ser Asn Ala Cys Lys Glu Leu Ala Ile Phe Leu Thr Thr Gly Ile
 1 5 10 15
 20 Val Val Ser Ala Phe Gly Leu Pro Ile Val Phe Ala Arg Ala His Leu
 20 25 30
 Ile Glu Trp Gly Ala Cys Ala Leu Val Leu Thr Gly Asn Thr Val Ile
 35 40 45
 25 Phe Ala Thr Ile Leu Gly Phe Phe Leu Val Phe Gly Ser Asn Asp Asp
 50 55 60
 Phe Ser Trp Gln Gln Trp
 30 65 70

35 (2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

Met Thr Leu Leu Ile Ile Phe Leu Pro Phe Xaa Phe Thr Thr Xaa Thr
 1 5 10 15
 45 Asn Ser Gly Gly Ser Phe Pro Val Arg
 20 25

50 (2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Met Lys Gly Glu Leu Leu Pro Phe Leu Phe Leu Thr Val Trp Leu Trp
 1 5 10 15
 60

Leu Tyr Lys Leu Xaa Phe Gly Glu Ser Pro Arg Tyr Pro Asn Val Ile
 20 25 30

5 Gly Lys Thr Tyr Phe Phe Phe Trp Thr Asp Gln Ile Ser Arg Glu Ser
 35 40 45

Arg Phe Leu Glu Arg Leu Ala Phe Ile Val Ser Glu Asn Cys Leu Ile
 50 55 60

10 Phe Leu Ile His Ala Ile Thr Gly Gln
 65 70

15 (2) INFORMATION FOR SEQ ID NO: 199:

 (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 289 amino acids

 (B) TYPE: amino acid

20 (D) TOPOLOGY: linear

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

Met Ser Gly Phe Ser Thr Glu Glu Arg Ala Ala Pro Phe Ser Leu Glu
 1 5 10 15

25 Tyr Arg Val Phe Leu Lys Asn Glu Lys Gly Gln Tyr Ile Ser Pro Phe
 20 25 30

30 His Asp Ile Pro Ile Tyr Ala Asp Lys Asp Val Phe His Met Val Val
 35 40 45

Glu Val Pro Arg Trp Ser Asn Ala Lys Met Glu Ile Ala Thr Lys Asp
 50 55 60

35 Pro Leu Asn Pro Ile Lys Gln Asp Val Lys Lys Gly Lys Leu Arg Tyr
 65 70 75 80

Val Ala Asn Leu Phe Pro Tyr Lys Gly Tyr Ile Trp Asn Tyr Gly Ala
 85 90 95

40 Ile Pro Gln Thr Trp Glu Asp Pro Gly His Asn Asp Lys His Thr Gly
 100 105 110

45 Cys Cys Gly Asp Asn Asp Pro Ile Asp Val Cys Glu Ile Gly Ser Lys
 115 120 125

Val Cys Ala Arg Gly Glu Ile Ile Gly Val Lys Val Leu Gly Ile Leu
 130 135 140

50 Ala Met Ile Asp Glu Gly Glu Thr Asp Trp Lys Val Ile Ala Ile Asn
 145 150 155 160

Val Asp Asp Pro Asp Ala Ala Asn Tyr Asn Asp Ile Asn Asp Val Lys
 165 170 175

55 Arg Leu Lys Pro Gly Tyr Leu Glu Ala Thr Val Asp Trp Phe Arg Arg
 180 185 190

60 Tyr Lys Val Pro Asp Gly Lys Pro Glu Asn Glu Phe Ala Phe Asn Ala
 195 200 205

Glu Phe Lys Asp Lys Asp Phe Ala Ile Asp Ile Ile Lys Ser Thr His
 210 215 220
 5 Asp His Trp Lys Ala Leu Val Thr Lys Lys Thr Asn Gly Lys Gly Ile
 225 230 235 240
 Ser Cys Met Asn Thr Thr Leu Ser Glu Ser Pro Phe Lys Cys Asp Pro
 245 250 255
 10 Asp Ala Ala Arg Ala Ile Val Asp Ala Leu Pro Pro Pro Cys Glu Ser
 260 265 270
 15 Ala Cys Thr Val Pro Thr Asp Val Asp Lys Trp Phe His His Gln Lys
 275 280 285
 Asn
 20
 (2) INFORMATION FOR SEQ ID NO: 200:
 (i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 625 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:
 30 Met Glu Ile Pro Gly Ser Leu Cys Lys Lys Val Lys Leu Ser Asn Asn
 1 5 10 15
 Ala Gln Asn Trp Gly Met Gln Arg Ala Thr Asn Val Thr Tyr Gln Ala
 20 25 30
 35 His His Val Ser Arg Asn Lys Arg Gly Gln Val Val Gly Thr Arg Gly
 35 40 45
 40 Gly Phe Arg Gly Cys Thr Val Trp Leu Thr Gly Leu Ser Gly Ala Gly
 50 55 60
 Lys Thr Thr Val Ser Met Ala Leu Glu Glu Tyr Leu Val Cys His Gly
 65 70 75 80
 45 Ile Pro Cys Tyr Thr Leu Asp Gly Asp Asn Ile Arg Gln Gly Leu Asn
 85 90 95
 Lys Asn Leu Gly Phe Ser Pro Glu Asp Arg Glu Glu Asn Val Arg Arg
 100 105 110
 50 Ile Ala Glu Val Ala Lys Leu Phe Ala Asp Ala Gly Leu Val Cys Ile
 115 120 125
 55 Thr Ser Phe Ile Ser Pro Tyr Thr Gln Asp Arg Asn Asn Ala Arg Gln
 130 135 140
 Ile His Glu Gly Ala Ser Leu Pro Phe Phe Glu Val Phe Val Asp Ala
 145 150 155 160
 60 Pro Leu His Val Cys Glu Gln Arg Asp Val Lys Gly Leu Tyr Lys Lys

	165	170	175
	Ala Arg Ala Gly Glu Ile Lys Gly Phe Thr Gly Ile Asp Ser Glu Tyr		
	180	185	190
5	Glu Lys Pro Glu Ala Pro Glu Leu Val Leu Lys Thr Asp Ser Cys Asp		
	195	200	205
10	Val Asn Asp Cys Val Gln Gln Val Val Glu Leu Leu Gln Glu Arg Asp		
	210	215	220
	Ile Val Pro Val Asp Ala Ser Tyr Glu Val Lys Glu Leu Tyr Val Pro		
	225	230	235
15	Glu Asn Lys Leu His Leu Ala Lys Thr Asp Ala Glu Thr Leu Pro Ala		
	245	250	255
20	Leu Lys Ile Asn Lys Val Asp Met Gln Trp Val Gln Val Leu Ala Glu		
	260	265	270
	Gly Trp Ala Thr Pro Leu Asn Gly Phe Met Arg Glu Arg Glu Tyr Leu		
	275	280	285
25	Gln Cys Leu His Phe Asp Cys Leu Leu Asp Gly Gly Val Ile Asn Leu		
	290	295	300
	Ser Val Pro Ile Val Leu Thr Ala Thr His Glu Asp Lys Glu Arg Leu		
	305	310	315
30	Asp Gly Cys Thr Ala Phe Ala Leu Met Tyr Glu Gly Arg Arg Val Ala		
	325	330	335
35	Ile Leu Arg Asn Pro Glu Phe Phe Glu His Arg Lys Glu Glu Arg Cys		
	340	345	350
	Ala Arg Gln Trp Gly Thr Thr Cys Lys Asn His Pro Tyr Ile Lys Met		
	355	360	365
40	Val Met Glu Gln Gly Asp Trp Leu Ile Gly Gly Asp Leu Gln Val Leu		
	370	375	380
	Asp Arg Val Tyr Trp Asn Asp Gly Leu Asp Gln Tyr Arg Leu Thr Pro		
	385	390	395
45	Thr Glu Leu Lys Gln Lys Phe Lys Asp Met Asn Ala Asp Ala Val Phe		
	405	410	415
50	Ala Phe Gln Leu Arg Asn Pro Val His Asn Gly His Ala Leu Leu Met		
	420	425	430
	Gln Asp Thr His Lys Gln Leu Leu Glu Arg Gly Tyr Arg Arg Pro Val		
	435	440	445
55	Leu Leu Leu His Pro Leu Gly Gly Trp Thr Lys Asp Asp Asp Val Pro		
	450	455	460
	Leu Met Trp Arg Met Lys Gln His Ala Ala Val Leu Glu Glu Gly Val		
	465	470	475
60	Leu Asn Pro Glu Thr Thr Val Val Ala Ile Phe Pro Ser Pro Met Met		

315

485 490 495
 Tyr Ala Gly Pro Thr Glu Val Gln Trp His Cys Arg Ala Arg Met Val
 500 505 510
 5 Ala Gly Ala Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met Pro
 515 520 525
 10 His Pro Glu Thr Gly Lys Asp Leu Tyr Glu Pro Ser His Gly Ala Lys
 530 535 540
 Val Leu Thr Met Ala Pro Gly Leu Ile Thr Leu Glu Ile Val Pro Phe
 545 550 555 560
 15 Arg Val Ala Ala Tyr Asn Lys Lys Lys Lys Arg Met Asp Tyr Tyr Asp
 565 570 575
 Ser Glu His His Glu Asp Phe Glu Phe Ile Ser Gly Thr Arg Met Arg
 580 585 590
 20 Lys Leu Ala Arg Glu Gly Gln Lys Pro Pro Glu Gly Phe Met Ala Pro
 595 600 605
 25 Lys Ala Trp Thr Val Leu Thr Glu Tyr Tyr Lys Ser Leu Glu Lys Ala
 610 615 620
 Xaa
 625

30

(2) INFORMATION FOR SEQ ID NO: 201:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 649 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

40 Met Ser Ala Ser Gln Asp Leu Glu Pro Lys Pro Leu Phe Pro Lys Pro
 1 5 10 15
 Ala Phe Gly Gln Lys Pro Pro Leu Ser Thr Glu Asn Ser His Glu Asp
 20 25 30
 45 Glu Ser Pro Met Lys Asn Val Ser Ser Ser Lys Gly Ser Pro Ala Pro
 35 40 45
 50 Leu Gly Val Arg Ser Lys Ser Gly Pro Leu Lys Pro Ala Arg Glu Asp
 50 55 60
 Ser Glu Asn Lys Asp His Ala Gly Glu Ile Ser Ser Leu Pro Phe Pro
 65 70 75 80
 55 Gly Val Val Leu Lys Pro Ala Ala Ser Arg Gly Gly Pro Gly Leu Ser
 85 90 95
 Lys Asn Gly Glu Glu Lys Lys Glu Asp Arg Lys Ile Asp Ala Ala Lys
 100 105 110
 60

316

Asn Thr Phe Gln Ser Lys Ile Asn Gln Glu Glu Leu Ala Ser Gly Thr
 115 120 125
 5 Pro Pro Ala Arg Phe Pro Lys Ala Pro Ser Lys Leu Thr Val Gly Gly
 130 135 140
 Pro Trp Gly Gln Ser Gln Glu Lys Glu Lys Gly Asp Lys Asn Ser Ala
 145 150 155 160
 10 Thr Pro Lys Gln Lys Pro Leu Pro Pro Leu Phe Thr Leu Gly Pro Pro
 165 170 175
 Pro Pro Lys Pro Asn Arg Pro Pro Asn Val Asp Leu Thr Lys Phe His
 180 185 190
 15 Lys Thr Ser Ser Gly Asn Ser Thr Ser Lys Gly Gln Thr Ser Tyr Ser
 195 200 205
 20 Thr Thr Ser Leu Pro Pro Pro Pro Pro Ser His Pro Ala Ser Gln Pro
 210 215 220
 Pro Leu Pro Ala Ser His Pro Ser Gln Pro Pro Val Pro Ser Leu Pro
 225 230 235 240
 25 Pro Arg Asn Ile Lys Pro Pro Phe Asp Leu Lys Ser Pro Val Asn Glu
 245 250 255
 Asp Asn Gln Asp Gly Val Thr His Ser Asp Gly Ala Gly Asn Leu Asp
 260 265 270
 30 Glu Glu Gln Asp Ser Glu Gly Glu Thr Tyr Glu Asp Ile Glu Ala Ser
 275 280 285
 35 Lys Glu Arg Glu Lys Lys Arg Glu Lys Glu Glu Lys Lys Arg Leu Glu
 290 295 300
 Leu Glu Lys Lys* Glu Gln Lys Glu Lys Glu Lys Lys Glu Gln Glu Ile
 305 310 315 320
 40 Lys Lys Lys Phe Lys Leu Thr Gly Pro Ile Gln Val Ile His Leu Ala
 325 330 335
 Lys Ala Cys Cys Asp Val Lys Gly Gly Lys Asn Glu Leu Ser Phe Lys
 340 345 350
 45 Gln Gly Glu Gln Ile Glu Ile Ile Arg Ile Thr Asp Asn Pro Glu Gly
 355 360 365
 50 Lys Trp Leu Gly Arg Thr Ala Arg Gly Ser Tyr Gly Tyr Ile Lys Thr
 370 375 380
 Thr Ala Val Glu Ile Asp Tyr Asp Ser Leu Lys Leu Lys Lys Asp Ser
 385 390 395 400
 55 Leu Gly Ala Pro Ser Arg Pro Ile Glu Asp Asp Gln Glu Val Tyr Asp
 405 410 415
 Asp Val Ala Glu Gln Asp Asp Ile Ser His Ser Gln Ser Gly Ser
 420 425 430
 60

317

Gly Gly Ile Phe Pro Pro Pro Pro Asp Asp Asp Ile Tyr Asp Gly Ile
 435 440 445
 5 Glu Glu Glu Asp Ala Asp Asp Gly Ser Thr Leu Gln Val Gln Glu Lys
 450 455 460
 Ser Asn Thr Trp Ser Trp Gly Ile Leu Lys Met Leu Lys Gly Lys Asp
 465 470 475 480
 10 Asp Arg Lys Lys Ser Ile Arg Glu Lys Pro Lys Val Ser Asp Ser Asp
 485 490 495
 Asn Asn Glu Gly Ser Ser Phe Pro Ala Pro Pro Lys Gln Leu Asp Met
 500 505 510
 15 Gly Asp Glu Val Tyr Asp Asp Val Asp Thr Ser Asp Phe Pro Val Ser
 515 520 525
 Ser Ala Glu Met Ser Gln Gly Thr Asn Val Gly Lys Ala Lys Thr Glu
 530 535 540
 Glu Lys Asp Leu Lys Lys Leu Lys Lys Gln Xaa Lys Xaa Xaa Lys Asp
 545 550 555 560
 25 Phe Arg Lys Lys Phe Lys Tyr Asp Gly Glu Ile Arg Val Leu Tyr Ser
 565 570 575
 Thr Lys Val Thr Thr Ser Ile Thr Ser Lys Lys Trp Gly Thr Arg Asp
 580 585 590
 30 Leu Gln Val Lys Pro Gly Glu Ser Leu Glu Val Ile Gln Thr Thr Asp
 595 600 605
 Asp Thr Lys Val Leu Cys Arg Asn Glu Glu Gly Lys Tyr Gly Tyr Val
 610 615 620
 35 Leu Arg Ser Tyr Leu Ala Asp Asn Asp Gly Glu Ile Tyr Asp Asp Ile
 625 630 635 640
 40 Ala Asp Gly Cys Ile Tyr Asp Asn Asp
 645

45 (2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Met Ala Trp Pro Ser Arg Ser Lys Met Phe Thr Leu Leu Pro Val Leu
 1 5 10 15
 55 Cys Tyr Leu Trp Ser Leu Trp Leu Pro Gln Phe Ser Trp Ile Gln Glu
 20 25 30
 60 Leu Lys Ala Val Leu Arg Asp Asp Gly Leu Ile Ser Ala Val Ala Trp
 35 40 45

Asn Ala Glu Phe Gln Thr Cys
50 55

5

(2) INFORMATION FOR SEQ ID NO: 203:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

15 Met Val Lys Val Thr Phe Asn Ser Ala Leu Ala Gln Lys Glu Ala Lys
1 5 10 15

Lys Asp Glu Pro Lys Ser Gly Glu Glu Ala Leu Ile Ile Pro Pro Asp
20 25 30

20

Ala Val Ala Val Asp Cys Lys Asp Pro Asp Asp Val Val Pro Val Gly
35 40 45

25 Gln Arg Arg Ala Trp Cys Trp Cys Met Cys Phe Gly Leu Ala Phe Met
50 55 60

Leu Ala Gly Val Ile Leu Gly Gly Ala Tyr Leu Tyr Lys Tyr Phe Ala
65 70 75 80

30 Leu Gln Pro Asp Asp Val Tyr Tyr Cys Gly Ile Lys Tyr Ile Lys Asp
85 90 95

Asp Val Ile Leu Asn Glu Pro Ser Ala Asp Ala Pro Ala Ala Leu Tyr
100 105 110

35

Gln Thr Ile Glu Glu Asn Ile Lys Ile Phe Glu Glu Glu Glu Val Glu
115 120 125

40 Phe Ile Ser Val Pro Val Pro Glu Phe Ala Asp Ser Asp Pro Ala Asn
130 135 140

Ile Val His Asp Phe Asn Lys Lys Leu Thr Ala Tyr Leu Asp Leu Asn
145 150 155 160

45 Leu Asp Lys Cys Tyr Val Ile Pro Leu Asn Thr Ser Ile Val Met Pro
165 170 175

Pro Arg Asn Leu Leu Glu Leu Leu Ile Asn Ile Lys Ala Gly Thr Tyr
180 185 190

50

Leu Pro Gln Ser Tyr Leu Ile His Glu His Met Val Ile Thr Asp Arg
195 200 205

55 Ile Glu Asn Ile Asp His Leu Gly Phe Phe Ile Tyr Arg Leu Cys His
210 215 220

Asp Lys Glu Thr Tyr Lys Leu Gln Arg Arg Glu Thr Ile Lys Gly Ile
225 230 235 240

60 Gln Lys Arg Glu Ala Ser Asn Cys Phe Ala Ile Arg His Phe Glu Asn

319

245 250 255

Lys Phe Ala Val Glu Thr Leu Ile Cys Ser Xaa
260 265

5

(2) INFORMATION FOR SEQ ID NO: 204:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe
1 5 10 15

Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro
20 25 30

Gln Leu Ser Asp Lys Val His Asn Asp Ala Gln Ser Phe Asp Tyr Asp
35 40 45

25 His Asp Ala Phe Leu Gly Ala Glu Glu Ala Lys Thr Phe Asp Gln Leu
50 55 60

Thr Pro Glu Glu Ser Lys Glu Arg Leu Gly Lys Ile Val Ser Lys Ile
65 70 75 80

30 Asp Gly Asp Lys Asp Gly Phe Val Thr Val Asp Glu Leu Lys Asp Trp
85 90 95

Ile Lys Phe Ala Gln Lys Arg Trp Ile Tyr Glu Asp Val Glu Arg Gln
35 100 105 110

Trp Lys Gly His Asp Leu Asn Glu Asp Gly Leu Val Ser Trp Glu Glu
115 120 125

40 Tyr Lys Asn Ala Thr Tyr Gly Tyr Val Leu Asp Asp Pro Asp Pro Asp
130 135 140

Asp Gly Phe Asn Tyr Lys Gln Met Met Val Arg Asp Glu Arg Arg Phe
145 150 155 160

45 Lys Met Ala Asp Lys Asp Gly Asp Leu Ile Ala Thr Lys Glu Glu Phe
165 170 175

Thr Ala Phe Leu His Pro Glu Glu Tyr Asp Tyr Met Lys Asp Ile Val
50 180 185 190

Val Gln Glu Thr Met Glu Asp Ile Asp Lys Asn Ala Asp Gly Phe Ile
195 200 205

55 Asp Leu Glu Glu Tyr Ile Gly Asp Met Tyr Ser His Asp Gly Asn Thr
210 215 220

Asp Glu Pro Glu Trp Val Lys Thr Glu Arg Glu Gln Phe Val Glu Phe
225 230 235 240

60

320

[illegible]

(2) INFORMATION FOR SEQ ID NO: 205:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 207 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

25	Met	Phe	Asp	Ala	Val	Leu	Ile	Leu	Leu	Ile	Pro	Leu	Lys	Asp	Lys	
	1				5				10					15		
30	Leu	Val	Asp	Pro	Ile	Leu	Arg	Arg	His	Gly	Leu	Leu	Pro	Ser	Ser	Leu
				20					25					30		
	Lys	Arg	Ile	Ala	Val	Gly	Met	Phe	Phe	Val	Met	Cys	Ser	Ala	Phe	Ala
			35					40					45			
35	Ala	Gly	Ile	Leu	Glu	Ser	Lys	Arg	Leu	Asn	Leu	Val	Lys	Glu	Lys	Thr
	50						55					60				
	Ile	Asn	Gln	Thr	Ile	Gly	Asn	Val	Val	Tyr	His	Ala	Ala	Asp	Leu	Ser
40	65					70					75					80
	Leu	Trp	Trp	Gln	Val	Pro	Gln	Tyr	Leu	Leu	Ile	Gly	Ile	Ser	Glu	Ile
				85					90						95	
45	Phe	Ala	Ser	Ile	Ala	Gly	Leu	Glu	Phe	Ala	Tyr	Ser	Ala	Ala	Pro	Lys
				100					105					110		
	Ser	Met	Gln	Ser	Ala	Ile	Met	Gly	Leu	Phe	Phe	Phe	Phe	Ser	Gly	Val
			115					120					125			
50	Gly	Ser	Phe	Val	Gly	Ser	Gly	Leu	Leu	Ala	Leu	Val	Ser	Ile	Lys	Ala
	130						135					140				
	Ile	Gly	Trp	Met	Ser	Ser	His	Thr	Asp	Phe	Gly	Asn	Ile	Asn	Gly	Cys
55	145					150					155					160
	Tyr	Leu	Asn	Tyr	Tyr	Phe	Phe	Leu	Leu	Ala	Ala	Ile	Gln	Gly	Ala	Thr
				165						170					175	
60	Leu	Leu	Leu	Phe	Leu	Ile	Ile	Ser	Val	Lys	Tyr	Asp	His	His	Arg	Asp
				180					185					190		

321

His Gln Arg Ser Arg Ala Asn Gly Val Pro Thr Ser Arg Arg Ala
 195 200 205

5

(2) INFORMATION FOR SEQ ID NO: 206:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

15 Met Arg Ser Arg Ile Arg Glu Phe Asp Ser Ser Thr Leu Asn Glu Ser
 1 5 10 15
 Val Arg Asn Thr Ile Met Arg Asp Leu Lys Ala Val Gly Lys Lys Phe
 20 20 25 30
 Met His Val Leu Tyr Pro Arg Lys Ser Asn Thr Leu Leu Arg Asp Trp
 35 40 45
 25 Asp Leu Trp Gly Pro Leu Ile Leu Cys Val Thr Leu Ala Leu Met Leu
 50 55 60
 Gln Arg Asp Ser Ala Asp Ser Glu Lys Asp Gly Gly Pro Gln Phe Ala
 65 70 75 80
 30 Glu Val Phe Val Ile Val Trp Phe Gly Ala Val Thr Ile Thr Leu Asn
 85 90 95
 Ser Lys Leu Leu Gly Gly Asn Ile Ser Phe Phe Gln Ser Leu Cys Val
 100 105 110
 35 Leu Gly Tyr Cys Ile Leu Pro Leu Thr Val Ala Met Leu Ile Cys Arg
 115 120 125
 Leu Val Leu Leu Ala Asp Pro Gly Pro Val Asn Phe Met Val Arg Leu
 130 135 140
 Phe Val Val Ile Val Met Phe Ala Trp Ser Ile Val Ala Ser Thr Ala
 145 150 155 160
 45 Phe Leu Ala Asp Ser Gln Pro Pro Asn Arg Arg Ala Leu Ala Val Tyr
 165 170 175
 Pro Val Phe Leu Phe Tyr Phe Val Ile Ser Trp Met Ile Leu Thr Phe
 180 185 190
 50 Thr Pro Gln Xaa
 195

55

(2) INFORMATION FOR SEQ ID NO: 207:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 amino acids
 (B) TYPE: amino acid

60

322

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

5 Met Ala Lys Asp Gln Ala Val Glu Asn Ile Leu Val Ser Pro Val Val
 1 5 10 15
 Val Ala Ser Ser Leu Gly Leu Val Ser Leu Gly Gly Lys Ala Thr Thr
 20 25 30
 10 Ala Ser Gln Ala Lys Ala Val Leu Ser Ala Glu Gln Leu Arg Asp Glu
 35 40 45
 Glu Val His Ala Gly Leu Gly Glu Leu Leu Arg Ser Leu Ser Asn Ser
 50 55 60
 15 Thr Ala Arg Asn Val Thr Trp Lys Leu Gly Ser Arg Leu Tyr Gly Pro
 65 70 75 80
 Ser Ser Val Ser Phe Ala Asp Asp Phe Val Arg Ser Ser Lys Gln His
 85 90 95
 Tyr Asn Cys Glu His Ser Lys Ile Asn Phe Arg Asp Lys Arg Ser Ala
 100 105 110
 25 Leu Gln Ser Ile Asn Glu Trp Ala Ala Gln Thr Thr Asp Gly Lys Leu
 115 120 125
 Pro Glu Val Thr Lys Asp Val Glu Arg Thr Asp Gly Ala Leu Leu Val
 130 135 140
 30 Asn Ala Met Phe Phe Lys Pro His Trp Asp Glu Lys Phe His His Lys
 145 150 155 160
 Met Val Asp Asn Arg Gly Phe Met Val Thr Arg Ser Tyr Thr Val Gly
 165 170 175
 Val Met Met Met His Arg Thr Gly Leu Tyr Asn Tyr Tyr Asp Asp Glu
 180 185 190
 40 Lys Glu Lys Leu Gln Ile Val Glu Met Pro Leu Ala His Lys Leu Ser
 195 200 205
 Ser Leu Ile Ile Leu Met Pro His His Val Glu Pro Leu Glu Arg Leu
 210 215 220
 45 Glu Lys Leu Leu Thr Lys Glu Gln Leu Lys Ile Trp Met Gly Lys Met
 225 230 235 240
 Gln Lys Lys Ala Val Ala Ile Ser Leu Pro Lys Gly Val Val Glu Val
 245 250 255
 50 Thr His Asp Leu Gln Lys His Leu Ala Gly Leu Gly Leu Thr Glu Ala
 260 265 270
 55 Ile Asp Lys Asn Lys Ala Asp Leu Ser Arg Met Ser Gly Lys Lys Asp
 275 280 285
 Leu Tyr Leu Ala Ser Val Phe His Ala Thr Ala Phe Glu Leu Asp Thr
 290 295 300
 60

323

Asp Gly Asn Pro Leu Thr Arg Ile Thr Gly Gly Gly Val Arg Thr Gln
 305 310 315 320

5 Val Phe Tyr Ala Asp His Pro Phe Ile Ser Xaa
 325 330

10 (2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

Met Cys Met Gln Leu Phe Gly Phe Leu Ala Phe Met Ile Phe Met Cys
 1 5 10 15

20 Trp Val Gly Asp Val Tyr Pro Val Tyr Gln Pro Val Gly Pro Lys Gln
 20 25 30

Tyr Pro Tyr Asn Asn Leu Tyr Leu Glu Arg Gly Gly Asp Pro Ser Lys
 35 40 45

25 Glu Pro Glu Arg Val Val His Tyr Glu Ile
 50 55

30 (2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 392 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

40 Met Asp Ala Leu Val Glu Asp Asp Ile Cys Ile Leu Asn His Glu Lys
 1 5 10 15

Ala His Lys Arg Asp Thr Val Thr Pro Val Ser Ile Tyr Ser Gly Asp
 20 25 30

45 Glu Ser Val Ala Ser His Phe Ala Leu Val Thr Ala Tyr Glu Asp Ile
 35 40 45

Lys Lys Arg Leu Lys Asp Ser Glu Lys Glu Asn Ser Leu Leu Lys Lys
 50 55 60

50 Arg Ile Arg Phe Leu Glu Lys Leu Ile Ala Arg Phe Glu Glu Glu
 65 70 75 80

55 Thr Ser Ser Val Gly Arg Glu Gln Val Asn Lys Ala Tyr His Ala Tyr
 85 90 95

Arg Glu Val Cys Ile Asp Arg Asp Asn Leu Lys Ser Lys Leu Asp Lys
 100 105 110

60 Met Asn Lys Asp Asn Ser Glu Ser Leu Lys Val Leu Asn Glu Gln Leu

324

	115	120	125
	Gln Ser Lys Glu Val	Glu Leu Leu Gln Leu Arg Thr	Glu Val Glu Thr
	130	135	140
5	Gln Gln Val Met Arg Asn Leu Asn Pro Pro Ser Ser Asn Trp Glu Val		
	145	150	155 160
10	Glu Lys Leu Ser Cys Asp Leu Lys Ile His Gly Leu Glu Gln Glu Leu		
		165 170	175
	Glu Leu Met Arg Lys Glu Cys Ser Asp Leu Lys Ile Glu Leu Gln Lys		
		180 185	190
15	Ala Lys Gln Thr Asp Pro Tyr Gln Glu Asp Asn Leu Lys Ser Arg Asp		
		195 200	205
	Leu Gln Lys Leu Ser Ile Ser Ser Asp Asn Met Gln His Ala Tyr Trp		
		210 215	220
20	Glu Leu Lys Arg Glu Met Ser Asn Leu His Leu Val Thr Gln Val Gln		
		225 230	235 240
25	Ala Glu Leu Leu Arg Lys Leu Lys Thr Ser Thr Ala Ile Lys Lys Ala		
		245 250	255
	Cys Ala Pro Val Gly Cys Ser Glu Asp Leu Gly Arg Asp Ser Thr Lys		
		260 265	270
30	Leu His Leu Met Asn Phe Thr Ala Thr Tyr Thr Arg His Pro Pro Leu		
		275 280	285
	Leu Pro Asn Gly Lys Ala Leu Cys His Thr Thr Ser Ser Pro Leu Pro		
		290 295	300
35	Gly Asp Val Lys Val Leu Ser Glu Lys Ala Ile Leu Gln Ser Trp Thr		
		305 310	315 320
40	Asp Asn Glu Arg Ser Ile Pro Asn Asp Gly Thr Cys Phe Gln Glu His		
		325 330	335
	Ser Ser Tyr Gly Arg Asn Ser Leu Glu Asp Asn Ser Trp Val Phe Pro		
		340 345	350
45	Ser Pro Pro Lys Ser Ser Glu Thr Ala Phe Gly Glu Thr Lys Thr Lys		
		355 360	365
	Thr Leu Pro Leu Pro Asn Leu Pro Pro Leu His Tyr Leu Asp Gln His		
		370 375	380
50	Asn Gln Asn Cys Leu Tyr Lys Asn		
		385 390	

55

(2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

60

325

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

5 Met His His His Thr Gln Leu Met Phe Ile Tyr Leu Phe Ile Tyr Leu
 1 5 10 15
 Phe Ile Leu Gly Val Phe Phe Phe Phe Phe Xaa
 20 25

10

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

20 Met Asn Cys Ile Leu Leu Leu Tyr Leu Leu Ile Pro Thr Ile Ser Ile
 1 5 10 15
 Ser Val Val Pro Tyr Val Ala Leu Asn Ile Lys Tyr Ile Lys Glu Cys
 20 25 30
 25 Thr Glu Asn Ser Phe Tyr Xaa
 35

30

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 71 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

40 Met Leu Leu His Leu Thr Ala Ala Phe Leu Gln Arg Ala Gln Phe Ser
 1 5 10 15
 Thr Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val
 20 25 30
 45 Phe Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr
 35 40 45
 Ala Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr
 50 55 60
 50 Arg Val Leu Phe Ile Tyr Xaa
 65 70

55

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 83 amino acids
 (B) TYPE: amino acid

326

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

5 Met Leu Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe
1 5 10 15
Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile
20 25 30
10 Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe
35 40 45
Ser Thr Tyr Phe Pro Ala Phe Met Asn Ser Leu Ser Arg Ser Lys Arg
50 55 60
15 Thr Pro Ala Gly Ser Glu Ser Arg Cys Arg Thr Gln Arg Asn Asn His
65 70 75 80
20 Leu Leu Xaa

(2) INFORMATION FOR SEQ ID NO: 214:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

Met Ser Lys Arg Ser Ala Ser Phe Ile Leu Leu Pro Leu Leu Phe Leu
1 5 10 15
35 Lys Gly Ser Phe Ala Lys Leu Asn Ala Arg Ile Ser Asp Cys Leu Glu
20 25 30
Glu Arg Tyr Cys His Asn Leu Trp Met Val Phe Gln Gly Cys Val Ile
35 40 45
40 Thr Glu Leu His Leu Ser Arg Met Ser Lys Thr Leu Ser Ser Leu Cys
50 55 60
45 Tyr Asp Phe Val Ile Asn Val Tyr Ile Phe Phe Lys Phe Leu Asp Ile
65 70 75 80
Thr

50

(2) INFORMATION FOR SEQ ID NO: 215:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

60

Met Cys Ser Leu Phe Glu Ser Arg Phe Phe Cys Phe Val Leu Phe Ser

327

1 5 10 15
 Glu Lys Ile Ile Gln Leu Cys Ala Ser Ile Ala Phe Leu Cys Phe Val
 20 25 30
 5 Lys His Val Pro Trp Pro Lys Trp Lys Arg Lys Cys Leu Ile Asn Ala
 35 40 45
 10 Phe

15 (2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

Met Thr Leu Arg Pro Ser Leu Leu Pro Leu His Leu Leu Leu Leu Leu
 1 5 10 15
 25 Leu Leu Ser Ala Ala Val Cys Arg Ala Glu Ala Gly Leu Glu Thr Glu
 20 25 30
 Ser Pro Val Arg Thr Leu Gln Val Glu Thr Leu Val Glu Pro Pro Glu
 35 40 45
 30 Pro Cys Ala Glu Pro Ala Ala Phe Gly Asp Thr Leu His Ile His Tyr
 50 55 60
 Thr Gly Ser Leu Val Asp Gly Arg Ile Ile Asp Thr Ser Leu Thr Arg
 35 65 70 75 80
 Asp Pro Leu Val Ile Glu Leu Gly Gln Lys Gln Val Ile Pro Gly Leu
 85 90 95
 40 Glu Gln Ser Leu Leu Asp Met Cys Val Gly Glu Lys Arg Arg Ala Ile
 100 105 110
 Ile Pro Ser His Leu Ala Tyr Gly Lys Arg Gly Phe Pro Pro Ser Val
 115 120 125
 45 Pro Ala Asp Ala Val Val Gln Tyr Asp Val Glu Leu Ile Ala Leu Ile
 130 135 140
 Arg Ala Asn Tyr Trp Leu Lys Leu Val Lys Gly Ile Leu Pro Leu Val
 50 145 150 155 160
 Gly Met Ala Met Val Pro Pro Ser Trp Ala Ser Leu Gly Ile Thr Tyr
 165 170 175
 55 Thr Glu Arg Pro Ile Asp Pro Lys Ser Pro Lys Arg Ser Ser Arg Lys
 180 185 190
 Arg Asn Glu Thr Arg Ala Lys Arg Asn Asn Lys
 195 200
 60

(2) INFORMATION FOR SEQ ID NO: 217:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

10

Met Lys Thr Leu Met Thr Ile Cys Pro Gly Thr Val Leu Leu Val Phe
 1 5 10 15

15

Ser Ile Ser Leu Trp Ile Ile Ala Ala Trp Thr Val Arg Val Cys Glu
 20 25 30

Ser Pro Glu Ser Pro Ala Gln Pro Ser Gly Ser Ser Leu Pro Ala Trp
 35 40 45

20

Tyr His Asp Gln Gln Asp Val Thr Ser Asn Phe Leu Gly Ala Met Trp
 50 55 60

25

Leu Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr Gly Asp Met Val Pro
 65 70 75 80

His Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu Thr Gly Ile Met Gly
 85 90 95

30

Ala Gly Cys Thr Ala Leu Val Val Ala Val Val Ala Arg Lys Leu Glu
 100 105 110

Leu Thr Lys Ala Glu Lys His Val His Xaa Phe Met Met Asp Thr Gln
 115 120 125

35

Leu Thr Lys Arg Ile Lys Asn Xaa Ala Ala Asn Val Leu Xaa Glu Thr
 130 135 140

40

Trp Leu Ile Tyr Lys His Thr Lys Leu Leu Lys Lys Ile Asp His Ala
 145 150 155 160

Lys Val Arg Asn Thr Arg Gly Ser Ser Ser Lys Tyr Pro Pro Val Glu
 165 170 175

45

Glu Arg Gln Asp Gly Thr Glu Glu Ala Glu
 180 185

50

(2) INFORMATION FOR SEQ ID NO: 218:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile Phe Leu
 1 5 10 15

60

Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr Tyr Pro

329

20 25 30

Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu Thr Thr Ala
35 40 45

5 Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr Ala Thr Thr Ala
50 55 60

10 Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val Leu Pro Lys Trp Val
65 70 75 80

Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
85 90

15

(2) INFORMATION FOR SEQ ID NO: 219:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

25 Met Ser Ser Ala Ala Ala Asp His Trp Ala Trp Leu Leu Val Leu Ser
1 5 10 15

Phe Val Phe Gly Cys Asn Val Leu Arg Ile Leu Leu Pro Ser Phe Ser
20 25 30

30 Ser Phe Met Ser Arg Val Leu Gln Lys Asp Ala Glu Gln Glu Ser Gln
35 40 45

35 Met Arg Ala Glu Ile Gln Asp Met Lys Gln Glu Leu Ser Thr Val Asn
50 55 60

Met Met Asp Glu Phe Ala Arg Tyr Ala Arg Leu Glu Arg Lys Ile Asn
65 70 75 80

40 Lys Met Thr Asp Lys Leu Lys Thr His Val Lys Ala Arg Thr Ala Gln
85 90 95

Leu Ala Lys Ile Lys Trp Val Ile Ser Val Ala Phe Tyr Val Leu Gln
100 105 110

45 Ala Ala Leu Met Ile Ser Leu Ile Trp Lys Tyr Tyr Ser Val Pro Val
115 120 125

50 Ala Val Val Pro Ser Lys Trp Ile Thr Leu Xaa
130 135

55

(2) INFORMATION FOR SEQ ID NO: 220:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

330

Met Ser Ser Ala Ala Ala Asp His Trp Ala Trp Leu Leu Val Leu Ser
 1 5 10 15
 5 Phe Val Phe Gly Cys Asn Val Leu Arg Ile Leu Leu Pro Ser Phe Ser
 20 25 30
 Ser Phe Met Ser Arg Val Leu Gln Lys Asp Ala Asp Arg Ser His Arg
 35 40 45
 10

15

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe Leu Ile
 1 5 10 15
 Val Phe Phe Ser Leu Gly Val Phe Cys Ile Cys His Ser His Trp Tyr
 20 25 30
 30 His Thr Leu Gln Gln Met Ala Gly Thr Glu Pro Lys Ala Leu Leu Leu
 35 40 45
 Ser Pro Pro Ala Ala Thr Thr Phe Val Thr Val Thr His Glu Val Trp
 50 55 60
 35 Lys Glu Gln Ala Leu Ala
 65 70

40

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 83 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

Met Thr Cys Ser Val Ala Leu Leu Leu Ile Leu Gly Leu Arg Cys Ser
 1 5 10 15
 Gly Val Arg Pro Gly Leu Val Gly Glu Gly His Asn Pro Ser Leu Leu
 20 25 30
 55 Val Cys Leu Leu Leu Lys Asp Ser Arg Thr Asn Gln Gly Ser Cys Pro
 35 40 45
 Gly Gly Pro Trp Ser Glu Arg Asp Ile Glu Ser Val Thr Ser Asp Asn
 50 55 60
 60

Cys Glu Ala Thr Leu Gly Tyr Arg Asn His Ser Leu Pro Ser Asn Tyr
 65 70 75 80

Tyr Asn Ser

5

(2) INFORMATION FOR SEQ ID NO: 223:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

Met Leu Thr Arg Ser Leu Lys Thr Leu Pro Ser Ala Cys Thr Ala Phe
 1 5 10 15

20

Leu Leu Leu Phe Phe Leu Phe Ser Ser Gly Asp Pro Glu Leu Ser Cys
 20 25 30

Ser Cys Thr Leu Arg Thr Gln Ser Ser Trp Ser
 35 40

25

(2) INFORMATION FOR SEQ ID NO: 224:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

35

Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His Gly
 1 5 10 15

40

Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly Arg
 20 25 30

Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala His
 35 40 45

45

Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val Ala
 50 55 60

50

Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu Gly
 65 70 75 80

Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp Val
 85 90 95

55

Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg His
 100 105 110

Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp Arg
 115 120 125

60

Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Xaa Thr Tyr Gly His

332

130 135 140

Xaa Xaa Pro Xaa Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr Tyr
 145 150 155 160

5 Lys Lys Met Leu Xaa Arg Asp Glu Arg Arg Phe Arg Val Ala Asp Gln
 165 170 175

10 Asp Gly Asp Ser Met Ala Thr Arg
 180

15 (2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

Met Trp Leu Phe Ile Leu Leu Ser Leu Ala Leu Ile Ser Asp Ala Met
 1 5 10 15

25 Val Met Asp Glu Lys Val Lys Arg Ser Leu Cys Trp Thr Arg Leu Leu
 20 25 30

Pro Ser Ala Thr Thr Met Pro Xaa Thr Arg Ile Thr Pro Asn Thr Gly
 35 40 45

30 Ala Glu Xaa Ile Ser Val Xaa Thr Ala Thr Ser Ser Pro Ser Pro Leu
 50 55 60

35 Thr Ala Pro Ile Met Trp Pro
 65 70

40 (2) INFORMATION FOR SEQ ID NO: 226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

Met His Val Phe Val Leu Glu Ile Phe Leu
 1 5 10

50

(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

60 Met Ala Val Ala Thr Leu Ala Ser Glu Thr Leu Pro Leu Leu Ala Leu

333

1 5 10 15
 Thr Phe Ile Thr Asp Asn Ser Leu Val Ala Ala Gly His Asp Cys Phe
 20 25 30
 5 Pro Val Leu Phe Thr Tyr Asp Ala Ala Ala Gly Met Leu Ser Phe Gly
 35 40 45
 10 Gly Arg Leu Asp Val Pro Lys Gln Ser Ser Gln Arg Gly Leu Thr Ala
 50 55 60
 Arg Glu Arg Phe Gln Asn Leu Asp Lys Lys Ala Ser Ser Glu Gly Gly
 65 70 75 80
 15 Thr Ala Ala Gly Ala Gly Leu Asp Ser Leu His Lys Asn Ser Val Ser
 85 90 95
 Gln Ile Ser Val Leu Ser Gly Gly Lys Ala Lys Cys Ser Gln Phe Cys
 100 105 110
 20 Thr Thr Gly Met Asp Gly Gly Met Ser Ile Trp Asp Val Lys Ser Leu
 115 120 125
 Glu Ser Ala Leu Lys Asp Leu Lys Ile Lys
 130 135
 25

(2) INFORMATION FOR SEQ ID NO: 228:
 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

Leu Gly Ser Leu Ser Thr Ala Pro Ser Ser Ala Leu Pro Thr Leu Gly
 1 5 10 15
 40 Ala Arg Arg Thr Arg Ser Lys
 20

(2) INFORMATION FOR SEQ ID NO: 229:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 133 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

Met Thr Tyr Phe Ser Gly Leu Leu Val Ile Leu Ala Phe Ala Ala Trp
 1 5 10 15
 55 Val Ala Leu Ala Glu Gly Leu Gly Val Ala Val Tyr Ala Ala Ala Val
 20 25 30
 Leu Leu Gly Ala Gly Cys Ala Thr Ile Leu Val Thr Ser Leu Ala Met
 35 40 45
 60

Thr Ala Asp Leu Ile Gly Pro His Thr Asn Ser Gly Ala Phe Val Tyr
 50 55 60
 5 Gly Ser Met Ser Phe Leu Asp Lys Val Ala Asn Gly Leu Ala Val Met
 65 70 75 80
 Ala Ile Gln Ser Leu His Pro Cys Pro Ser Glu Leu Cys Cys Arg Ala
 85 90 95
 10 Cys Val Ser Phe Tyr His Trp Ala Met Val Ala Val Thr Gly Gly Val
 100 105 110
 15 Gly Val Ala Ala Ala Leu Cys Leu Cys Ser Leu Leu Leu Trp Pro Thr
 115 120 125
 Arg Leu Arg Arg Xaa
 130

20

(2) INFORMATION FOR SEQ ID NO: 230:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

30 Gly Lys Pro Thr Gly Lys Ser Leu Pro Leu Met Trp Met Ile Leu Met
 1 5 10 15
 Gln Pro Ile Ile Met Ile Ser Met Met Ser Asn Gly
 20 25
 35

(2) INFORMATION FOR SEQ ID NO: 231:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

45 Met Gln Gly Lys Phe Met Lys Val Gln Val Tyr Arg Phe Leu Lys Tyr
 1 5 10 15
 50 Leu Leu Met Leu Leu Cys Met Phe Val Asn Arg Gly Met Ser Lys Asp
 20 25 30
 Ser Thr Lys Lys Pro Gly Gln Glu Lys Leu Lys Val Ser Leu Gly Ser
 35 40 45
 55 Ile Leu Asn Met Lys Ser Gln Arg Pro Leu Ser Trp Cys
 50 55 60

60 (2) INFORMATION FOR SEQ ID NO: 232:

335

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

Met Met Glu Arg Ser Met Met Ile Leu Leu Met Ala Ala Ser Met Thr
1 5 10 15
Met Thr Ser Thr Gln Leu Trp Ser Phe Cys Cys Val His
20 25

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

Met Trp Tyr Gln Leu Ala Lys Glu Glu Pro Gly Val Gly Ala Cys Ala
1 5 10 15
Leu Asp

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

Leu Xaa
1

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

Met Leu Ile Cys Arg Leu Val Leu Leu Ala Asp Pro Gly Pro Val Asn
1 5 10 15
Phe Met Val Arg Leu Phe Val Val Ile Val Met Phe Ala Trp Ser Ile
20 25 30
Val Ala Ser Thr Ala Phe Leu Ala Asp Ser Gln Pro Pro Asn Arg Arg
35 40 45

336

Ala Leu Ala Val Tyr Pro Val Phe Leu Phe Tyr Phe Val Ile Ser Trp
 50 55 60

5 Met Ile Leu Thr Phe Thr Pro Gln
 65 70

10 (2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

Met Arg Ser Leu Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala
 1 5 10 15
 20 Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Ala Pro Gly Thr
 20 25 30
 25 Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Xaa Pro
 35 40 45
 Ala Trp Pro Ser Ala Cys Thr Arg Pro Trp Pro Arg Thr Arg Gln Trp
 50 55 60
 30 Arg Thr Ser Trp Cys His Pro Trp Trp Trp Pro Arg Arg Trp Gly Ser
 65 70 75 80
 Cys Arg Trp Ala Ala Arg Arg Pro Arg Arg Arg Pro Arg Gln Cys
 85 90 95
 35

40 (2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 143 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

Met Arg Ser Leu Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala
 1 5 10 15
 Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Ala Pro Gly Thr
 20 25 30
 55 Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Lys Arg
 35 40 45
 Pro Gly Leu Gln Leu Val Pro Gly His Gly Gln Gly Pro Gly Ser Gly
 50 55 60
 60

337

Glu His Pro Gly Val Thr Arg Gly Gly Gly Leu Val Ala Gly Ala Arg
 65 70 75 80
 Val Ala Gly Arg Gln Gly Asp His Gly Val Ala Gly Gln Gly Ser Ala
 5 85 90 95
 Glu Arg Arg Ala Ala Ala Arg Arg Gly Gly Ala Arg Arg Pro Gly Arg
 100 105 110
 Ala Ala Ala Leu Thr Gln Gln Leu His Gly Ala Gln Arg Asp Leu Glu
 10 115 120 125
 Ala Gly Gln Pro Thr Val Arg Thr Gln Leu Ser Glu Leu Arg Xaa
 130 135 140
 15

(2) INFORMATION FOR SEQ ID NO: 238:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 142 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:
 25 Met Arg Ser Leu Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala
 1 5 10 15
 Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Ala Pro Gly Thr
 30 20 25 30
 Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Xaa Arg
 35 35 40 45
 Pro Gly Leu Gln Leu Val Pro Gly His Gly Gln Gly Pro Gly Ser Gly
 50 55 60
 Glu His Pro Gly Val Thr Arg Gly Gly Gly Leu Val Ala Gly Ala Arg
 40 65 70 75 80
 Val Ala Gly Arg Gln Gly Asp His Gly Val Ala Gly Gln Gly Ser Ala
 85 90 95
 Glu Arg Arg Ala Ala Ala Arg Arg Gly Gly Ala Arg Arg Pro Gly Arg
 45 100 105 110
 Ala Ala Ala Leu Thr Gln Gln Leu Xaa Gly Ala Gln Arg Asp Leu Glu
 115 120 125
 Ala Gly Gln Pro Thr Val Arg Thr Gln Leu Ser Glu Leu Arg
 50 130 135 140

55 (2) INFORMATION FOR SEQ ID NO: 239:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

Asp Pro Glu Ala Ala Asp Ser Gly Glu Pro Gln Asn Lys Arg Thr Pro
 1 5 10 15
 Asp Leu Pro Glu Glu Glu Tyr Val Lys Glu Glu Ile Gln Glu Asn Glu
 20 25 30
 Glu Ala Val Lys Lys Met Leu Val Glu Ala Thr Arg Glu Phe Glu Glu
 35 40 45
 Val Val Val Asp Glu Ser
 50

15

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

Gln Lys Leu Lys Arg Lys Ala Glu Glu Asp Pro Glu Ala Ala Asp Ser
 1 5 10 15
 Gly Glu Pro Gln Asn Lys Arg Thr Pro Asp Leu Pro Glu Glu Glu Tyr
 20 25 30
 Val Lys Glu Glu Ile Gln Glu Asn Glu Glu Ala Val Lys Lys Met Leu
 35 40 45
 Val Glu Ala Thr Arg Glu Phe Glu Glu Val Val Val Asp Glu Ser
 50 55 60

35

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

Lys Ala Met Glu Lys Ser Ser Leu Thr Gln His Ser Trp Gln Ser Leu
 1 5 10 15
 Lys Asp Arg Tyr Leu Lys His Leu Arg Gly Gln Glu His Lys Tyr Leu
 20 25 30
 Leu Gly Asp Ala Pro Val Ser Pro Ser Ser Gln Lys Leu Lys Arg Lys
 35 40 45
 Ala Glu Glu Asp Pro Glu Ala Ala Asp Ser Gly Glu Pro Gln Asn Lys
 50 55 60
 Arg Thr Pro Asp Leu Pro Glu Glu Glu Tyr Val Lys Glu Glu Ile Gln
 65 70 75 80

55

60

339

Glu Asn Glu Glu Ala Val Lys Lys Met Leu Val Glu Ala Thr Arg Glu
 85 90 95

5 Phe Glu Glu Val Val Val Asp Glu Ser Pro Pro Asp Phe Glu Ile His
 100 105 110

Ile

10

(2) INFORMATION FOR SEQ ID NO: 242:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

20

Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr Ile
 1 5 10 15

25

Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp Phe
 20 25 30

Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met Leu
 35 40 45

30

Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu Ser
 50 55 60

Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser Gly
 65 70 75 80

35

Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Thr
 85 90 95

40

Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val Phe
 100 105 110

Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr Ala
 115 120 125

45

Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr Arg
 130 135 140

Val Leu Phe Ile
 145

50

(2) INFORMATION FOR SEQ ID NO: 243:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

60

340

Ala Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys
 1 5 10 15

5 Trp Ile Leu Ile Val Arg Phe Ser
 20

10 (2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

Met Lys His Leu Ser Ala Trp Asn Phe Thr Lys Leu Thr Phe Leu Gln
 1 5 10 15

20 Leu Trp Glu Ile Phe Glu Gly Ser Val Glu Asn Cys Gln Thr Leu Thr
 20 25 30

Ser Tyr Ser Lys Leu Gln Ile Lys Tyr Thr Phe Ser Arg Gly Ser Thr
 35 40 45

25 Phe Tyr Ile
 50

30 (2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

40 Phe Ser Ser Asp Phe Arg Thr Ser Pro Trp Glu Ser Arg Arg Val Glu
 1 5 10 15

Ser Lys Ala Thr Ser Ala Arg Cys Gly Leu Trp Gly Ser Gly Pro Arg
 20 25 30

45 Arg Arg Pro Ala Ser Gly Met Phe Arg Gly Leu Ser Ser Trp Leu Gly
 35 40 45

50 Leu Gln Gln Pro Val Ala Gly Gly Gly Gln Pro Asn Gly Asp Ala Pro
 50 55 60

Pro Glu Gln Pro Ser Glu Thr Val Ala Glu Ser Ala Glu Glu Glu Leu
 65 70 75 80

55 Gln Gln Ala Gly Asp Gln Glu Leu Leu His Gln Ala Lys Asp Phe Gly
 85 90 95

Asn Tyr Leu Phe Asn Phe Ala Ser Ala Ala Thr Lys Lys Ile Thr Glu
 100 105 110

60 Ser Val Ala Glu Thr Ala Gln Thr Ile Lys Lys Ser Val Glu Glu Gly

341

115 120 125
 Lys Ile Asp Gly Ile Ile Asp Lys Thr Ile Ile Gly Asp Phe Gln Lys
 130 135 140
 5 Glu Gln Lys Lys Phe Val Glu Glu Gln His Thr Lys Lys Ser Glu Ala
 145 150 155 160
 10 Ala Val Pro Pro Trp Val Asp Thr Asn Asp Glu Glu Thr Ile Gln Gln
 165 170 175
 Gln Ile Leu Ala Leu Ser Ala Asp Lys Arg Asn Phe Leu Arg Asp Pro
 180 185 190
 15 Pro Ala Gly Val Gln Phe Asn Phe Asp Phe Asp Gln Met Tyr Pro Val
 195 200 205
 Ala Leu Val Met Leu
 210
 20

(2) INFORMATION FOR SEQ ID NO: 246:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

30 Met Arg Phe Ala Leu Val Pro Lys Leu Val Lys Glu Glu Val Phe Trp
 1 5 10 15
 35 Arg Asn Tyr Phe Tyr Arg Val Ser Leu Ile Lys Gln Ser Ala Gln Leu
 20 25 30
 Thr Ala Leu Ala Ala Gln Gln Gln Ala Ala Gly Lys Gly Gly Glu Glu
 35 40 45
 40 Gln

(2) INFORMATION FOR SEQ ID NO: 247:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 50 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

55 Ser Thr Ser Pro Gly Val Ser Glu Phe Val Ser Asp Ala Phe Asp Ala
 1 5 10 15
 Cys Asn Leu Asn Gln Glu Asp Leu Arg Lys Glu Met Glu Gln Leu Val
 20 25 30
 60 Leu Asp Lys Lys Gln Glu Glu Thr Ala Val Leu Glu Glu Asp Ser Ala
 35 40 45

342

Asp Trp Glu Lys Glu Leu Gln Gln Glu Leu Gln Glu Tyr Glu Val Val
 50 55 60

5 Thr Glu Ser Glu Lys Arg Asp Glu Asn Trp Asp Lys
 65 70 75

10 (2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

Ser Pro Trp Glu Ser Arg Arg Val Glu Ser Lys Ala Thr Ser Ala Arg
 1 5 10 15

20 Cys Gly Leu Trp Gly Ser Gly Pro Arg Arg Arg Pro Ala Ser Gly Met
 20 25 30

25 Phe Arg Gly Leu Ser Ser Trp Leu Gly Leu Gln Gln Pro Val Ala Gly
 35 40 45

Gly Gly Gln Pro Asn Gly Asp Ala Pro Pro Glu Gln Pro Ser
 50 55 60

30

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

40 Pro Val Ala Gly Gly Gly Gln Pro Asn Gly Asp Ala Pro Pro Glu Gln
 1 5 10 15

Pro Ser Glu Thr Val Ala Glu Ser Ala Glu Glu Glu Leu Gln Gln Ala
 20 25 30

45 Gly Asp Gln Glu Leu Leu His Gln Ala Lys Asp Phe Gly Asn Tyr Leu
 35 40 45

50 Phe Asn Phe Ala Ser Ala Ala Thr Lys Lys Ile Thr Glu Ser Val Ala
 50 55 60

Glu
 65

55

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

60

343

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

5 Phe Gln Lys Glu Gln Lys Lys Phe Val Glu Glu Gln His Thr Lys Lys
 1 5 10 15

Ser Glu Ala Ala Val Pro Pro Trp Val Asp Thr Asn Asp Glu Glu Thr
 20 25 30

10 Ile Gln Gln Gln Ile Leu Ala Leu Ser Ala Asp Lys Arg Asn Phe Leu
 35 40 45

Arg Asp Pro Pro Ala Gly Val Gln Phe Asn Phe Asp Phe Asp Gln Met
 15 50 55 60

Tyr Pro Val Ala Leu Val Met Leu
 65 70

20

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

30 Pro Phe Ile Cys Val Ala Arg Asn Pro Val Ser Arg Asn Phe Ser Ser
 1 5 10 15

Pro Ile Leu Ala Arg Lys Leu Cys Glu Gly Ala Ala
 20 25

35

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

40 Lys Glu Asp Pro Ala Asn Thr Val Tyr Ser Thr Val Glu Ile Pro Lys
 1 5 10 15

Lys Met Glu Asn Pro His Ser Leu Leu Thr Met Pro Asp Thr Pro Arg
 50 20 25 30

Leu

55

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 amino acids

60

344

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

5 Ala Ser Ala Val Leu Leu Asp Leu Pro Asn Ser Gly Gly Glu Ala Gln
 1 5 10 15
 Ala Lys Lys Leu Gly Asn Asn Cys Val Phe Ala Pro Ala Asp Val Thr
 20 25 30
 10 Ser Glu Lys Asp Val Gln Thr Ala Leu Ala Leu Ala Lys Gly Lys Phe
 35 40 45
 Gly Arg Val Asp Val Ala Val Asn Cys Ala Gly Ile Ala Val Ala Ser
 15 50 55 60
 Lys Thr Tyr Asn Leu Lys Lys Gly Gln Thr His Thr Leu Glu Asp Phe
 65 70 75 80
 20 Gln Arg Val Leu Asp Val Asn Leu Met Gly Thr Phe Asn Val Ile Arg
 85 90 95
 Leu Val Ala Gly Glu Met Gly Gln Asn Glu Pro Asp Gln Gly Gly Gln
 100 105 110
 25 Arg Gly Val Ile Ile Asn Thr Ala Ser Val Ala Ala Phe Glu Gly Gln
 115 120 125
 Val Gly Gln Ala Ala Tyr Ser Ala Ser Lys Gly Gly Ile Val Gly Met
 30 130 135 140
 Thr Leu Pro Ile Ala Arg Asp Leu Ala Pro Ile Gly Ile Arg Val Met
 145 150 155 160
 35 Thr Ile Ala Pro Gly Leu Phe Gly Thr Pro Leu Leu Thr Ser Leu Pro
 165 170 175
 Glu Lys Val Cys Asn Phe Leu Ala Ser Gln Val Pro Phe Pro Ser Arg
 180 185 190
 40 Leu Gly Asp Pro Ala Glu Tyr Ala His Leu Val Gln Ala Ile Ile Glu
 195 200 205
 Asn Pro Phe Leu Asn Gly Glu Val Ile Arg Leu Asp Gly Ala Ile Arg
 45 210 215 220
 Met Gln Pro
 225

50

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

60

Ser Val Ala Ala Phe Glu Gly Gln Val Gly Gln Ala Ala Tyr Ser Ala

345

1 5 10 15
 Ser Lys Gly Gly Ile Val Gly Met Thr Leu Pro Ile Ala
 20 25

5

(2) INFORMATION FOR SEQ ID NO: 255:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

15

Ala Arg Arg Ser Gly Ala Glu Leu Ala Trp Asp Tyr Leu Cys Arg Trp
 1 5 10 15

20

Ala Gln Lys His Lys Asn Trp Arg Phe Gln Lys Thr Arg Gln Thr Trp
 20 25 30

Leu Leu Leu His Met Tyr Asp Ser Asp Lys Val Pro Asp Glu His Phe
 35 40 45

25

Ser Thr Leu Leu Ala Tyr Leu Glu Gly Leu Gln Gly Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO: 256:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

His Pro Ile Glu Trp Ala Ile Asn Ala Ala Thr Leu Ser Gln Phe Tyr
 1 5 10 15

40

Ile Asn Lys Leu Cys Phe
 20

45

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

Cys Trp Ile Lys Tyr Cys Leu Thr Leu Met Gln Asn Ala Gln Leu Ser
 1 5 10 15

55

Met Gln Asp Asn Ile Gly
 20

60

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

Lys Val Ser Tyr Leu Arg Pro Leu Asp Phe Glu Glu Ala Arg Glu Leu
1 5 10 15
Phe Leu Leu Gly Gln His Tyr Val Phe
20 25

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

Met Glu Arg Arg Cys Lys Met His Lys Arg Xaa Ile Ala Met Leu Glu
1 5 10 15
Pro Leu Thr Val Asp Leu Asn Pro Gln
20 25

(2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

Ser His Ile Val Lys Lys Ile Asn Asn Leu Asn Lys Ser Ala Leu Lys
1 5 10 15
Tyr Tyr Gln Leu Phe Leu Asp
20

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

Phe Thr His Leu Ser Thr Cys Leu Leu Ser Leu Leu Leu Val Arg Met
1 5 10 15
Ser Gly Phe Leu Leu Leu Ala Arg Ala Ser Pro Ser Ile Cys Ala Leu

347

20 25 30

Asp Ser Ser Cys Phe Val Gln Glu Tyr Cys Ser Ser Tyr Ser Ser Ser
35 40 45

5 Cys Phe Leu His Gln His Phe Pro Ser Leu Leu Asp His Leu Cys Gln
50 55 60

10

(2) INFORMATION FOR SEQ ID NO: 262:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

Phe Leu Leu Leu Ala Arg Ala Ser Pro Ser Ile Cys Ala Leu Asp Ser
1 5 10 15

25

Ser Cys Phe Val Gln Glu Tyr
20

30

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

Pro Asp Gly Arg Val Thr Asn Ile Pro Gln Gly Met Val Thr Asp Gln
1 5 10 15

40

Phe Gly Met Ile Gly Leu Leu Thr Phe Ile Arg Ala Ala Glu Thr Asp
20 25 30

45

Pro Gly Met Val His Leu Ala Leu Gly Ser Asp Leu Thr Thr Leu Gly
35 40 45

Leu Asn Leu Asn Ser
50

50

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

60

Glu Asp Leu Leu Phe Tyr Leu Tyr Tyr Met Asn Gly Gly Asp Val Leu

348

1 5 10 15
 Gln Leu Leu Ala Ala Val Glu Leu Phe Asn Arg Asp Trp Arg Tyr His
 20 25 30
 5 Lys Glu Glu Arg Val Trp Ile Thr Arg
 35 40

10

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

20 Val His Leu Ala Leu Gly Ser Asp Leu Thr Thr Leu Gly Leu Asn Leu
 1 5 10 15
 Asn Ser Pro Glu Asn Leu Tyr Pro
 20

25

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

35 His Asn Glu Asp Phe Pro Ala Leu Pro Gly Ser
 1 5 10

40

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

50 Gly Arg Ile Ile Asp Thr Ser Leu Thr Arg Asp Pro Leu Val Ile Glu
 1 5 10 15
 Leu Gly Gln Lys Gln Val Ile Pro Gly Leu Glu Gln Ser Leu Leu Asp
 20 25 30
 55 Met Cys Val Gly Glu Lys Arg Arg Ala Ile Ile Pro Ser His Leu Ala
 35 40 45
 Tyr Gly Lys Arg Gly Phe Pro Pro Ser Val Pro Ala Asp Ala Val Val
 50 55 60
 60 Gln Tyr Asp Val Glu Leu Ile Ala Leu Ile Arg

349

65

70

75

5 (2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

Ile His Tyr Thr Gly Ser Leu Val Asp Gly Arg Ile Ile Asp Thr Ser
1 5 10 15

15

20

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

25 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

Cys Glu Ser Pro Glu Ser Pro Ala Gln Pro Ser Gly Ser Ser Leu Pro
1 5 10 15

30

Ala Trp Tyr His
20

35

(2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

45 Glu Glu Ala Gly Ala Gly Arg Arg Cys Ser His Gly Gly Ala Arg Pro
1 5 10 15

Ala Gly Leu Gly Asn Glu Gly Leu Gly Leu Gly Gly Asp Pro Asp His
20 25 30

50

Thr Asp Thr Gly Ser Arg Ser Lys Gln Arg Ile Asn Asn Trp Lys Glu
35 40 45

55

Ser Lys His Lys Val Ile Met Ala Ser Ala Ser Ala Arg Gly Asn Gln
50 55 60

Asp Lys Asp Ala His Phe Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe
65 70 75 80

60 Cys Pro Lys Ser Lys Leu His Ile His Arg Ala Glu Ile Ser Lys

350

85

90

95

5 (2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

Ser Lys Gln Arg Ile Asn Asn Trp Lys Glu Ser Lys His Lys Val Ile
 1 5 10 15
 Met Ala Ser Ala Ser Ala Arg
 20

15

20

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

Leu Phe His Trp Ala Cys Leu Asn Glu Arg Ala Ala Gln Leu Pro Arg
 1 5 10 15
 Asn Thr Ala Xaa Ala Gly Tyr Gln Cys Pro Ser Cys Asn Gly Pro Ser
 20 25 30

35

40 (2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

Phe Tyr Ile Tyr Tyr Arg Pro Thr Asp Ser Asp Asn Asp Ser Asp Tyr
 1 5 10 15
 Lys Lys Asp Met Val Glu Gly Asp Lys Tyr Trp His Ser Ile Ser His
 20 25 30
 Leu Gln Pro Glu Thr Ser Tyr Asp Ile Lys Met Gln Cys Phe Asn Glu
 35 40 45
 Gly Gly Glu Ser Glu Phe Ser Asn Val Met Ile Cys Glu Thr Lys Ala
 50 55 60
 Arg Lys Ser Ser Gly Gln Pro Gly Arg Leu Pro Pro Pro Thr Leu Ala

50

55

60

351

	65					70						75					80
	Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg	Pro	Val	Gly	Thr	
					85					90					95		
5	Gly	Ala	Met	Val	Ala	Arg	Ser	Ser	Asp	Leu	Pro	Tyr	Leu	Ile	Val	Gly	
				100					105					110			
	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile	Val	Thr	Phe	Ile	Pro	Phe	
10			115					120					125				
	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln	Lys	His	Thr	Thr	Asp	Leu	Gly	
		130					135					140					
15	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro	Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	
	145					150					155					160	
	Leu	Gly	Gly	Leu	Pro	Gly	His	Gln	Ala	Val	Asp	Ser	Pro	Thr	Ser	Val	
					165					170					175		
20	Ala	Ser	Val	Asp	Gly	Pro	Val	Leu	Met								
				180					185								

25 (2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

30 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

35 Tyr Ile Tyr Tyr Arg Pro Thr Asp Ser Asp Asn Asp Ser Asp Tyr Lys
1 5 10 15

Lys Asp Met Val Glu Gly Asp Lys Tyr Trp His Ser Ile Ser His Leu
20 25 30

40 Gln Pro Glu Thr Ser Tyr Asp Ile Lys Met Gln Cys Phe Asn Glu Gly
35 40 45

Gly Glu Ser Glu Phe Ser Asn Val Met Ile Cys Glu Thr Lys Ala Arg
50 55 60

45 Lys Ser
65

50 (2) INFORMATION FOR SEQ ID NO: 275:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

55 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

60 Asn Val Arg Ala Leu Leu His Arg Met Pro Glu Pro Pro Lys Ile Asn
 1 5 10 15

352

Thr Ala Lys Phe Asn Asn Asn Lys Arg Lys Asn Leu Ser Leu
 20 25 30

5

(2) INFORMATION FOR SEQ ID NO: 276:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

15 Asn Thr Asn Gln Arg Glu Ala Leu Gln Tyr Ala Lys Asn Phe Gln Pro
 1 5 10 15

Phe Ala Leu Asn His Gln Lys Asp Ile Gln Val Leu Met Gly Ser Leu
 20 25 30

20

Val Tyr Leu Arg Gln Gly Ile Glu Asn Ser Pro Tyr Val His Leu Leu
 35 40 45

25 Asp Ala Asn Gln Trp Ala Asp Ile Cys Asp Ile Phe Thr Arg Asp Ala
 50 55 60

Cys Ala Leu Leu Gly Leu Ser Val Glu Ser Pro Leu Ser Val Ser Phe
 65 70 75 80

30 Ser Ala Gly Cys Val Ala Leu Pro Ala Leu Ile Asn Ile Lys Ala Val
 85 90 95

Ile Glu Gln Arg Gln Cys Thr Gly Val Trp Asn Gln Lys Asp Glu Leu
 100 105 110

35

Pro Ile Glu Val Asp Leu Gly Lys Lys Cys Trp Tyr His Ser Ile Phe
 115 120 125

40 Ala Cys Pro Ile Leu Arg Gln Gln Thr Thr Asp Asn Asn Pro Pro Met
 130 135 140

Lys Leu Val Cys Gly His Ile Ile Ser Arg Asp Ala Leu Asn Lys Met
 145 150 155 160

45 Phe Asn Gly Ser Lys Leu Lys Cys Pro Tyr Cys Pro Met Glu Gln Ser
 165 170 175

Pro Gly Asp Ala Lys Gln Ile Phe Phe
 180 185

50

(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

55

60

353

Ser Tyr Leu Ser Ala Cys Phe Ala Gly Cys Asn Ser Thr Asn Leu Thr
 1 5 10 15
 Gly Cys Ala Cys Leu Thr Thr Val Pro Ala Glu Asn Ala Thr Val Val
 5 20 25 30
 Pro Gly Lys Cys Pro Ser Pro Gly Cys Gln Glu Ala Phe Leu Thr Phe
 35 40 45
 10 Leu Cys Val Met Cys Ile Cys Ser Leu Ile Gly Ala Met Ala Arg His
 50 55 60
 Pro
 65
 15

(2) INFORMATION FOR SEQ ID NO: 278:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

25 Pro Ser Val Ile Ile Leu Ile Arg Thr Val Ser Pro Glu Leu Lys Ser
 1 5 10 15
 Tyr Ala Leu Gly Val Leu Phe Leu Leu Leu Arg Leu Leu Gly Phe Ile
 30 20 25 30
 Pro Pro Pro Leu Ile Phe Gly Ala Gly Ile Asp Ser Thr Cys Leu Phe
 35 35 40 45
 35 Trp Ser Thr Phe Cys Gly Glu Gln Gly Ala Cys Val Leu Tyr Asp Asn
 50 55 60
 Val Val Tyr Arg Tyr Leu Tyr Val Ser Ile Ala Ile Ala Leu Lys Ser
 65 70 75 80
 40 Phe Ala Phe Ile

45

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 182 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

50 Gln Ser Leu Phe Thr Arg Phe Val Arg Val Gly Val Pro Thr Val Asp
 1 5 10 15
 Leu Asp Ala Gln Gly Arg Ala Arg Ala Ser Leu Cys Xaa Xaa Tyr Asn
 20 25 30
 60 Trp Arg Tyr Lys Asn Leu Gly Asn Leu Pro His Val Gln Leu Leu Pro

354

35 40 45
 Glu Phe Ser Thr Ala Asn Ala Gly Leu Leu Tyr Asp Phe Gln Leu Ile
 50 55 60
 5 Asn Val Glu Asp Phe Gln Gly Val Gly Glu Ser Glu Pro Asn Pro Tyr
 65 70 75 80
 10 Phe Tyr Gln Asn Leu Gly Glu Ala Glu Tyr Val Val Ala Leu Phe Met
 85 90 95
 Tyr Met Cys Leu Leu Gly Tyr Pro Ala Asp Lys Ile Ser Ile Leu Thr
 100 105 110
 15 Thr Tyr Asn Gly Gln Lys His Leu Ile Arg Asp Ile Ile Asn Arg Arg
 115 120 125
 Cys Gly Asn Asn Pro Leu Ile Gly Arg Pro Asn Lys Val Thr Thr Val
 130 135 140
 20 Asp Arg Phe Gln Gly Gln Gln Asn Asp Tyr Ile Leu Leu Ser Leu Val
 145 150 155 160
 25 Arg Thr Arg Ala Val Gly His Leu Arg Asp Val Arg Arg Leu Val Val
 165 170 175
 Ala Met Ser Arg Ala Arg
 180

30

(2) INFORMATION FOR SEQ ID NO: 280:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

40 Leu Val Lys Glu Ala Lys Ile Ile Ala Met Thr Cys Thr His Ala Ala
 1 5 10 15
 Leu Lys Arg His Asp Leu Val Lys Leu Gly Phe Lys Tyr Asp Asn Ile
 20 25 30
 45 Leu Met Glu Glu Ala Ala Gln Ile Leu Glu Ile Glu Thr Phe Ile Pro
 35 40 45
 50 Leu Leu Leu Gln Asn Pro Gln Asp Gly Phe Ser Arg Leu Lys Arg Trp
 50 55 60
 Ile Met Ile Gly Asp His His Gln Leu Pro Pro Val Ile
 65 70 75

55

(2) INFORMATION FOR SEQ ID NO: 281:

- 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids

355

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

5 Asp Thr Tyr Pro Asn Glu Glu Lys Gln Gln Glu Arg Val Phe Pro Xaa
 1 5 10 15
 Xaa Ser Ala Met Val Asn Asn Gly Ser Leu Ser Tyr Asp His Glu Arg
 20 25 30
 10 Asp Gly Arg Pro Thr Glu Leu Gly Gly Cys Xaa Ala Ile Val Arg Asn
 35 40 45
 Leu His Tyr Asp Thr Phe Leu Val Ile Arg Tyr Val Lys Arg His Leu
 15 50 55 60
 Thr Ile Met Met Asp Ile Asp Gly Lys His Glu Trp Arg Asp Cys Ile
 65 70 75 80
 20 Glu Val Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr Phe Gly Thr Ser
 85 90 95
 Ser Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys
 100 105 110
 25 Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu
 115 120 125

30

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

40 Leu Lys Arg Glu His Ser Leu Ser Lys Pro Tyr Gln Gly Val Gly Thr
 1 5 10 15
 Gly Ser Ser Ser Leu Trp Asn Leu Met Gly Asn Ala Met Val Met Thr
 20 25 30
 45 Gln Tyr Ile Arg Leu Thr Pro Asp Met Gln Ser Lys Gln Gly Ala Leu
 35 40 45
 Trp Asn Arg Val Pro Cys Phe Leu Arg Asp Trp Glu Leu Gln Val His
 50 55 60
 50 Phe Lys Ile His Gly Gln Gly Lys Lys Asn Leu His Gly Asp Gly Leu
 65 70 75 80
 Ala Ile Trp Tyr Thr
 85

60

(2) INFORMATION FOR SEQ ID NO: 283:

356

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

Pro Gly Thr Leu Gln Cys Ser Ala Leu His His Asp Pro Gly Cys Ala
1 5 10 15

10 Asn Cys Ser Arg Phe Cys Arg Asp Cys Ser Pro Pro Ala Cys Gln Cys
20 25 30

15

(2) INFORMATION FOR SEQ ID NO: 284:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

Phe Leu Tyr Asp Val Leu Met Xaa His Glu Ala Val Met Arg Thr His
1 5 10 15

30 Gln Ile Gln Leu Pro Asp Pro Glu Phe Pro Ser
20 25

35 (2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

Gly Trp Tyr Trp Cys Gly
1 5

45

(2) INFORMATION FOR SEQ ID NO: 286:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

55 Met Lys Val Gly Ala Arg Ile Arg Val Lys Met Ser Val Asn Lys Ala
1 5 10 15

His Pro Val Val Ser Thr His Trp Arg Trp Pro Ala Glu Trp Pro Gln
20 25 30

60

357

Met Phe Leu His Leu Ala Gln Glu Pro Arg Thr Glu Val Lys Ser Arg
 35 40 45

5 Pro Leu Gly Leu Ala Gly Phe Ile Arg Gln Asp Ser Lys Thr Arg Lys
 50 55 60

Pro Leu Glu Gln Glu Thr Ile Met Ser Ala Ala Asp Thr Ala Leu Trp
 65 70 75 80

10 Pro Tyr Gly His Gly Asn Arg Glu His Gln Glu Asn Glu Leu Gln Lys
 85 90 95

Tyr Leu Gln Tyr Lys Asp Met His Leu Leu Asp Ser Gly Gln Ser Leu
 100 105 110

15 Gly His Thr His Thr Leu Gln Gly Ser His Asn Leu Thr Ala Leu Asn
 115 120 125

Ile

20

(2) INFORMATION FOR SEQ ID NO: 287:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

Ser Leu His Lys Asn Ser Val Ser Gln Ile Ser Val Leu Ser Gly Gly
 1 5 10 15

35 Lys Ala Lys Cys Ser Gln Phe Cys Thr Thr Gly Met Asp Gly Gly Met
 20 25 30

Ser Ile Trp Asp Val Lys Ser Leu Glu Ser Ala Leu Lys Asp Leu Lys
 35 40 45

40 Ile

45

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

50

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

55 Glu Ala Ser Lys Ser Ser His Ala Gly Leu Asp Leu Phe Ser Val Ala
 1 5 10 15

Ala Cys His Arg Phe
 20

60

(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

5 Tyr Met Gly Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe
1 5 10 15

Glu Arg Ser Phe Thr
20

15

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

20 Val Thr Gly Ile Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg
1 5 10 15

30 Val Gly Leu Leu Gln Tyr Ser Thr Gln Val His
20 25

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

35 Thr Glu Phe Thr Leu Arg Asn Phe Asn Ser Ala Lys Asp Met Lys Lys
1 5 10 15

45 Ala Val Ala His Met Lys Tyr Met
20

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

50 Gly Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg
1 5 10 15

60

359

Ser Phe Thr Gln Gly Glu Gly Ala Arg Pro Phe
20 25

5

(2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

15 Ser Thr Arg Val Pro Arg Ala Ala Ile Val Phe Thr Asp Gly Arg Ala
1 5 10 15

Gln Asp Asp Val Ser Glu Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile
20 25 30

20 Thr Met Tyr Ala Val Gly Val Gly Lys Ala Ile Glu
35 40

25

(2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

35 Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro Thr Asn Lys His Leu Phe
1 5 10 15

Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu Ile Ser Glu Lys Leu Lys
20 25 30

40

Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser
35 40

45

(2) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

Thr Gln Arg Leu Glu Glu Met Thr Gln Arg Met
1 5 10

55

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

60

360

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

5 Pro Gln Gly Cys Pro Glu Gln Pro Leu His
 1 5 10

10 (2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

Arg Cys Lys Lys Cys Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile
 1 5 10 15
 20 Asp Gly Ser Lys Ser Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln
 20 25 30

25 Phe

30 (2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

Met Ala Ala Leu Leu Leu Arg His Val Gly Arg His Cys Leu Arg Ala
 1 5 10 15

40 His Phe Ser Pro Gln Leu Cys Ile Arg Asn Ala Val Pro Leu Gly Thr
 20 25 30

Thr Ala Lys Glu Glu Met Glu Arg Phe Trp Asn Lys Asn Ile Gly Ser
 35 40 45

45 Asn Arg Pro Leu Ser Pro His Ile Thr Ile Tyr Ser
 50 55 60

50 (2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

60 Val Phe Pro Leu Met Tyr His Thr Trp Asn Gly Ile Arg His Leu Met
 1 5 10 15

361

Trp Asp Leu Gly Lys Gly Leu Lys Ile Pro Gln Leu Tyr Gln Ser Gly
20 25 30

5

10 (2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

Met Ala Ala Leu Leu Leu Arg His Val Gly Arg His Cys Leu Arg Ala
1 5 10 15

20

His

25

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

Val Lys Ser Leu Cys Leu Gly Pro Ala Leu Ile His Thr Ala Lys Phe
1 5 10 15

35

Ala Leu

40

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

Val Phe Pro Leu Met Tyr His Thr Trp Asn Gly Ile Arg His Leu Met
1 5 10 15

50

Trp Asp Leu Gly Lys Gly Leu
20

55

(2) INFORMATION FOR SEQ ID NO: 303:

60

(i) SEQUENCE CHARACTERISTICS:

362

(A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

Arg Val Trp Asp Val Arg Pro Phe Ala Pro Lys Glu Arg Cys Val Lys
 1 5 10 15
 Ile Phe Gln Gly Asn Val
 20

(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

His Asn Phe Glu Lys Asn Leu Leu Arg Cys Ser Trp Ser Pro Asp Gly
 1 5 10 15
 Ser Lys Ile Ala Ala Gly Ser Ala Asp Arg Phe Val Tyr Val
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

Trp Asp Thr Thr Ser Arg Arg Ile Leu Tyr Lys Leu Pro Gly His Ala
 1 5 10 15
 Gly Ser Ile Asn Glu Val Ala Phe His Pro Asp Glu Pro Ile
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

Val Arg Gly Arg Thr Val Leu Arg Pro Gly Leu Asp Ala Glu Pro Glu
 1 5 10 15
 Leu Ser Pro Glu
 20

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

10 Glu Gln Arg Val Leu Glu Arg Lys Leu Lys Lys Glu Arg Lys Lys Glu
 1 5 10 15

Glu Arg Gln

15

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

25 Arg Leu Arg Glu Ala Gly Leu Val Ala Gln His Pro Pro
 1 5 10

30

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

40 Gly Arg Ile Pro Ala Pro Ala Pro Ser Val Pro Ala Gly Pro Asp Ser
 1 5 10 15

Arg

45

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

55 Thr Gly Cys Val Leu Val Leu Ser Arg Asn Phe Val Gln Tyr Ala Cys
 1 5 10 15

Phe Gly Leu Phe Gly Ile Ile Ala Leu Gln Thr Ile Ala Tyr Ser Ile
 20 25 30

60

Leu Trp Asp Leu Lys Phe Leu Met Arg Asn
 35 40

5

(2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

15

Ser Arg Ser Glu Gly Lys Ser Met Phe Ala Gly Val Pro Thr Met Arg
 1 5 10 15

Glu Ser Ser Pro Lys Gln Tyr Met Gln Leu Gly Gly Arg Val Leu Leu
 20 25 30

20

Val Leu Met Phe Met Thr Leu Leu His Phe Asp Ala Ser Phe Phe Ser
 35 40 45

Ile Val Gln Asn Ile Val Gly
 50 55

25

(2) INFORMATION FOR SEQ ID NO: 312:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

35

Gly Thr Ala Glu Asp Phe Ala Asp Gln Phe Leu Arg Val Thr Lys Gln
 1 5 10 15

40

Tyr Leu Pro His Val Ala Arg Leu Cys Leu Ile Ser Thr Phe Leu Glu
 20 25 30

Asp Gly Ile Arg Met Trp Phe Gln Trp Ser Glu Gln Arg Asp Tyr Ile
 35 40 45

45

Asp Thr Thr Trp Asn Cys Gly Tyr Leu Leu Ala Ser
 50 55 60

50

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

Ala Ser Phe Leu Leu Ser Arg Thr Ser Trp Gly Thr Ala Leu Met Ile
 1 5 10 15

60

365

Leu

5

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

Leu Met Arg Asn Glu Ser Arg Ser

15

1

5

(2) INFORMATION FOR SEQ ID NO: 315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

Ala Ser Phe Leu Leu Ser Arg Thr Ser Trp Gly Thr Ala

1

5

10

30

(2) INFORMATION FOR SEQ ID NO: 316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

40

Phe Ile Ser Phe Ala Asn Ser Arg Ser Ser Glu Asp Thr Lys Gln Met

1

5

10

15

Met Ser Ser Phe

20

45

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

55

Asp Pro Arg Arg Pro Asn Lys Val Leu Arg Tyr Lys Pro Pro Pro Ser

1

5

10

15

Glu Cys Asn Pro Ala Leu Asp Asp Pro Thr Pro

20

25

60

(2) INFORMATION FOR SEQ ID NO: 318:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Asp Tyr Met Asn Leu Leu Gly Met Ile Phe Ser Met Cys Gly Leu Met
1 5 10 15

15

Leu Lys Leu Lys Trp Cys Ala Trp Val Ala Val Tyr Cys Ser
20 25 30

(2) INFORMATION FOR SEQ ID NO: 319:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

Met Leu Ser Ile Ser Ala Val Val Met Ser Tyr Leu Gln Asn Pro Gln
1 5 10 15

30

Pro Met Thr Pro Pro Trp
20

(2) INFORMATION FOR SEQ ID NO: 320:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

Ala Ala Gly Asp Gly Asp Val Lys Leu Gly Thr Leu Gly Ser Gly Ser
1 5 10 15

45

Glu Ser Ser Asn Asp Gly Gly Ser Glu Ser Pro Gly Asp Ala Gly Ala
20 25 30

50

Ala Ala Xaa Gly Gly Gly Trp Ala Ala Ala Ala Leu Ala Leu Leu Thr
35 40 45

Gly Gly Gly Glu
50

55

(2) INFORMATION FOR SEQ ID NO: 321:

60

(i) SEQUENCE CHARACTERISTICS:

367

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

5
Ala Ala Asp Asn Tyr Gly Ile Pro Arg Ala Cys Arg Asn Ser Ala Arg
1 5 10 15
10
Ser Tyr Gly Ala Ala Trp Leu Leu Leu Xaa Pro Ala Gly Ser Ser Arg
20 25 30
Val Glu Pro Thr Gln Asp Ile Ser Ile Ser Asp Gln Leu Gly Gly Gln
35 40 45
15
Asp Val Pro Val Phe Arg Asn Leu Ser Leu Leu Val Val Gly Val Gly
50 55 60
Ala Val Phe Ser Leu Leu Phe His Leu Gly Thr Arg Glu Arg Arg Arg
65 70 75 80
20
Pro His Ala Xaa Glu Pro Gly Glu His Thr Pro Leu Leu Ala Pro Ala
85 90 95
25
Thr Ala Gln Pro Leu Leu Leu Trp Lys His Trp Leu Arg Glu Xaa Ala
100 105 110
Phe Tyr Gln Val Gly Ile Leu Tyr Met Thr Thr Arg Leu Ile Val Asn
115 120 125
30
Leu Ser Gln Thr Tyr Met Ala Met Tyr Leu Thr Tyr Ser Leu His Leu
130 135 140
Pro Lys Lys Phe Ile Ala Thr Ile Pro Leu Val Met Tyr Leu Ser Gly
145 150 155 160
35
Phe Leu Ser Ser Phe Leu Met Lys Pro Ile Asn Lys Cys Ile Gly Arg
165 170 175
40
Asn

(2) INFORMATION FOR SEQ ID NO: 322:

45
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:
50
Arg Ile Thr Asp Asn Pro Glu Gly Lys Trp Leu Gly Arg Thr Ala Arg
1 5 10 15
55
Gly Ser Tyr Gly Tyr Ile Lys Thr Thr Ala Val Glu Ile Xaa Tyr Asp
20 25 30
Ser Leu Lys Leu Lys Lys Asp Ser Leu Gly Ala Pro Ser Arg Pro Ile
35 40 45
60
Glu Asp Asp Gln Glu Val Tyr Asp Asp Val Ala Glu Gln Asp Asp Ile

368

50 55 60

Ser Ser His Ser Gln Ser Gly Ser Gly Gly Ile Phe Pro Pro Pro Pro
65 70 75 80

5 Asp Asp Asp Ile Tyr Asp Gly Ile Glu Glu Glu Asp Ala Asp Asp Gly
 85 90 95

10 Phe Pro Ala Pro Pro Lys Gln Leu Asp Met Gly Asp Glu Val Tyr Asp
 100 105 110

Asp Val Asp Thr Ser Asp Phe Pro Val Ser Ser Ala Glu Met Ser Gln
115 120 125

15 Gly Thr Asn Val Gly Lys Ala Lys Thr Glu Glu Lys Asp Leu Lys Lys
130 135 140

Leu Lys Lys Gln Xaa Lys Glu Xaa Lys Asp Phe Arg Lys Lys Phe Lys
145 150 155 160

20 Tyr Asp Gly Glu Ile Arg Val Leu Tyr Ser Thr Lys Val Thr Thr Ser
 165 170 175

25 Ile Thr Ser Lys Lys Trp Gly Thr Arg Asp Leu Gln Val Lys Pro Gly
180 185 190

Glu Ser Leu Glu Val Ile Gln Thr Thr Asp Asp Thr Lys Val Leu Cys
195 200 205

30 Arg Asn Glu Glu Gly Lys Tyr Gly Tyr Val Leu Arg Ser Tyr Leu Ala
210 215 220

Asp Asn Asp Gly Glu Ile Tyr Asp Asp Ile Ala Asp Gly Cys Ile Tyr
225 230 235 240

35 Asp Asn Asp

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

50 Ser Met Ser Ala Leu Thr Arg Leu Ala Ser Phe Ala Arg Val Gly Gly
1 5 10 15

Arg Leu Phe Arg Ser Gly Cys Ala Arg Thr Ala Gly Asp Gly Gly Val
20 25 30

55 Arg His Ala Gly Gly Gly Val His Ile Glu Pro Arg Tyr Arg Gln Phe
35 40 45

Pro Gln Leu Thr Arg Ser Gln Val Phe Gln Ser Glu Phe Phe Ser Gly
50 55 60

60 Leu Met Trp Phe Trp Ile Leu Trp Arg Phe Trp His Asp Ser Glu Glu

369

65

70

75

80

Val Leu Gly His Phe Pro Tyr Pro Asp Pro Ser Gln Trp Thr Asp Glu
85 90 95

5

Glu Leu Gly Ile Pro Pro Asp Asp Glu Asp
100 105

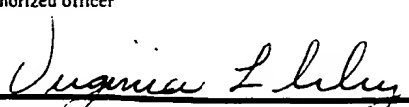
370

Applicant's or agent's file reference number	2004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 73 . line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit March 7, 1997	Accession Number 97923
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

For receiving Office use only	For International Bureau use only
<input checked="checked" type="checkbox"/> This sheet was received with the international application	<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer 	Authorized officer

371

Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>73</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit <u>May 22, 1997</u>	Accession Number <u>209071</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
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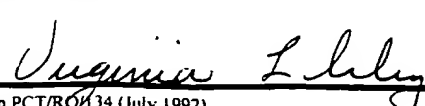
372

Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 73, line N/A	
B. IDENTIFICATION OF DEPOSIT	
Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit February 25, 1998	Accession Number 209641
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 75, line N/A	
B. IDENTIFICATION OF DEPOSIT	
Further deposits are identified on an additional sheet: <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit July 24, 1997	Accession Number 209179
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 77, line N/A	
B. IDENTIFICATION OF DEPOSIT	
Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit March 7, 1997	Accession Number 97924
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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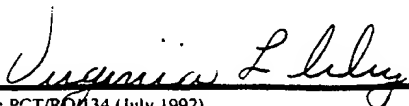
375

Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>80</u> . line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit March 13, 1997	Accession Number 97958
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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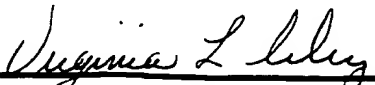
376

Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 80, line N/A	
B. IDENTIFICATION OF DEPOSIT	
Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit May 22, 1997	Accession Number 209072
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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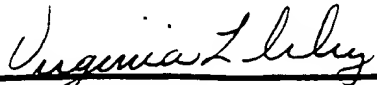
377

Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 80 . line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit September 4, 1997	Accession Number 209235
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications. e.g. "Accession Number of Deposit")	

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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>84</u> . line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>August 28, 1997</u>	Accession Number <u>209226</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit") 	

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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>84</u> . line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit March 13, 1997	Accession Number 97957
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 84, line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit May 22, 1997	Accession Number 209073
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:

5 (a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit No:Z,
10 which is hybridizable to SEQ ID NO:X;

(c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a
15 polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(e) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X, having biological activity;

20 (f) a polynucleotide which is a variant of SEQ ID NO:X;

(g) a polynucleotide which is an allelic variant of SEQ ID NO:X;

(h) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;

(i) a polynucleotide capable of hybridizing under stringent conditions to any
one of the polynucleotides specified in (a)-(h), wherein said polynucleotide does not
25 hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.

2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein.

30

3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

35

4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

5

5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

10

6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

15

7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.

8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.

20

9. A recombinant host cell produced by the method of claim 8.

10. The recombinant host cell of claim 9 comprising vector sequences.

25

11. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(b) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z, having biological activity;

30

(c) a polypeptide domain of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(d) a polypeptide epitope of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

35

(e) a secreted form of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(f) a full length protein of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

- (g) a variant of SEQ ID NO:Y;
- (h) an allelic variant of SEQ ID NO:Y; or
- (i) a species homologue of the SEQ ID NO:Y.

12. The isolated polypeptide of claim 11, wherein the secreted form or the
5 full length protein comprises sequential amino acid deletions from either the C-terminus
or the N-terminus.

13. An isolated antibody that binds specifically to the isolated polypeptide of
claim 11.

10

14. A recombinant host cell that expresses the isolated polypeptide of claim
11.

15

15. A method of making an isolated polypeptide comprising:
(a) culturing the recombinant host cell of claim 14 under conditions such that
said polypeptide is expressed; and
(b) recovering said polypeptide.

20

16. The polypeptide produced by claim 15.

17. A method for preventing, treating, or ameliorating a medical condition,
comprising administering to a mammalian subject a therapeutically effective amount of
the polypeptide of claim 11 or the polynucleotide of claim 1.

25

18. A method of diagnosing a pathological condition or a susceptibility to a
pathological condition in a subject comprising:

(a) determining the presence or absence of a mutation in the polynucleotide of
claim 1; and

(b) diagnosing a pathological condition or a susceptibility to a pathological
30 condition based on the presence or absence of said mutation.

35

19. A method of diagnosing a pathological condition or a susceptibility to a
pathological condition in a subject comprising:

(a) determining the presence or amount of expression of the polypeptide of
claim 11 in a biological sample; and

(b) diagnosing a pathological condition or a susceptibility to a pathological
condition based on the presence or amount of expression of the polypeptide.

20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:

(a) contacting the polypeptide of claim 11 with a binding partner; and

(b) determining whether the binding partner effects an activity of the polypeptide.

21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.

22. A method of identifying an activity in a biological assay, wherein the method comprises:

(a) expressing SEQ ID NO:X in a cell;

(b) isolating the supernatant;

(c) detecting an activity in a biological assay; and

(d) identifying the protein in the supernatant having the activity.

23. The product produced by the method of claim 22.



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/12, 5/10, 1/21, C07K 14/47, 16/18, C12Q 1/68, G01N 33/50, 33/53, 33/68, A61K 38/17		A1	(11) International Publication Number: WO 98/42738
			(43) International Publication Date: 1 October 1998 (01.10.98)
(21) International Application Number: PCT/US98/05311		60/056,370	19 August 1997 (19.08.97) US
		60/060,862	2 October 1997 (02.10.97) US
(22) International Filing Date: 19 March 1998 (19.03.98)			
(30) Priority Data:		(71) Applicant (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US).	
60/041,281	21 March 1997 (21.03.97) US	(72) Inventors; and	
60/041,276	21 March 1997 (21.03.97) US	(75) Inventors/Applicants (for US only): YOUNG, Paul [US/US];	
60/042,344	21 March 1997 (21.03.97) US	122 Beckwith Street, Gaithersburg, MD 20878 (US).	
60/041,277	21 March 1997 (21.03.97) US	GREENE, John, M. [US/US]; 872 Diamond Avenue,	
60/048,355	30 May 1997 (30.05.97) US	Gaithersburg, MD 20878 (US). FERRIE, Ann, M. [US/US];	
60/048,096	30 May 1997 (30.05.97) US	13203 L Astoria Hill Court, Germantown, MD 20874 (US).	
60/048,351	30 May 1997 (30.05.97) US	RUBEN, Steven, M. [US/US]; 18528 Heritage Hills Drive,	
60/048,154	30 May 1997 (30.05.97) US	Olney, MD 20832 (US). ROSEN, Craig, A. [US/US];	
60/048,160	30 May 1997 (30.05.97) US	22400 Rolling Hill Road, Laytonsville, MD 20882 (US).	
60/048,069	30 May 1997 (30.05.97) US	DUAN, Roxanne [US/US]; 4541 Fairfield Drive, Bethesda,	
60/048,131	30 May 1997 (30.05.97) US	MD 20814 (US). HU, Jing-Shan [CN/US]; 1247 Lakeside	
60/048,186	30 May 1997 (30.05.97) US	Drive #3034, Sunnyvale, CA 94086 (US). FLORENCE,	
60/048,095	30 May 1997 (30.05.97) US	Kimberly, A. [US/US]; 12805 Atlantic Avenue, Rockville,	
60/048,187	30 May 1997 (30.05.97) US	MD 20851 (US). OLSEN, Henrik, S. [DK/US]; 182	
60/048,099	30 May 1997 (30.05.97) US	Kendrick Place #24, Gaithersburg, MD 20878 (US).	
60/050,937	30 May 1997 (30.05.97) US	EBNER, Reinhard [DE/US]; 9906 Shelburne Terrace #316,	
60/048,352	30 May 1997 (30.05.97) US	Gaithersburg, MD 20878 (US). BREWER, Laurie, A.	
60/048,135	30 May 1997 (30.05.97) US	[US/US]; 14920 M. Nebo Road, Poolesville, MD 20837	
60/048,188	30 May 1997 (30.05.97) US	(US). MOORE, Paul, A. [GB/US]; Apartment 104, 1908	
60/048,094	30 May 1997 (30.05.97) US	Holly Ridge Drive, McLean, VA 22102 (US). SHI, Yangu	
60/048,350	30 May 1997 (30.05.97) US	[CN/US]; 437 West Side Drive, Gaithersburg, MD 20878	
60/054,804	5 August 1997 (05.08.97) US	(US). LAFLEUR, David, W. [US/US]; 1615 Q Street, N.W.	
		#807, Washington, DC 20009 (US). NI, Jian [CN/US];	
		5502 Manorfield Road, Rockville, MD 20853 (US).	
		(74) Agents: BROOKES, Anders, A. et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 10850 (US).	
		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).	
		Published With international search report.	
(54) Title: 87 HUMAN SECRETED PROTEINS			
(57) Abstract			
<p>The present invention relates to 87 novel human secreted proteins and isolated nucleic acids containing the coding regions of the genes encoding such proteins. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human secreted proteins.</p>			

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87 Human Secreted Proteins

Field of the Invention

This invention relates to newly identified polynucleotides and the polypeptides encoded by these polynucleotides, uses of such polynucleotides and polypeptides, and
5 their production.

Background of the Invention

Unlike bacterium, which exist as a single compartment surrounded by a membrane, human cells and other eucaryotes are subdivided by membranes into many functionally distinct compartments. Each membrane-bounded compartment, or
10 organelle, contains different proteins essential for the function of the organelle. The cell uses "sorting signals," which are amino acid motifs located within the protein, to target proteins to particular cellular organelles.

One type of sorting signal, called a signal sequence, a signal peptide, or a leader sequence, directs a class of proteins to an organelle called the endoplasmic reticulum
15 (ER). The ER separates the membrane-bounded proteins from all other types of proteins. Once localized to the ER, both groups of proteins can be further directed to another organelle called the Golgi apparatus. Here, the Golgi distributes the proteins to vesicles, including secretory vesicles, the cell membrane, lysosomes, and the other organelles.

20 Proteins targeted to the ER by a signal sequence can be released into the extracellular space as a secreted protein. For example, vesicles containing secreted proteins can fuse with the cell membrane and release their contents into the extracellular space - a process called exocytosis. Exocytosis can occur constitutively or after receipt of a triggering signal. In the latter case, the proteins are stored in secretory vesicles (or
25 secretory granules) until exocytosis is triggered. Similarly, proteins residing on the cell membrane can also be secreted into the extracellular space by proteolytic cleavage of a "linker" holding the protein to the membrane.

Despite the great progress made in recent years, only a small number of genes encoding human secreted proteins have been identified. These secreted proteins include
30 the commercially valuable human insulin, interferon, Factor VIII, human growth hormone, tissue plasminogen activator, and erythropoietin. Thus, in light of the pervasive role of secreted proteins in human physiology, a need exists for identifying and characterizing novel human secreted proteins and the genes that encode them. This knowledge will allow one to detect, to treat, and to prevent medical disorders by using
35 secreted proteins or the genes that encode them.

Summary of the Invention

The present invention relates to novel polynucleotides and the encoded polypeptides. Moreover, the present invention relates to vectors, host cells, antibodies, and recombinant methods for producing the polypeptides and polynucleotides. Also provided are diagnostic methods for detecting disorders related to the polypeptides, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying binding partners of the polypeptides.

Detailed Description

Definitions

The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide.

In the present invention, a "secreted" protein refers to those proteins capable of being directed to the ER, secretory vesicles, or the extracellular space as a result of a signal sequence, as well as those proteins released into the extracellular space without necessarily containing a signal sequence. If the secreted protein is released into the extracellular space, the secreted protein can undergo extracellular processing to produce a "mature" protein. Release into the extracellular space can occur by many mechanisms, including exocytosis and proteolytic cleavage.

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X or the cDNA contained within the clone deposited with the ATCC. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, with or without the signal sequence, the secreted protein coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having the translated amino acid sequence generated from the polynucleotide as broadly defined.

In the present invention, the full length sequence identified as SEQ ID NO:X was often generated by overlapping sequences contained in multiple clones (contig

analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X was deposited with the American Type Culture Collection ("ATCC"). As shown in Table 1, each clone is identified by a cDNA Clone ID (Identifier) and the ATCC Deposit Number. The ATCC is located at 10801 University Boulevard,
5 Manassas, Virginia 20110-2209, USA. The ATCC deposit was made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for purposes of patent procedure.

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained
10 in SEQ ID NO:X, the complement thereof, or the cDNA within the clone deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42°C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM sodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the
15 filters in 0.1x SSC at about 65°C.

Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages
20 of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 µg/ml salmon sperm blocking DNA; followed by washes at 50°C with 1XSSPE, 0.1% SDS. In addition, to achieve even
25 lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include
30 Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

Of course, a polynucleotide which hybridizes only to polyA+ sequences (such
35 as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a

complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone).

5 The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and
10 double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability
15 or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

 The polypeptide of the present invention can be composed of amino acids joined
20 to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs,
25 as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be
30 branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a
35 nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine,

formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990); Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

"SEQ ID NO:X" refers to a polynucleotide sequence while "SEQ ID NO:Y" refers to a polypeptide sequence, both sequences identified by an integer specified in Table 1.

"A polypeptide having biological activity" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention.)

Polynucleotides and Polypeptides of the Invention

FEATURES OF PROTEIN ENCODED BY GENE NO: 1

The translation product of this gene shares sequence homology with nucleolin, which is thought to be important in macromolecule binding, as well as some membrane proteins. Preferred polypeptide fragments comprise the amino acid sequence:
 DPEAADSGEPQNKRTDLPDEEYVKEEIQENEEAVKKMLVEATREFEEVVDES
 (SEQ ID NO:239); QKLKRKAEEDPEAADSGEPQNKRTDLPDEEYVKEEIQENEE
 AVKKMLVEATREFEEVVDES (SEQ ID NO:240); KAMEKSSLTQHSWQSLKDR
 YLKHLLRGQEHKYLLGDAPVSPSSQKLKRKAEEDPEAADSGEPQNKRTDLPDEE
 EYVKEEIQENEEAVKKMLVEATREFEEVVDESPPDFEIH (SEQ ID NO:241).
 Also preferred are the polynucleotide fragments encoding these polypeptide fragments.

This gene maps to chromosome 16, and therefore can be used as a marker in linkage analysis for chromosome 16.

This gene is expressed primarily in brain and kidney and to a lesser extent in wide range of tissues.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cell-cell interaction or cell-matrix interaction. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes
10 for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and kidney, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., brain and other tissue of the nervous system, and kidney, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
15 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:125 as residues: Met-1 to Trp-10.

20 The tissue distribution and homology to nucleolin indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of diseases involving cell-cell interaction or cell-extracellular matrix interaction.

FEATURES OF PROTEIN ENCODED BY GENE NO: 2

25 The translation product of this gene shares sequence homology with a porcine zona pellucida protein ZPDS.1711. (See Accession No. R39356.) These two proteins have weak homology with *Drosophila* commissureless and metal homeostasis proteins which are thought to be important in controlling growth cone guidance across the CNS midline and protecting cells against reactive oxygen toxicity. thus, based on homology, it is likely that this gene also be involved in development. Preferred polypeptide
30 fragments comprise the amino acid sequence: LPSYDEAERTKAEATIPLVGRDEDF VGRDDFDADQLRIGNDGIFMLTFFMAFLFNWIGFFLSFCLTTSAAGRYGAISG FGLSLIKWILIVRFSTYFPGYFDGQYWLWWVFLVLGFLFLRGRFINYAKVRKM PETFSNLPRTRVLFI (SEQ ID NO:242); and/or AGRYGAISGFGLSLIKWILIVRFS (SEQ ID NO:243). Also preferred are polynucleotide fragments encoding these
35 polypeptide fragments. This gene maps to chromosome 5, and therefore can be used in linkage analysis as a marker for chromosome 5.

This gene is expressed primarily in kidney, adrenal gland, brain and to a lesser extent in wide range of tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, fertilization control or tissue damages by metabolites or other toxic agents. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive and urosecretion system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., kidney, adrenal gland, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to zona pellucida protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for fertility control such as contraceptive development. The homology with metal homeostasis and commissureless genes indicates the gene's function in spermatozoa guidance and protection. It would also be useful for the treatment/diagnosis of tissue damages caused by toxic metabolites and other agents since the gene product is also expressed in urosecretive tissues.

25 **FEATURES OF PROTEIN ENCODED BY GENE NO: 3**

This gene is expressed primarily in liver and to a lesser extent in placenta. Preferred polypeptide fragments comprise the amino acid sequence: MKHLSAWNFT KLTFLQLWEI FEGSVENCQTLTSYSKLQIKYTFSRGSTFYI (SEQ ID NO:244). Also preferred are polynucleotide fragments encoding these polypeptide fragments.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, digestive and nutrient transport/utilization disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive and

circulatory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., liver, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in liver and placenta indicates that the protein product is either an extracellular enzyme or a molecule carrier. Therefore, polynucleotides and polypeptides corresponding to this gene are useful for diagnosis/treatment of digestive and nutrient transport/utilization disorders, including malabsorption and malnutrition.

FEATURES OF PROTEIN ENCODED BY GENE NO: 4

This gene shares homology with the sap47 gene of *Drosophila melanogaster*, a gene which codes for a conserved neuronal protein associated with synaptic terminals. (See Mol. Brain Res. 32:45-54 (1995); see also, Accession No. 929571.) Thus, based on homology, the gene of the present invention also should be associated with synaptic terminals. Preferred polypeptide fragments comprise the amino acid sequence:
 FSSDFRTSPWESRRVESKATSARCGLWGSGPRRRPASGMFRGLSSWLGLQQP
 VAGGGQPNGDAPPEQPSETVAESAEEELQQAGDQELLHQA KDFGN YLFNFASA
 ATKKITESVAETAQTIKKSVEEGKIDGIIDKTIIGDFQKEQKKFVEEQHTKKSEA
 AVPPWVD TNDEETIQQQILALSADKRNFLRDPPAGVQFNFDQMY PVALV ML
 (SEQ ID NO:245); MRFALVPKLVKEEVFWRNYFYRVSLIKQSAQLTALAAQQQA
 AGKGGEEQ (SEQ ID NO:246); STSPGVSEFVS DAFDACNLNQEDLRKEMEQL
 VLDKKQEETAVLEEDSADWEKELQQELQEYEVVTESEKRDENWDK (SEQ ID
 NO:247); SPWESRRVESKATSARCGLWGSGPRRRPASGMFRGLSSWLGLQQ
 PVAGGGQPNGDAPPEQPS (SEQ ID NO:248); PVAGGGQPNGDAPPEQPSETV
 ESAEEELQQAGDQELLHQA KDFGN YLFNFASAATKKITESVAE (SEQ ID NO:
 249); and/or FQKEQKKFVEEQHTKKSEAAVPPWVD TNDEETIQQQILALSADKR
 NFLRDPPAGVQFNFDQMY PVALV ML (SEQ ID NO:250). Also preferred are
 polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in kidney pyramids and to a lesser extent in lung and other tissues of various types. This gene fluxes calcium in human aortic smooth muscle cells, and therefore is involved in signal transduction.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, renal and nervous disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the kidney and/or nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., kidney, lung, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in kidney and lung and homology with sap47 indicates that the protein product has regulatory or direct functions in molecular exchange with body fluids and nervous system signaling. Polynucleotides and polypeptides corresponding to this gene are useful for treatment of disorders in kidney and nervous system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 5

The translation product of this gene shares sequence homology with the mouse Ly-9.2 antigen which is thought to be an important cell surface marker in lymphoids, myeloids and hematopoietic progenitors. (See Accession No. gil198932.) Preferred polypeptide fragments comprise the amino acid sequence: PFICVARNPVSERNFSSPI LARKLCEGAA (SEQ ID NO:251); and/or KEDPANTVYSTVEIPKKMENPHSLLT MPDTPRL (SEQ ID NO:252). Also preferred are polynucleotide fragments encoding these polypeptide fragments. Based on homology, it is likely that this gene is also a cell surface marker, involved in hematopoiesis.

This gene is expressed primarily in activated macrophages, monocytes and T-cells and to a lesser extent in spleen and bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune and hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., blood cells, and bone marrow, and cancerous and wounded

tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those
5 comprising a sequence shown in SEQ ID NO:129 as residues: Lys-26 to Tyr-33, Arg-44 to Ile-49, Ser-53 to Lys-71, Lys-86 to Pro-91.

The tissue distribution and homology to Ly-9.2 surface immunoglobulin family indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis of immune and hematopoietic disorders. Polypeptides and polynucleotides
10 corresponding to this gene are also be used as a marker for leukemia or a modulator of the functions of the cells of macrophage/monocyte or T-cell types.

FEATURES OF PROTEIN ENCODED BY GENE NO: 6

The translation product of this gene shares sequence homology with the
15 *Drosophila* glutactin gene which is thought to be important in cell-cell interaction or cell-extracellular matrix contact.

This gene is expressed primarily in colon tissue, aorta endothelial cells and to a lesser extent in skin, breast tissue and T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as
20 reagents for differential identification of these tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the gastrointestinal tract, vascular system or T-cell development. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these
25 tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive system, cardiovascular system, and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., colon, cardiovascular tissue, skin, mammary tissue, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine,
30 synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to glutactin indicates that polynucleotides
35 and polypeptides corresponding to this gene are useful for the development and maintenance of the integrity of the basal membrane in the gastrointestinal tract and

cardiovascular system. The expression in T-cells also indicate the protein may be involved in T-cell adhesion, cell-cell interaction and development.

FEATURES OF PROTEIN ENCODED BY GENE NO: 7

5 The translation product of this gene shares sequence homology with MURF4 protein, an ATPase homolog, which is thought to be important in ATP hydrolysis. This gene is expressed primarily in breast tissue.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, breast cancer and non-neoplastic breast diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the breast tissue, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., mammary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

20 The tissue distribution and homology to MURF4 gene indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neoplastic or non-neoplastic breast diseases because ATPase like protein may be involved in changed metabolic states of the breast.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 8

 This gene shares homology to the alcohol dehydrogenase gene. Preferred polypeptide fragments comprise the amino acid sequence: ASAVLLDL PNSG GEAQAKKLGNNCVFAPADV TSEKDVQTALALAKGKFGRVDVAVNCAGIAVAS

30 KTYNLKKGQTH TLEDFQRVLDVNL MGT FNVIRLVAGEMGQNEPDQGGQRGVI INTASVAAFEGQVGQAAYSASKGGIVGMTLPIARDLAPIGIRVMTIAPGLFGTPL LTSLPEKVCNFLASQVPFPSRLGDP AEY AHLVQAIENPFLNGEVIRLDGAIRMQ P (SEQ ID NO:253); and/or SVAAFEGQVGQAAYSASKGGIVGMTLPIA (SEQ ID NO:254). Polynucleotides encoding these fragments are also encompassed by the invention. Other groups have also recently cloned this gene, recognizing its homology to alcohol dehydrogenase. (See Accession No. 1778355.) Moreover, a second group

35

recently cloned the mouse homologue of this gene. (See Accession No. 2078284.) They found that the mouse homologue binds to amyloid beta-peptide and mediates neurotoxicity in Alzheimer's disease, calling the protein ERAB. This gene maps to chromosome X, and therefore can be used in linkage analysis as a marker for chromosome X. Therefore, mutations in the translated product of this gene may be involved in Alzheimer's disease in humans, as well as other sex linked diseases. This gene can be used as a diagnostic marker for these diseases.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:132 as residues: Arg-45 to Ser-53.

FEATURES OF PROTEIN ENCODED BY GENE NO: 9

The translation product of this gene shares weak sequence homology with rat N-methyl-D-aspartate receptor subunit and other proline-rich proteins which are thought to be important in neurotransmission or protein-protein interaction.

This gene is expressed primarily in synovial hypoxia and to a lesser extent in ovary, senescent cells and brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, synovial hypoxia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the synovia and brain, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., synovial tissue, ovary and other reproductive tissue, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in synovial hypoxia and nerve tissues, and homology to N-methyl-D-aspartate receptor subunit and other proline-rich proteins indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of synovial hypoxia and other synovial disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 10

This gene is expressed primarily in prostate and to a lesser extent in placenta and ovary.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, male and female infertility, cancer, and other hyperproliferative disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system and neoplasia, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., prostate, placenta, ovary and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 134 as residues: Pro-17 to Met-23, Ala-30 to Trp-38, Ile-49 to Trp-54, Lys-68 to Gly-74, Thr-93 to Gly-99, Met-126 to Glu-132, Gly-173 to Ser-178, Lys-205 to Tyr-214.

The tissue distribution of this gene in the prostate, placenta and ovary indicates that this gene product is useful for treatment/diagnosis of male or female infertility, endocrine disorders, fetal deficiencies, ovarian failure, amenorrhea, ovarian cancer, benign prostate hyperplasia, prostate cancer, and other forms of cancer of the reproductive system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 11

This gene is expressed primarily in the thyroid and to a lesser extent in the pineal gland. This gene maps to chromosome 10, and therefore can be used as a marker in linkage analysis for chromosome 10. Preferred polypeptide fragments comprise the amino acid sequence: HPIEWAINAATLSQFY (SEQ ID NO:256); CWIKYCLTLMQN AQLSMQDNIG (SEQ ID NO:257); KVSYLRLPLDFEEARELFLLGQHYVF (SEQ ID NO:258); MERRCKMHKRXIAMLEPLTVDLNPQ (SEQ ID NO:259); and/or SHIV KKINNLNKSALKY YQLFLD (SEQ ID NO:260). Also preferred are polynucleotides encoding these polypeptide fragments.

Therefore, polynucleotides and polypeptides of the invention are useful as

reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune, thyroid and pineal gland disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes
5 for differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., thyroid and pineal gland, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another
10 tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:135 as residues: Ser-2 to Ser-8, Thr-38 to Arg-44.

15 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating/detecting immune disorders such as arthritis, asthma, immune deficiency diseases (e.g., AIDS), and leukemia, as well as treating/detecting thymus disorders (e.g., Graves Disease, lymphocytic thyroiditis, hyperthyroidism, and hypothyroidism), and treating/detecting pineal gland disorders
20 (e.g., circadian rhythm disturbances associated with shift work, jet lag, blindness, insomnia and old age).

FEATURES OF PROTEIN ENCODED BY GENE NO: 12

This gene is expressed primarily in lung and tonsils.

25 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, pulmonary or immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for
30 differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the pulmonary and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., pulmonary tissue, and tonsils, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
35 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily

fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:136 as residues: Glu-28 to Gly-49.

The tissue distribution of this gene only in lung indicates that it could play a role in the treatment/detection of lung lymphoma or sarcoma formation, pulmonary edema and embolism, bronchitis and cystic fibrosis. Its expression in tonsils indicates a potential role in the treatment/detection of immune disorders such as arthritis, asthma, immune deficiency diseases (e.g., AIDS), and leukemia, in addition to the treatment/detection of tonsillitis.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 13**

This gene is expressed primarily in lymphoid, myeloid and erythroid cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hematopoietic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, myeloid cells, and bone marrow, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The predominant tissue distribution of this gene in hematopoietic cell types indicates that the gene could be important for the treatment or detection of immune or hematopoietic disorders including arthritis, asthma, immunodeficiency diseases and leukemia. Preferred embodiments of the present invention are polypeptide fragments comprising the amino acid sequence: FTHLSTCLLSLLLVRMSGFLLLARASPSI CALDSSCFVEYCSSYSSSCFLHQHFPSLLDHLCQ (SEQ ID NO:261); or FLLL ARASPSICALDSSCFVQEY (SEQ ID NO:262). Also preferred are polynucleotide fragments encoding these polypeptide fragments.

FEATURES OF PROTEIN ENCODED BY GENE NO: 14

This gene is homologous to the *Drosophila Regena* (*Rga*) gene. (See Accession No. 1658504.) This *Drosophila* gene is thought to be a homolog of the global negative

transcriptional regulator NOT2 (CDC36) from yeast, which modifies gene expression and suppresses position effect variegation. Preferred polypeptide fragments comprise the amino acid sequence: PDGRVTNIPQGMVTDQFGMIGLLTFIRAAETDPGMVHL
 5 ALGSDLTTLGLNLNS (SEQ ID NO:263); VHLALGSDLTTLGLNLNSPENLYP (SEQ ID NO:265); EDLLFYLYYMNGGDVLQLLA AVELFN RDWRYHKEERVWI
 TR (SEQ ID NO:264); and/or HNEDFPALPGS (SEQ ID NO:266).

This gene is expressed primarily in placenta and to a lesser extent in infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as
 10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurodegenerative and developmental disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of
 15 disorders of the above tissues or cells, particularly of the neurological system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., placenta, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having
 20 such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:138 as residues: Leu-9 to Tyr-15, Asp-34 to Gln-46, Pro-51 to Asp-57, Gly-88 to Thr-104, Thr-123 to Ser-128.

25 The tissue distribution of this gene indicates that it could be used in the detection and/or treatment of neurological disorders such as such as Alzheimer's Disease, Parkinson's Disease, Huntington's Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, and panic disorder.

30 **FEATURES OF PROTEIN ENCODED BY GENE NO: 15**

This gene is expressed primarily in adrenal gland tumor and osteoclastoma.

Therefore, polynucleotides and polypeptides of the invention are useful as
 reagents for differential identification of the tissue(s) or cell type(s) present in a
 biological sample and for diagnosis of diseases and conditions, which include, but are
 35 not limited to, endocrine and bone disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for

differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine system and in bone, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., adrenal gland, and bone, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:139 as residues: Ile-52 to Trp-57.

The tissue distribution of this gene indicates that it may be involved in the treatment and/or detection of adrenal gland tumors, osteosarcomas, endocrine disorders and bone disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 16

The translation product of this gene shares sequence homology with the FK506 binding protein, a protein which plays an important role in immunosuppression. (See Accession No. M75099.) Specifically, a 12-kDa FK506-binding protein (FKBP-12) is a cytosolic receptor for the immunosuppressants FK506 and rapamycin. (See, Proc. Natl. Acad. Sci. 88: 6677-6681 (1991).) Thus, based on homology, it is likely that this gene also has immunosuppression activity. Preferred polypeptides comprise the amino acid sequence: GRIIDTSLTRDPLVIELGQKQVIPGLEQSLLDMCVGEKRRRAIIPSH LAYGKRGFPSPADAVVQYDVELIALIR (SEQ ID NO:267); and/or IHYTGSLV DGR IIDTS (SEQ ID NO:268). Also preferred are the polynucleotide fragments encoding these polypeptides.

This gene is expressed primarily in melanocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer and other hyperproliferative disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and cancer, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., melanocytes, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to

the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:140 as residues: Ala-118 to Phe-124, Arg-178 to Lys-201.

- 5 The tissue distribution and homology to the FK506 binding proteins which are believed to a role in immunosuppression mediated by the immunosuppressant drugs rapamycin and cyclosporin, indicates that this gene could serve as a novel target for the identification of novel immunosuppressant drugs.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 17**

- The translation product of this gene shares sequence homology with the rat calcium-activated potassium channel rSK3, which is thought to be important in regulating vascular tone. (See Accession No. gil2564072, gil1575663, and
15 gil1575661.) Although homologous to these proteins, this gene contains an 18 amino acid insert, not previously identified in the homologs. Preferred polypeptide fragments comprise the amino acid sequence: CESPESPAQPSGSSLPAWYH (SEQ ID NO:269). Also preferred are the polynucleotide fragments encoding these polypeptides.

 This gene is expressed primarily in B-cells, frontal cortex and endothelial cells.

- Therefore, polynucleotides and polypeptides of the invention are useful as
20 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cardiovascular (hyper/hypotension, asthma, pulmonary edema, pneumonia, heart disease, restenosis, atherosclerosis, stroke, angina and thrombosis) and neurological disorders. Similarly, polypeptides and antibodies directed to these
25 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cardiovascular and nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, brain and other tissue of the nervous system, and endothelium,
30 and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID
35 NO:141 as residues: Glu-72 to Gly-82, His-90 to Val-95, Gln-168 to Lys-174, Val-202 to Ser-212.

The tissue distribution and homology to calcium-activated potassium channels indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of vascular disorders (hyper/hypotension, athesma, pulmonary edema, pneumonia, heart disease, restenosis, atherosclerosis, stoke, angina and thrombosis).

FEATURES OF PROTEIN ENCODED BY GENE NO: 18

This gene is expressed primarily in smooth muscle and to a lesser extent in brain (amygdala, corpus colosum, hippocampus).

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cardiovascular (hypertension, heart disease, athesma, pulmonary edema, restenosis, atherosclerosis, stoke, angina, thrombosis, and wound healing), and neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cardiovascular and neurological systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., smooth muscle, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:142 as residues: Lys-43 to Arg-49, Tyr-58 to Glu-65.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of cardiovascular disorders (hypertension, heart disease, athesma, pulmonary edema, restenosis, atherosclerosis, stoke, angina, thrombosis, and wound healing). Expression in brain indicates a role in the treatment and diagnosis of behavioral or neurological disorders, such as depression, schizizophrenia, Alzheimer's disease, mania, dementia, paranoia, and addictive behavior.

FEATURES OF PROTEIN ENCODED BY GENE NO: 19

This gene is expressed primarily in T-cells (Jurkats, resting, activated, and

anergic T-cells), endothelial cells, pineal gland, and to a lesser extent in a variety of other tissues and cell types. Preferred polypeptide fragments comprise the amino acid sequence: EEAGAGRRCSHG GARPAGLGNEGLGLGGDPDHTDTGSRSKQRINN WKESKHKVIMASASARGNQDKDAHFP PPSKQSLLFCPKSKLHIHRAEISK (SEQ ID NO:270); and/or SKQRINNWKESKHKVIMASASAR (SEQ ID NO:271). Also preferred are the polynucleotide fragments encoding these polypeptides.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation, immune and cardiovascular disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, neurological and vascular systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., T-cells and other blood cells, endothelial cells, and pineal gland, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:143 as residues: Phe-71 to Arg-76, Pro-82 to His-87, Glu-103 to Ala-111.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of immune disorders including: leukemias, lymphomas, auto-immune, immuno-suppressive (e.g. transplantation) and immunodeficiencies (e.g. AIDS) and hematopoietic disorders. In addition, expression in the pineal gland might suggest a role in the diagnosis of specific brain tumors and treatment of neurological disorders. Endothelial cell expression might suggest a role in cardiovascular or respiratory/pulmonary disorders or infections (athesma, pulmonary edema, pneumonia).

FEATURES OF PROTEIN ENCODED BY GENE NO: 20

This gene is expressed primarily in brain and embryo and to a lesser extent in leukocytes. This gene maps to chromosome 15, and therefore can be used as a marker in linkage analysis to chromosome 15.

Therefore, polynucleotides and polypeptides of the invention are useful as

reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental and neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 144 as residues: Met-1 to Gly-8.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of immune disorders including: leukemias, lymphomas, auto-immune, immuno-suppressive (e.g. transplantation) and immunodeficiencies (e.g. AIDS) and hematopoietic disorders. The expression in the brain -- and in particular the fetal brain -- would suggest a possible role in the treatment and diagnosis of developmental and neurodegenerative diseases of the brain and nervous system (depression, schizophrenia, Alzheimer's disease, mania, dementia, paranoia, and addictive behavior).

FEATURES OF PROTEIN ENCODED BY GENE NO: 21

This gene is expressed primarily in brain, kidney, lung, liver, spleen, and a variety of leukocytes (especially T-cells) and to a lesser extent in a variety of other tissues and cell types.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, leukemias, lymphomas, autoimmune, immunosuppressive, and immunodeficiencies, hematopoietic disorders, as well as renal disorders, and neoplasms. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the renal, pulmonary, immune, and central nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.,

brain and other tissue of the nervous system, kidney, pulmonary tissue, liver, spleen, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of renal conditions, such as acute renal failure, kidney fibrosis, and kidney tubule regeneration. The expression in leukocytes and other immune tissues indicates a role in immune disorders including: leukemias, lymphomas, auto-immune, immuno-suppressive (e.g. transplantation) and immunodeficiencies (e.g. AIDS) and hematopoietic disorders. The expression in the brain -- and in particular the fetal brain -- indicates a possible role in the treatment and diagnosis of developmental and neurodegenerative diseases of the brain and nervous system (depression, schizophrenia, Alzheimer's disease, mania, dementia, paranoia, and addictive behavior).

FEATURES OF PROTEIN ENCODED BY GENE NO: 22

This gene is expressed primarily in skin (fetal epithelium, keratinocytes and skin). This gene also maps to chromosome 19, and therefore can be used in linkage analysis as a marker for chromosome 19.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, skin cancers (e.g., melanomas), eczema, psoriasis or other disorders of the skin. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skin, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., skin and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:146 as residues: Pro-28 to Glu-35, Ser-39 to Phe-44, Ala-94 to Gln-99.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of skin cancers (e.g., melanomas), eczema, psoriasis or other disorders of the skin.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 23

This gene maps to chromosome 11. Another group recently isolated this same gene, associating the sequence to the region thought to harbor the gene involved in Multiple Endocrine Neoplasia Type 1, or MEN 1. (See Accession No. 2529721 and Genome Res. 7(7), 725-735 (1997), incorporated herein by reference in its entirety.)

10 Preferred polypeptide fragments comprise the amino acid sequence: LFHWACLNERA AQLPRNTAXAGYQCPSCNGPS (SEQ ID NO:272).

This gene is expressed primarily in epididymus, pineal gland, T-cells, as well as fetal epithelium, lung and kidney.

Therefore, polynucleotides and polypeptides of the invention are useful as
15 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune, metabolic mediated disorders, and MEN. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a
20 number of disorders of the above tissues or cells, particularly of the immune, renal, neurological and pulmonary systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., epididymus and other reproductive tissue, pineal gland, T-cells and other blood cells, epithelium, lung, and kidney, and cancerous and wounded tissues) or bodily fluids
25 (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
30 corresponding to this gene are useful for the treatment and diagnosis of developmental deficiencies or abnormalities as well as a host of different disorders which arise as a result of conditions in the indicated tissues or cell types. An area of particular interest is in the treatment and diagnosis of immune disorders including: leukemias, lymphomas, auto-immune, immuno-suppressive (e.g. transplantation) and immunodeficiencies (e.g.
35 AIDS) and hematopoietic disorders. The expression in the brain, and in particular the fetal brain, would suggest a possible role in the treatment and diagnosis of

developmental and neurodegenerative diseases of the brain and nervous system (depression, schizophrenia, Alzheimer's disease, mania, dementia, paranoia, and addictive behavior). Respiratory/pulmonary disorders, such as atesma, pulmonary edema are also potential therapeutic areas, as well as renal conditions such as acute renal failure, kidney fibrosis and kidney tubule regeneration. Moreover, this gene can be used in the treatment and/or detection of MEN I.

FEATURES OF PROTEIN ENCODED BY GENE NO: 24

This gene is expressed primarily in fetal spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, leukemia, lymphoma, AIDS, hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., spleen and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of immune disorders including: leukemias, lymphomas, auto-immune, immuno-suppressive (e.g. transplantation) and immunodeficiencies (e.g. AIDS) and hematopoietic disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 25

A closely related homolog of this gene was recently cloned by another group, calling the gene CDO, an oncogene-, serum-, and anchorage-regulated member of the Ig/fibronectin type III repeat family. (See Accession No. 2406628, and J. Cell Biol. 138(1): 203-213 (1997), herein incorporated by reference in its entirety.) Preferred polypeptide fragments comprise the amino acid sequence: FYIYYRPTDSDNDSYKK DMVEGDKYWHSISHLQPETSIDIKMQCFNEGGESEFSNVMICETKARKSSGQP GRLPPPTLAPPQPPLPETIERPVG TGAMVARSSDLPYLIVGVVLGSIIVLITFIPF CLWRAWKQKHTTDLGFPR SALPPSCPYTMVPLGGLPGHQA VDSPTS VASVD

GPVLM (SEQ ID NO:273); or YIYYRPTDSDNDSYKKDMVEGDKYWHSISHLQ
PETSYDIKMQCFNEGGESEFSNVMICETKARKS (SEQ ID NO:274).

This gene is expressed primarily in fetal lung and kidney, human embryo and
osteoclastoma stromal cells and to a lesser extent in a variety of other tissues and cell
5 types.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
not limited to, developmental disorders and cancers, as well as pulmonary and renal
10 disorders. Similarly, polypeptides and antibodies directed to these polypeptides are
useful in providing immunological probes for differential identification of the tissue(s)
or cell type(s). For a number of disorders of the above tissues or cells, particularly of
the respiratory/pulmonary, skeletal and renal systems, expression of this gene at
significantly higher or lower levels may be routinely detected in certain tissues and cell
15 types (e.g., lung, kidney, embryonic tissue, and bone cells, and cancerous and
wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
fluid) or another tissue or cell sample taken from an individual having such a disorder,
relative to the standard gene expression level, i.e., the expression level in healthy tissue
or bodily fluid from an individual not having the disorder. Preferred epitopes include
20 those comprising a sequence shown in SEQ ID NO:149 as residues: Thr-5 to Pro-18,
Ala-76 to Thr-84.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for the detection and treatment of: osteoporosis,
fracture, osteosarcoma, ossification, and osteonecrosis, as well as
25 respiratory/pulmonary disorders, such as atesma, pulmonary edema, and renal
conditions such as acute renal failure, kidney fibrosis and kidney tubule regeneration.

FEATURES OF PROTEIN ENCODED BY GENE NO: 26

This gene is homologous to the HIV envelope glycoprotein. (See Accession
30 No. 2641463.) Preferred polypeptide fragments comprise the amino acid sequence:
NVRALLHRMPEPPKINTAKFNNNKRKNLSL (SEQ ID NO:275).

This gene is expressed primarily in pineal gland and skin, and to a lesser extent
in lung.

Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, neurological and behavior disorders: respiratory/pulmonary disorders, such as atesma, pulmonary edema; skin conditions such as eczema, psoriasis, acne and skin cancer, as well as AIDS. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential

5 identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous and respiratory systems, as well as skin and AIDS, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, pineal gland, epidermis, and pulmonary tissue, and cancerous and wounded tissues) or bodily fluids

10 (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:150 as residues: Gln-15 to Gln-20.

15 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of conditions which affect the above tissues, such as: skin cancer, eczema, psoriasis, acne, atesma, pulmonary edema, neuro-degenerative or developmental disorders such as Alzheimer's, depression, schizophrenia, dementia, and AIDS.

20 **FEATURES OF PROTEIN ENCODED BY GENE NO: 27**

Preferred polypeptide encoded by this gene comprise the following amino acid sequence: NTNQREALQYAKNFQPFALNHQKDIQVLMGSLVYLRQGIENSPYVHL

LDANQWADICDIFTRDACALLGLSVESPLSVSFSAGCVALPALINIKAVIEQRQC

25 TGVWNQKDELPIEVDLGKKCWYHSIFACPILRQQTDDNNPPMKLVCGHIISRDLNKMFGSKLKCPYCPMEQSPGDAKQIFF (SEQ ID NO:276). Polynucleotides encoding such polypeptides are also provided as are complementary polynucleotides thereto.

30 This gene is expressed primarily in liver (adult and fetal) and spleen tissue, and to a lesser extent in placenta, T helper cells, kidney tumor, ovarian tumor, melanocytes and fetal heart.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

35 not limited to, immune and developmental diseases and disorders and liver diseases such as liver cancer. Similarly, polypeptides and antibodies directed to these

polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, circulatory and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, placenta, blood cells, kidney, ovary and other reproductive tissue, melanocytes, and heart, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful for study, diagnosis and treatment of growth, hematopoietic and immune system disorders particularly related to the liver.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 28**

The translation product of this gene shares sequence homology with prostaglandin transporter which is thought to be important in metabolic and endocrine disorders. See, for example, Gastroenterology Oct:109(4):1274-1282 (1995). Preferred polypeptides encoded by this gene comprise the following amino acid sequence:

20 SYLSACFAGCNSTNLTGACLTTPAENATVVPKGKCPSPGCQEAFLTFLCVMCI
CSLIGAMARHP (SEQ ID NO:277); and/or PSVILIRTVSPELKSIALGVLFLLRL
LGFIPPPLIFGAGIDSTCLFWSTFCGEQGACVLYDNVVYRYLYVSIAIALKSFAFI
(SEQ ID NO:278).

This gene is expressed primarily in hematopoietic and brain tissues.

25 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, metabolic, immune and endocrine diseases and disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing

30 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the metabolic, immune and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., endocrine tissue, hematopoietic tissue, and brain and other tissue of the nervous system, and cancerous and wounded

35 tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to

the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to prostaglandin (and anion) transporter indicates that polynucleotides and polypeptides corresponding to this gene are useful for
5 study, diagnosis and treatment of endocrine, metabolic, immune and kidney disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 29

This gene is expressed primarily in early stage human lung.

Therefore, polynucleotides and polypeptides of the invention are useful as
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, growth and respiratory disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of
15 the above tissues or cells, particularly of the developmental and respiratory systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., pulmonary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the
20 standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:153 as residues: Val-50 to Trp-55.

The tissue distribution indicates that the protein products of this gene are useful for study, diagnosis and treatment of respiratory and growth diseases and disorders.
25

FEATURES OF PROTEIN ENCODED BY GENE NO: 30

The translation product of this gene shares sequence homology with human DNA helicase which is thought to be important in accurate and complete DNA replication in creation of new cells. Preferred polypeptides encoded by this gene
30 comprise the following amino acid sequence: QSLFTRFVRVGVPTVDLDAQGRARA SLCXXYNWRYKNLGNLPHVQLLPEFSTANAGLLYDFQLINVEDFQGVGESEPN PYFYQNLGEAEYVVALFMYMCLLGYPADKISILTTYNGQKHLIRDIINRRCGNN PLIGRPNKVTTVDRFQGGQNDYILLSLVRTRAVGHLLRDVRRLLVAMSRAR (SEQ ID NO:279); and/or LVKEAKIIAMTCTHAALKRHDLVKLGFKYDNILMEE
35 AAQILEIETFIPLLLQNPQDGFSRLKRWIMIGDHHQLPPVI (SEQ ID NO:280).

This gene is expressed primarily in testes tumor and to a lesser extent in adrenal

gland tumor and placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancers and endocrine/growth disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine, developmental, and reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., testes and other reproductive tissue, adrenal gland, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to DNA helicase indicates that the protein products of this gene are useful for study, treatment, and diagnosis of many cancer types, including testicular cancer; as well as disorders involving endocrine function and normal growth and development.

FEATURES OF PROTEIN ENCODED BY GENE NO: 31

The translation product of this gene shares sequence homology with BID-apoptotic death gene (mouse), Genbank accession no. PID g1669514, which is thought to be important in programmed cell death.

This gene is expressed primarily in jurkat membrane bound polysomes and activated neutrophils and to a lesser extent in endothelial cells and human cerebellum.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancers and other proliferative disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, endothelium, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,

urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID
5 NO:155 as residues: Glu-4 to Leu-11, Cys-28 to Arg-35, Gln-50 to His-66, Glu-73 to Gln-79, Gly-94 to Ser-100, Arg-114 to Asp-126, Pro-139 to Lys-146.

The tissue distribution and homology to BID-apoptotic death gene indicates that the protein products of this gene are useful for study of cell death, and treatment and diagnosis of proliferative disorders and cancers. Apoptosis - programmed cell death - is
10 a physiological mechanism involved in the deletion of peripheral T lymphocytes of the immune system, and its dysregulation can lead to a number of different pathogenic processes. Diseases associated with increased cell survival, or the inhibition of apoptosis, include cancers (such as follicular lymphomas, carcinomas with p53 mutations, and hormone-dependent tumors, such as breast cancer, prostate cancer,
15 Kaposi's sarcoma and ovarian cancer); autoimmune disorders (such as systemic lupus erythematosus and immune-related glomerulonephritis rheumatoid arthritis) and viral infections (such as herpes viruses, pox viruses and adenoviruses), inflammation; graft vs. host disease, acute graft rejection, and chronic graft rejection. Diseases associated with increased apoptosis include AIDS; neurodegenerative disorders (such as
20 Alzheimer's disease, Parkinson's disease, Amyotrophic lateral sclerosis, Retinitis pigmentosa, Cerebellar degeneration); myelodysplastic syndromes (such as aplastic anemia), ischemic injury (such as that caused by myocardial infarction, stroke and reperfusion injury), toxin-induced liver disease (such as that caused by alcohol), septic shock, cachexia and anorexia. Thus, the invention provides a method of enhancing
25 apoptosis in an individual by treating the individual with a polypeptide encoded by this gene.

FEATURES OF PROTEIN ENCODED BY GENE NO: 32

30 The translation product of this gene shares sequence homology with human fructose transporter which is thought to be important in normal metabolic function and activity.

This gene is expressed primarily in T-cell lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, leukemia and other cancers, and metabolic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic, lymph and metabolic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., T-cells and other blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:156 as residues: Pro-22 to Gly-48, Ser-54 to Pro-61.

The tissue distribution indicates that the protein products of this gene are useful for study of mechanisms leading to cancer, treatment and diagnosis of cancerous and pre-cancerous conditions; as well as the study and treatment of various metabolic diseases and disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 33

This gene is expressed primarily in human meningima.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation and other disorders of the CNS. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the CNS and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., meningima and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:157 as residues: Asn-23 to Pro-31.

The tissue distribution indicates that the protein products of this gene are useful for study, diagnosis and treatment of disorders of the CNS and inflammatory responses.

FEATURES OF PROTEIN ENCODED BY GENE NO: 34

This gene is expressed primarily in activated monocytes and wound healing tissues and to a lesser extent in fetal epithelium.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune and inflammatory disorders and wound healing and tissue repair dysfunctions. Similarly, polypeptides and antibodies directed to these polypeptides are
10 useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, epithelial and gastrointestinal systems, and healing wounds, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., monocytes and other blood cells, and epithelium, and
15 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:158 as residues:
20 Ala-28 to Ala-33, Gly-35 to Glu-45.

The tissue distribution indicates that the protein products of this gene are useful for diagnosis, study and treatment of immune and inflammatory disorders and wound healing dysfunctions.

25 **FEATURES OF PROTEIN ENCODED BY GENE NO: 35**

This gene is expressed primarily in human osteosarcoma and prostate cancer.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
30 not limited to, skeletal and neoplastic conditions such as bone and prostate cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and skeletal systems, expression of this gene at significantly higher or lower
35 levels may be routinely detected in certain tissues (e.g., bone, and prostate, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial

fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:159 as residues:

5 Ser-14 to Gly-22, Leu-37 to Gln-43.

The tissue distribution indicates that the protein products of this gene are useful for diagnosis and treatment of skeletal disorders and cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 36

10 This gene encodes a protein which is highly homologous to a protein called congenital heart disease protein 5, presumably implicated in congenital heart disease (see Genbank PID g2810996).

This gene is expressed primarily in Hodgkin's lymphoma, erythroleukemia cells, and TNF activated synovial fibroblasts, to a lesser extent in ovarian cancer, 15 cerebellum, spleen, fetal liver and placenta and finally to a lesser extent in various other mesenchymal tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are 20 not limited to, cancer, immune, hematopoietic and cardiovascular disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, hematopoietic and cardiovascular systems, expression of this gene at significantly 25 higher or lower levels may be routinely detected in certain tissues and cell types (e.g., heart and other cardiovascular tissue, lymphoid tissue, blood cells, bone marrow, ovary and other reproductive tissue, brain and other tissue of the nervous system, spleen, liver, and mesenchymal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell 30 sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:160 as residues: Lys-41 to Met-49, Gln-54 to Glu-59, Glu-76 to Thr-88.

35 The homology of this gene and translation product to congenital heart disease protein 5 indicates a role for this protein in the diagnosis, prognosis and/or treatment of

heart disease or other cardiovascular related disorders. In addition, predominant expression in cells associated with the immune and hematopoietic system indicates a role for this protein in the treatment, diagnosis and/or prognosis of immune and autoimmune diseases, such as lupus, transplant rejection, allergic reactions, arthritis, asthma, immunodeficiency diseases, leukemia, AIDS, thymus disorders such as Graves Disease, lymphocytic thyroiditis, hyperthyroidism and hypothyroidism, graft versus host reaction, graft versus host disease, transplant rejection, myelogenous leukemia, bone marrow fibrosis, and myeloproliferative disease. The protein could also be used to enhance or protect proliferation, differentiation and functional activation of hematopoietic progenitor cells such as bone marrow cells, which could be useful for cancer patients undergoing chemotherapy or patients undergoing bone marrow transplantation. The protein may also be useful to increase the proliferation of peripheral blood leukocytes, which could be useful in the combat of a range of hematopoietic disorders including immunodeficiency diseases, leukemia, and septicemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 37

This gene is expressed primarily in ovarian cancer.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, urogenital neoplasias. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., ovary and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:161 as residues: Asn-22 to Asn-27.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis and treatment of ovarian and other tumors.

FEATURES OF PROTEIN ENCODED BY GENE NO: 38

The translation product of this gene shares sequence homology with zinc finger proteins.

This gene is expressed primarily in various fetal, cancer, and endothelial lines.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune and growth disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for
10 differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cardiovascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., fetal tissue, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
15 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful for study, diagnosis and treatment of immune and developmental conditions and cancer.

20

FEATURES OF PROTEIN ENCODED BY GENE NO: 39

This gene is expressed primarily in fetal, infant, and adult brain and to a lesser extent in other brain and endocrine organs and blastomas.

25 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, brain tumors and neurodegenerative conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of
30 disorders of the above tissues or cells, particularly of the nervous and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., brain and other tissue of the nervous system, endocrine tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an
35 individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the

disorder.

The tissue distribution indicates that the protein products of this gene are useful for the study, diagnosis and treatment of brain cancer and other neurological disorders.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 40

The translation product of this gene shares sequence homology with vesicular glycoproteins and lectins. Preferred polypeptides encoded by this gene comprise the following amino acid sequence: DTYPNEEKQQERVFPXXSAMVNNGSLSYDHER DGRPTELGGCXAIVRNLHYDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGV
10 RLPRGYFYTSSITGDLSDNHDVISLKLFEFTVERTPEEE (SEQ ID NO:281);
and/or LKREHSLSKPYQGVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQGA
LWNRVPCFLRDWELQVHFKIHGQGGKKNLHGDGLAIWYT (SEQ ID NO:282).

This gene is expressed primarily in infant brain and to a lesser extent in various normal and transformed neural, endocrine, and immune organs.

15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological and neurodevelopmental conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological
20 probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and hormonal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., brain and other tissue of the nervous system, endocrine tissue, and tissue and cells of the immune system, and cancerous and wounded tissues)
25 or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:164 as residues: Pro-64 to Gly-71, Gly-
30 94 to Leu-100, Thr-110 to Pro-116, Thr-135 to Arg-145, Glu-164 to Glu-171, Asp-204 to Asp-211, Arg-253 to His-261, Asn-312 to Tyr-323.

The tissue distribution indicates that the protein products of this gene are useful for the study, diagnosis and treatment of mental retardation and other neurological disorders and neoplasias.

FEATURES OF PROTEIN ENCODED BY GENE NO: 41

This gene displays homology to the glycosyltransferase family, which catalyze the addition of sialic acids to carbohydrate groups which are present on glycoproteins.

This gene is expressed primarily in smooth muscle and to a lesser extent in
5 pineal gland, fetal liver, and infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, gastrointestinal injury, inflammatory and neurodegenerative conditions.
10 Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., smooth muscle, pineal gland,
15 liver, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those
20 comprising a sequence shown in SEQ ID NO:165 as residues: Ser-12 to Trp-21, Arg-24 to Pro-32, Asp-73 to Lys-82, Lys-90 to Ala-97.

The tissue distribution indicates that the protein products of this gene are useful for the study, diagnosis and treatment of neurodegenerative and growth disorders and gastrointestinal repair.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 42

The translation product of this gene shares sequence similarity with metallothionein polypeptides. See, for example, Proc. Natl. Acad. Sci. U S A 1992 Jul 15;89(14):6333-6337. Metallothioneins are believed to inhibit neuronal survival among
30 other biological functions. Based on the sequence similarity (especially the conserved cysteine motifs characteristic of the metallothionein family) the translation product of this gene is expected to share certain biological activities with other members of the metallothionein polypeptide family. Preferred polypeptides encoded by this gene comprise the following amino acid sequence: PGTLQCSALHHDPGCANCSRFCRD
35 CSPPACQC (SEQ ID NO:283).

This gene is expressed exclusively in placenta and fetal liver.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hematopoietic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., placenta, liver, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to metallothionein indicates that the protein products of this gene are useful for diagnosis and treatment of immune and hematopoietic system disorders and neurological diseases, especially in fetal development.

FEATURES OF PROTEIN ENCODED BY GENE NO: 43

Preferred polypeptides encoded by this gene comprise the following amino acid sequence: FLYDVLMXHEAVMRTHQIQLPDPEFPS (SEQ ID NO:284).

This gene is expressed primarily in T-cells and synovial tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune system disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., synovial tissue, and T-cells and other blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful for treatment and diagnosis of disorders of the immune system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 44

5 The translation product of this gene shares sequence similarity with several methyltransferases (e.g., see Genbank gil1065505).

 This gene is expressed primarily in ovary, thymus, infant adrenal gland, tissues of the nervous system and the hematopoietic tissue, and to a lesser extent in adipose tissue and many other tissues.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders of the reproductive system, the endocrine system, the hematopoietic system and the CNS. Similarly, polypeptides and antibodies directed to
15 these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, endocrine, CNS and reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., ovary and other reproductive tissue, thymus, adrenal gland,
20 brain and other tissue of the nervous system, hematopoietic tissue, and adipose tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the
25 disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:168 as residues: Ser-3 to Gly-12, Asp-19 to Arg-31, Tyr-70 to Tyr-77, Asn-130 to Lys-140, Pro-165 to Gln-170, Pro-192 to Lys-199, Leu-216 to Glu-227, Glu-254 to Phe-281.

 The tissue distribution and homology to methyltransferase indicates that the
30 protein products of this gene are useful for diagnosis and treatment of disorders of the CNS, the hematopoietic system and reproductive organs and tissues. For example, the abundant expression in the ovary may indicate that the gene product can be used as a hormone with either systemic or reproductive functions; as growth factors for germ cell maintenance and in vitro culture; as a fertility control agent; remedy for sexual
35 dysfunction or sex development disorders; diagnostics/treatment for ovarian tumors, such as serous adenocarcinoma, dysgerminoma, embryonal carcinoma,

choriocarcinoma, teratoma, etc; The expression in thymus may indicate its utilities in T-cell development and thus its applications in immune related medical conditions, such as infection, allergy, immune deficiency, tissue/organ transplantation, etc.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 45

The translation product of this gene shares sequence homology with cytochrome C oxidase which is thought to be important in metabolic function of cells. This gene has now recently been published as estrogen response gene. See Genbank accession no. AB007618 and Mol. Cell. Biol. 18 (1), 442-449 (1998). See also J Immunol. Mar 1:154(5): 2384-2392 (1995), where the mouse homologue was published and implicated in siliocis.

This gene is expressed primarily in adipose tissue, kidney and fetal brain and to a lesser extent in several other tissues and organs.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, metabolic diseases involving especially adipose tissue, brain and kidney. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the CNS and vascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., adipose tissue, kidney, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:169 as residues: Thr-5 to Ser-14.

The tissue distribution and homology to cytochrome C oxidase, estrogen response gene product and siliocis related gene product indicates that the protein products of this gene are useful for diagnosis and treatment of metabolic disorders in the CNS, adipose tissue and kidney, particularly siliocis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 46

The translation product of this gene shares sequence homology with reticulocalbin. See, for example, J. Biochem. 117 (5), 1113-1119 (1995). Based on the

sequence similarity, the translation product of this gene is expected to share certain biological activities with reticulocalbin, e.g., Ca^{++} binding activities. This gene product is sometimes hereinafter referred to as "Reticulocalbin-2".

5 This gene is expressed primarily in breast, endothelial cells, synovial, heart and smooth muscle cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the breast, vascular and skeletal/cardiac muscular system.

10 Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the breast, vascular and skeleto-muscular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g.,

15 mammary tissue, endothelial cells, synovial tissue, heart and other cardiovascular tissue, and smooth muscle, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an

20 individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:170 as residues: Gly-16 to Arg-32, Ala-42 to Asn-50, Glu-66 to Gln-76, Arg-85 to Gly-94, Thr-108 to Asp-115, Trp-121 to Gly-130, Leu-137 to His-144, Glu-155 to Lys-161, Asp-175 to Ser-180, Glu-209 to Gly-217, Glu-232 to Glu-237, Thr-243 to Asp-261, Glu-287 to Arg-295.

25 The tissue distribution indicates that the protein products of this gene are useful for diagnosis and treatment of diseases of the vascular and skeletal/cardiac muscular system. The homology of the gene with reticulocalbin indicates its biological function in regulating calcium store, a particularly important function in muscular cell types. The gene expression in the heart may indicate its utilities in diagnosis and remedy in heart

30 failure, ischemic heart diseases, cardiomyopathy, hypertension, arrhythmia, etc. The abundant expression in the breast may indicate its applications in breast neoplasia and breast cancers, such as fibroadenoma, papillary carcinoma, ductal carcinoma, Paget's disease, medullary carcinoma, mucinous carcinoma, tubular carcinoma, secretory carcinoma and apocrine carcinoma; juvenile hypertrophy and gynecomastia, mastitis

35 and abscess, duct ectasia, fat necrosis and fibrocystic diseases, etc.

FEATURES OF PROTEIN ENCODED BY GENE NO: 47

The translation product of this gene shares weak sequence homology with H⁺-transporting ATP synthase which is thought to be important in cell metabolism or signal transduction.

5 This gene is expressed only in testis.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of some types of diseases and conditions.

10 Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and hematopoietic tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., testes and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, 15 synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

20 Since only one out of about a million expressed sequence tag is found in testes indicates that its expression is low and selectively in testes. Since some of the genes only expressed in testes are usually expressed in brain or in certain induced hematopoietic cells/tissues, it is speculated that this gene to be expressed in brain or hematopoietic cells/tissues and is useful for diagnosis and treatment of disorders these systems.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 48

30 The translation product of this gene shares sequence homology with human polymeric immunoglobulin receptor (accession No.X73079) which is thought to be important in antibody recognition and immune defenses. In one embodiment, polypeptides of the invention comprise the sequence GWYWCG (SEQ ID NO:285). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in placenta and to a lesser extent in corpus callosum and fetal liver and spleen.

35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, disorders of the immune system, e.g. autoimmune diseases and immunodeficiency. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., placenta, liver, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:172 as residues: Tyr-37 to Cys-49, Gly-51 to Tyr-56, Lys-88 to Trp-93, Leu-130 to Glu-136.

The tissue distribution and homology to human polymeric immunoglobulin receptor indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of immune disorders, e.g. autoimmune diseases and immunodeficiencies.

FEATURES OF PROTEIN ENCODED BY GENE NO: 49

This gene is expressed in thymus.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune disorder. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., thymus and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of immune disorders, e.g. autoimmunity and immunodeficiency.

FEATURES OF PROTEIN ENCODED BY GENE NO: 50

Preferred polypeptide encoded by this gene comprise the following amino acid sequence: MKVGARIRVKMSVNKAHPVVSTHWRWPAEWPQMFLHLAQEP RTE
5 VKSRPLGLAGFIRQDSKTRKPLEQETIMSAADTALWPYGHGNREHQENELQKY
LQYKDMHLLDSGQSLGHTHTLQGSHNLTALNI (SEQ ID NO:286).

Polynucleotides encoding this polypeptide are also provided as are complementary polynucleotides thereto.

10 This gene is expressed primarily in adrenal gland, pituitary, T helper cells, and breast cells and to a lesser extent in a wide variety of tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of the some diseases and conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
15 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., adrenal gland, pituitary, T-cells and other blood cells, and mammary tissue, and cancerous and wounded tissues) or bodily fluids
20 (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:174 as residues: Gln-39 to Ser-47, Arg-57 to Glu-67,
25 Tyr-82 to Gln-95.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of a wide range of disorders, such as immune and endocrine disorders.

30 FEATURES OF PROTEIN ENCODED BY GENE NO: 51

The translation product of this gene shares sequence homology with human Sop2p-like protein which is important in cytoskeleton structure. In one embodiment, polypeptides of the invention comprise the sequence SLHKNSVSQISVLGGKAKCS
35 QFCTTGMDGGMSIWDVKSLESALKDLKI (SEQ ID NO:287). Polynucleotides encoding this polypeptide are also encompassed by the invention. This gene maps to chromosome 7. Therefore, polynucleotides of the invention can be used in linkage

analysis as a marker for chromosome 7.

This gene is expressed primarily in immune and hematopoietic tissues/cells and to a lesser extent in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immunological and hematopoietic disorders and inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a
10 number of disorders of the above tissues or cells, particularly of the immune and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., immune and hematopoietic tissue/cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample
15 taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:175 as residues: Lys-49 to Gln-54, Ala-61 to Arg-66, Lys-82 to Lys-87, Glu-126 to Val-133, His-136 to Ile-141, Glu-175 to Ser-187, Asp-
20 286 to Leu-296, Ala-298 to Ser-310.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of immunological, hematopoietic, and inflammatory disorders, e.g., immunodeficiency, autoimmunity, inflammation.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 52

The translation product of this gene shares sequence homology with *Caenorhabditis elegans* R53.5 gene encoding a putative secreted protein without known function.

30 This gene is expressed primarily in endothelial cells, brain and several highly vascularized, and tumor tissues and to a lesser extent in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
35 not limited to, aberrant angiogenesis and tumorigenesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes

for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vascular and brain system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endothelial cells, brain and other tissue of the nervous
5 system, and vascular tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a
10 sequence shown in SEQ ID NO:176 as residues: Thr-43 to Asn-60, Thr-106 to Phe-115, Asp-122 to Arg-133, Arg-186 to Asp-192, Leu-211 to Lys-216.

The tissue distribution and homology to a *C. elegans* secreted protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis or treatment of disorders in vascular or brain system, e.g. aberrant
15 angiogenesis, ischemia, neurodegeneration, etc.

FEATURES OF PROTEIN ENCODED BY GENE NO: 53

In one embodiment, polypeptides of the invention comprise the sequence EASKSSHAGLDLFSVAACHRF (SEQ ID NO:288). Polynucleotides encoding this
20 polypeptide are also encompassed by the invention.

This gene is expressed primarily in T-cells and to a lesser extent in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
25 not limited to, lymphocytic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the lymphoid system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell
30 types (e.g., T-cells and other blood cells, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the
35 disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:177 as residues: Pro-3 to Thr-8, Arg-37 to Asp-46.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis, treatment, and cure of lymphocytic disorders.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 54

The translation product of this gene shares sequence homology with secreted cartilage matrix protein, a major component of the extracellular matrix of nonarticular cartilage which is thought to be important in cartilage structure. In specific
 10 embodiment, polypeptides of the invention comprise the sequence: RCKKCTEGPI
 DLVFVIDGSKSLGEENFEVVKQF (SEQ ID NO:297); VTGIIDSLTISPKAARVGL
 LQYSTQVH (SEQ ID NO:290); TEFTLRNFNSAKDMKKAVAHMKYM (SEQ ID
 NO:291); GKGSMTGLALKHMFERSFTQGEARPF (SEQ ID NO:292); STRVP
 RAAIVFTDGRAQDDVSEWASKAKANGITMYAVGVGKAIE (SEQ ID NO:293);
 EELQEIASEPTNKHLYAEDFSTMDEISEKLKKGICEALED (SEQ ID NO:294);
 15 TQRLEEMTQRM (SEQ ID NO:295); PQGCPEQPLH (SEQ ID NO:296); and/or
 YMGKGSMTGLALKHMFERSFT (SEQ ID NO:289). Polynucleotides encoding these
 polypeptides are also encompassed by the invention.

This gene is expressed primarily in placenta, infant brain, prostate, fetal lung and to a lesser extent in endometrium and fetal tissues.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, abnormal placenta and pregnancy, disorder and injury in brain, prostate, and vasculature. Similarly, polypeptides and antibodies directed to these polypeptides
 25 are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproduction, neuronal, and vascular systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., placenta, brain and other tissue of the nervous system, prostate, lung and
 30 endometrium, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

35 The tissue distribution and homology to cartilage matrix protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis,

treatment, and cure of abnormalities in placenta and pregnancy, disorder and injury in brain, prostate, and vasculature.

FEATURES OF PROTEIN ENCODED BY GENE NO: 55

5 The translation product of this gene is the human ortholog of bovine and hamster CII-3, a succinate-ubiquinone oxidoreductase complex II membrane-intrinsic subunit, which is thought to be important in mitochondrial electron transport chain during metabolism. In specific embodiments, the polypeptides of the invention comprise MAALLLRHVGRHCLRAHFSPQLCIRNAVPLGTTAKEEMERFWNKNIG
10 SNRPLSPHITIYS (SEQ ID NO:298); VFPLMYHTWNGIRHLMWDLGKGLKIPQL YQSG (SEQ ID NO:299); MAALLLRHVGRHCLRAH (SEQ ID NO:300); VKSLCL GPALIHTAKFAL (SEQ ID NO:301); VFPLMYHTWNGIRHLMWDLGKGL (SEQ ID NO:302).

 This gene is expressed in 8-week old early stage human.

15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, metabolism disorder. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential
20 identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the [insert system where a related disease state is likely, e.g., immune], expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or
25 cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

 The tissue distribution and homology to indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis, treatment, and cure of
30 metabolism disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 56

 This gene is expressed primarily in umbilical vein endothelial cells, human ovarian tumor cells, human meningioma cells, and human Jurkat membrane bound
35 polysomes. In specific embodiments, polypeptides of the invention comprise the amino acid sequence: RVWDVRPFAPKERCVKIFQGNV (SEQ ID NO:303); HNFEKNLL

RCSWSPDGSKIAAGSADRFVYV (SEQ ID NO:304); and/or WDTTSRRILYKLPG HAGSINEVAFHPDEPI (SEQ ID NO:305). Polynucleotides encoding these polypeptides are also encompassed by the invention.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation, immune and cardiovascular disorders and urogenital neoplasias. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, neurological, urogenital, reproductive system and vascular systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, cells, endothelial cells, ovary and other reproductive tissue, meningima, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:143 as residues: Phe-71 to Arg-76, Pro-82 to His-87, Glu-103 to Ala-111.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of immune disorders including: leukemias, lymphomas, auto-immune, immuno-suppressive (e.g. transplantation) and immunodeficiencies (e.g. AIDS) and hematopoietic disorders. In addition, expression in ovarian tumor cells suggests that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis, and treatment of ovarian tumors, and other tumors and neoplasias. Further, endothelial cell expression suggests a role in cardiovascular or respiratory/pulmonary disorders or infections (athsma, pulmonary edema, pneumonia).

FEATURES OF PROTEIN ENCODED BY GENE NO: 57

The translation product of this gene shares sequence homology with type I collagen. In specific embodiments, the polypeptides of the invention comprise the sequence: GRIPAPAPSVPA GPDSR (SEQ ID NO:309); VRGRTVLRPGLDAEPE LSPE (SEQ ID NO:306); EQRVLERKCLKKERKKEERQ (SEQ ID NO:307); ARRSG

AELAWDYLCRWAQKHKNWRFQKTRQTWLLHMYDSKVPDEHFSTLLAYLE
GLQGR (SEQ ID NO:255); and/or RLREAGLVAQHPP (SEQ ID NO:308).

Polynucleotides encoding these polypeptides are also encompassed by the invention.

5 This gene is expressed primarily in epididymus, prostate cell line (LNCAP),
and pituitary gland; and to a lesser extent in many other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
not limited to, abnormalities of the epididymus, prostate (especially prostate cancer),
10 and pituitary gland. Similarly, polypeptides and antibodies directed to these
polypeptides are useful in providing immunological probes for differential identification
of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
particularly of the male reproductive system and neuroendocrine system, expression of
this gene at significantly higher or lower levels may be routinely detected in certain
15 tissues (e.g., epididymus and other reproductive tissue, prostate, and pituitary gland,
and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine,
synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual
having such a disorder, relative to the standard gene expression level, i.e., the
expression level in healthy tissue or bodily fluid from an individual not having the
20 disorder.

The tissue distribution and homology to type I collagen, indicates that
polynucleotides and polypeptides corresponding to this gene are useful for diagnosis
and treatment of abnormalities of the epididymus, prostate (especially prostate cancer),
and pituitary gland.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 58

This gene is expressed primarily in the frontal cortex of the brain from a
schizophrenic individual.

Therefore, polynucleotides and polypeptides of the invention are useful as
30 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
not limited to, schizophrenia. Similarly, polypeptides and antibodies directed to these
polypeptides are useful in providing immunological probes for differential identification
of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
35 particularly of the nervous system, expression of this gene at significantly higher or
lower levels may be routinely detected in certain tissues (e.g., brain and other tissue of

the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of schizophrenia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 59

The polypeptide encoded by Gene 59 is homologous to human surface 4 integral membrane protein. In specific embodiments, the polypeptides of the invention comprise the sequence: TGCVLVLSRNFVQYACFGLFGIILQTIAYSILWDLKF LMRN (SEQ ID NO:310); SRSEGKSMFAGVPTMRESSPKQYMQLGGRVLLV LMFMTLLHFDASFFSIVQNIVG (SEQ IDNO:311); GTAEDFADQFLRVTKQYLP HVARLCLISTFLEDGIRMFQWSEQRDYIDTTWNCGYLLAS (SEQ ID NO:312); LMRNESRS (SEQ ID NO:314); ASFLLSRTSWGTA (SEQ ID NO:315); and/or ASFLLSRTSWGTA LMIL (SEQ ID NO:313). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in Hodgkin's lymphoma and lung; and to a lesser extent in many other human tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, Hodgkin's lymphoma, tumors or other abnormalities of the lung. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and respiratory systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., lymphoid tissue, and pulmonary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:183 as residues: Met-20 to Trp-27.

The tissue distribution indicates that polynucleotides and polypeptides

corresponding to this gene are useful for diagnosis and treatment of Hodgkin's lymphoma, tumors or other abnormalities of the lung.

FEATURES OF PROTEIN ENCODED BY GENE NO: 60

5 This gene is expressed primarily in bone cancer and stomach cancer, and to a lesser extent in many other tissues.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
10 not limited to, bone cancer and stomach cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the bone, and the stomach, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues
15 (e.g., bone, and stomach, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

20 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of bone cancer and stomach cancer and possibly other cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 61

25 This gene is expressed primarily in epididymus, and lymph node of breast cancer, and to a lesser extent in many other tissues.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
30 not limited to, abnormalities of the epididymus, and breast cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the epididymus and breast, expression of this gene at significantly higher or lower levels may be routinely
35 detected in certain tissues (e.g., epididymus and other reproductive tissue, lymphoid tissue, and mammary tissue, and cancerous and wounded tissues) or bodily fluids

(e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:185 as residues: Arg-57 to Ser-65.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of abnormalities of the epididymus, and breast cancer.

10 FEATURES OF PROTEIN ENCODED BY GENE NO: 62

The translation product of this gene appears to be the human homolog of bovine NADH dehydrogenase which is thought to be important in cellular metabolism. In specific embodiments, the polypeptides of the invention comprise the amino acid sequence: SMSALTRLASFARVGGRLFRSGCARTAGDGGVRHAGGGVHIEPRY
15 RQFPQLTRSQVFQSEFFSGLMFWILWRFWHDSEEVLGHFPYPDPSQWTDEEL
GIPDDED (SEQ ID NO:323), or fragments thereof. Polynucleotides encoding this polypeptide are also encompassed by the invention.

This gene is expressed in larynx tumor, lymph node, brain amygdala, human cardiomyopathy, and retina.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases affecting cellular metabolism. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes
25 for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., larynx, lymphoid tissue, brain and other tissue of the nervous system, heart and cardiovascular tissue, and retina, and cancerous and wounded tissues) or
30 bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:208 as residues: Pro-27 to Gln-32, Arg-
35 42 to Glu-51.

The tissue distribution and homology to NADH dehydrogenase indicates that

polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of diseases involving cellular metabolism.

FEATURES OF PROTEIN ENCODED BY GENE NO: 63

5 This gene is expressed primarily in amygdala, and to a lesser extent in many other tissues.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
10 not limited to, abnormalities of the amygdala. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the amygdala, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.,
15 amygdala, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a
20 sequence shown in SEQ ID NO:187 as residues: Gln-17 to Glu-29, Pro-41 to Phe-46, Ser-59 to Ile-70, Thr-97 to Leu-105.

 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of abnormalities of
25 amygdala.

FEATURES OF PROTEIN ENCODED BY GENE NO: 64

 This gene is expressed primarily in female bladder, and to a lesser extent in chronic synovitis and hemangiopericytoma.

 Therefore, polynucleotides and polypeptides of the invention are useful as
30 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, bladder cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
35 particularly of the urinary tract, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., bladder, synovial tissue, and

vascular tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:188 as residues: Pro-2 to Gln-7, Pro-27 to Phe-34.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatments of defects of the urinary tract, especially bladder cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 65

This gene is expressed primarily in fetal spleen, and to a lesser extent in hemangiopericytoma, thymus, and synovial sarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, defects of immune or hematopoietic systems. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., spleen, vascular tissue, thymus, blood cells, and synovial tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The protein product of this gene is useful for treatment of defects of the immune or hematopoietic systems, because of the gene's expression in thymus and spleen.

FEATURES OF PROTEIN ENCODED BY GENE NO: 66

This gene is expressed primarily in human pituitary and to a lesser extent in placenta and fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, endocrine growth disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., pituitary and other endocrine tissue, placenta, and pulmonary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:190 as residues: Val-38 to Asn-44, Gly-53 to Ser-65.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of growth disorders related to pituitary dysfunction.

FEATURES OF PROTEIN ENCODED BY GENE NO: 67

The translation product of this gene shares sequence homology with a *Caenorhabditis elegans* gene of unknown function. In specific embodiments, the polypeptides of the invention comprise the sequence: DPRRPNKVLRYKPPPSE CNPALDDPTP (SEQ ID NO:317); DYMNLLGMIFSMCGLMLKLKWCWVA VYCS (SEQ ID NO:318); FISFANSRSEDTKQMMSSF (SEQ ID NO:316); and/or MLSISAVVMSYLQNPQPMTPPW (SEQ ID NO:319). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in primary breast cancer and lymph node breast cancer and to a lesser extent in adult brain, lung cancer, colon cancer, epithelioid sarcoma, and Caco-2 cell line.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cancer and tumor tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., mammary tissue, lymphoid tissue, brain and other tissue of the nervous system, lung, colon, and

epithelium, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:191 as residues: Asn-34 to Lys-42.

The tissue distribution in a variety of cancer tissues indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of a variety of cancer and tumor types.

10

FEATURES OF PROTEIN ENCODED BY GENE NO: 68

The translation product of this gene shares sequence homology with steroid membrane binding protein. The translation product of this gene has recently been published as progesterone binding protein. See Genbank AJ002030. Preferred polypeptides encoded by this gene comprise the following amino acid sequence: AAGDGDVKLGLTSGSESSNDGGSESPGDAGAAAXGGGWAAAALALLTG GGE (SEQ ID NO:320).

This gene is expressed primarily in breast, and to a lesser extent in placenta and fetal tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, breast cancer or developmental disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of breast or fetal tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., mammary tissue, placenta, and fetal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:192 as residues: Pro-43 to Asp-49, Gln-54 to Pro-64, Asp-110 to Asp-118, Lys-138 to Tyr-143, Pro-150 to Asp-170.

The tissue distribution and homology to steroid membrane binding protein and to progesterone binding protein indicates that the protein products of this gene are

useful for treatment of breast cancers, especially those caused by estrogen and progesterone binding.

FEATURES OF PROTEIN ENCODED BY GENE NO: 69

5 Preferred polypeptides encoded by this gene comprise the following amino acid sequence: AADNYGIPRACRNSARSYGAAWLLXPAGSSRVEPTQDISISDQLGG QDVPVFRNLSLLVVGVGAVFSLLFHLGTRERRRPHAXEPGEHTPLLAPATAQPL LLWKHWLREXAFYQVGILYMTTRLIVNLSQTYMAMYLTYSLHLPKKFIATIPLV MYLSGFLSSFLMKPINKCIGRN (SEQ ID NO:321).

10 This gene is expressed primarily in macrophage (GM-CSF treated), and to a lesser extent in monocytes and dendritic cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation and infection. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., macrophages and other blood cells, and dendritic cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

25 The tissue distribution indicates that the protein products of this gene are useful for treatment of infection or inflammation or other events or defects involving the immune system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 70

30 This gene is expressed primarily in adult brain and to a lesser extent in thyroid, 12 week old early stage human, and stromal cell TF274.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological or neuro-endocrine diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes

for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous or endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, thyroid, and stromal cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:194 as residues: Pro-65 to Cys-71.

The tissue distribution indicates that the protein products of this gene are useful for treatment and diagnosis of neurological diseases or metabolic conditions involving the neuro-endocrine system.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 71**

This gene is expressed in T-cell helper and to a lesser extent in adult brain and adult testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune disorders, meningitis or reproductive problems. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, neural and reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., T-cells and other blood cells, brain and other tissue of the nervous system, testes and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:195 as residues: Val-18 to Tyr-24, Ala-89 to Asp-99, Asp-104 to Ala-117, Leu-121 to Pro-136.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis immune and

reproductive disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 72

5 The translated polypeptide of this contig has a high degree of identity with the Ob Receptor-Associated Protein deposited as GenBank Accession No. 2266638. No function has been determined for the Ob Receptor-Associated Protein, however it is expressed upon stimulation of the Ob Receptor by Leptin.

This gene is expressed in T-cells and to a lesser extent in endothelial and bone marrow cells.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, acute lymphoblastic leukemia, hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
15 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., T-cells and other blood cells, endothelial cells, and bone marrow, and cancerous and wounded tissues) or
20 bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:196 as residues: Ser-61 to Trp-70.

25 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of leukemia and other disorders of the primary immune system. In addition, since this gene appears to be related to the Ob Receptor-Related Protein, it is likely that this polypeptide is also involved in the Ob/Leptin signal transduction cascade. As a result, this protein may be
30 of use in the molecular diagnosis and therapeutic intervention of obesity and related disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 73

35 The translation product of this contig has homology with furin, a protein thought to be a key endopeptidase in the constitutive secretory pathway. The identification and initial characterization of Furin was reported by Takahasi and.

colleagues (Biochem Biophys Res Commun 1993 Sep 15;195(2):1019-1026).

This gene is expressed in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the immune system such as allergies, wound healing and antigen recognition. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., neutrophils and other blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of allergies or other immune disorders since neutrophils are an important part of an allergic response. Further, since this protein appears to be related to Furin, it can be used diagnostically and therapeutically to treat secretory protein processing disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 74

This gene is expressed in the frontal cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, of the motor activity and sensory functions that involve the central nervous system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene

expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of neural disorders that affect cognitive functions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 75

The translation product of this gene shares sequence homology with inorganic pyrophosphatase which is thought to be important in the catalysis the hydrolysis of diphosphate bonds, chiefly in nucleoside di- and triphosphates and essential enzymes that are important for controlling the cellular levels of inorganic pyrophosphate (PPi). The bovine homolog of this gene has been identified by Yang and Wensel (J. Biol. Chem. 267:24641-24647 (1992)).

This gene is expressed in osteoclastoma cells and to a lesser extent in epithelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, osteoporosis and other bone weakening diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone, and epithelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:199 as residues: Lys-22 to Tyr-28, Asp-64 to Lys-77, Pro-86 to Ile-91, Gln-99 to Pro-119, Tyr-169 to Asp-174, Lys-176 to Gly-181, Trp-189 to Asn-202, Lys-233 to Gly-239, Ser-250 to Asp-257.

The tissue distribution and homology to inorganic pyrophosphatase indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of osteoporosis through the removal of bone by demineralization.

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 76

The translation product of this gene shares exact sequence homology with ATP sulfurylase/APS kinase (GenBank Accession No. 2673862) which is thought to be important in biosynthesis of the activated sulfate donor, adenosine 3'-phosphate 5'-phosphosulfate, involves the sequential action of two enzyme activities: ATP sulfurylase, which catalyzes the formation of adenosine 5'-phosphosulfate (APS) from ATP and free sulfate, and APS kinase, which subsequently phosphorylates APS to produce adenosine 3'-phosphate 5'-phosphosulfate.

This gene is expressed in osteoclastoma cells and to a lesser extent in developmental tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, antibiotic resistant bacterial infections, osteoarthritis and other autoimmune diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or skeletal structure expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., bone, and developmental tissues, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:200 as residues: Asn-15 to Trp-20, Ser-36 to Gly-41, Pro-103 to Val-110, Pro-134 to Arg-143, Leu-173 to Arg-178, Ser-190 to Ala-197, His-314 to Arg-319, Arg-354 to Asn-362, Asp-391 to Arg-397, Glu-402 to Asp-409, Asp-434 to Leu-439, Glu-441 to Arg-446, Gly-455 to Asp-462, Pro-528 to His-541, Asn-566 to Arg-571, Tyr-574 to Glu-581, Thr-589 to Glu-603.

The tissue distribution and homology to ATP sulfurylase/APS kinase indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment or detection of autoimmune diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 77

This polypeptide is identical to the SLP-76-associated protein reported by Musci and colleagues (J. Biol. Chem. 272 (18), 11674-11677 (1997)) and to the FYB protein

reported by da Silva and coworkers (Proc. Natl. Acad. Sci. U.S.A. (1997) In press).

These proteins have been reported to be novel T-cell Proteins which bind FYN and SLP-76 and regulate IL-2 production. Preferred polypeptides encoded by this gene

comprise the following amino acid sequence: RITDNPEGKWLGR TARGSYGYIK

5 TTAVEIXYDSLKLKKDSL GAPSRIEDDQEVYDDVAEQDDISSHSQSGSGGIFPP
PPDDDIYDGIEEDADDGFP APPKQLDMGDEVYDDVDTSDFPVSSAEMSQGTNV
GKAKTEEKDLKKLKKQXKEXKDFRKKFKYDGEIRVL YSTKVTTTSITSKKWGT
RDLQVKPGESLEVIQTDDTKVLCRNEEGKYGYVLR SYLADNDGEIYDDIADGC
IYDND (SEQ ID NO:322).

10 This gene is expressed in CD34 positive cells (hematopoietic progenitor cells) and to a lesser extent in adult spleen derived from a chronic lymphocytic leukemia patient.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
15 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, chronic lymphocytic leukemia; hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and
20 hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., T-cells and other blood cells, bone marrow, hematopoietic cells, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the
25 standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Further, nucleic acids and polypeptides of the present invention are useful both diagnostically and therapeutically in the intervention of immune and other disorders in which the ability to alter IL-2 expression is desired. Preferred epitopes include those comprising a sequence shown in
30 SEQ ID NO:201 as residues: Ala-17 to Lys-37, Val-39 to Ser-45, Lys-59 to His-70, Arg-90 to Leu-95, Lys-97 to Lys-107, Ser-117 to Leu-124, Phe-133 to Ser-138, Trp-146 to Leu-167, Pro-175 to Asn-185, Lys-190 to Ser-211, Pro-213 to Ser-222, His-230 to Pro-235, Pro-240 to Pro-246, Pro-253 to Gly-261, Leu-271 to Leu-303, Leu-305 to Leu-326, Lys-343 to Leu-349, Thr-363 to Leu-371, Arg-373 to Tyr-381, Tyr-391 to Leu-401, Pro-404 to Val-414, Ser-426 to Ser-432, Ile-448 to Ser-457, Gln-462
35 to Trp-468, Lys-477 to Ser-501, Asp-518 to Ser-523, Ala-541 to Gln-554.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of a variety of hematopoietic disorders. The noted expression of this gene in the hematopoietic progenitor cell compartment - as determined by its expression on CD34 positive hematopoietic stem and progenitor cells - indicates that it plays a critical role in the expansion or proliferation of hematopoietic stem/progenitor cells, as well as in the differentiation of the various blood cell lineages. Thus it could be useful in the reconstitution of the hematopoietic system of patients with leukemias and other hematopoietic diseases.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 78**

This gene is homologous to heparin cofactor II (HCII) which is a 66-kDa plasma glycoprotein that inhibits thrombin rapidly in the presence of dermatan sulfate or heparin.

This gene is expressed in apoptotic and anergic T-cells.

15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, thrombopenia T-cell lymphomas; Hodgkin's lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system - most notably the T-cell compartment, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., T-cells and other blood cells, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

25 The homology to heparin cofactor II (HCII) and the tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoietic disorders particularly in thrombopoiesis, most notably of the T-cell compartment. This could include immune modulation, inflammation, immune surveillance, graft rejection, and autoimmunity.

35 **FEATURES OF PROTEIN ENCODED BY GENE NO: 79**

The translation product of this gene shares sequence homology with a mouse

protein believed to represent an integral membrane protein.

This gene is expressed in fetal cochlea and epididymus and to a lesser extent in adult spleen and osteoclastoma.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, osteoclastoma; disorders of the inner ear; male fertility disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell
10 type(s). For a number of disorders of the above tissues or cells, particularly of the inner ear; male reproductive tract; bone; and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cochlea, epididymus and other reproductive tissue, spleen, and bone, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or
15 spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:203 as residues: Lys-13 to Gly-23, Cys-38 to Asp-43, Gly-48 to Trp-53, Cys-223 to Ile-237, Ile-240 to
20 Ser-246.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of hearing and fertility disorders. Likewise, it may have a role in the modulation of immune function and in the treatment of osteoporosis.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 80

The translation product of this gene shares sequence homology with reticulocalbin which is thought to be important in the binding of calcium, particularly within the endoplasmic reticulum.

30 This gene is expressed in endothelial cells and stromal cells and to a lesser extent in osteoblasts, osteoclasts, and T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
35 not limited to, osteoporosis; osteoclastomas; T-cell lymphomas; Hodgkin's disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in

providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vasculature, bone, and immune systems - particularly the T-cell compartments, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endothelial cells, stromal cells, bone, T-cells and other blood cells, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:204 as residues: Lys-20 to Arg-27, Pro-32 to Asp-48, Leu-64 to Arg-72, Asp-108 to Lys-114, Glu-128 to Thr-133, Asp-139 to Phe-147, Thr-196 to Ala-204, Tyr-218 to Glu-228, Val-230 to Gln-236, Arg-241 to Lys-255, Glu-276 to Lys-287.

The tissue distribution and homology to reticulocalbin indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of bone disorders such as osteoporosis; the diagnosis and treatment of T-cell lymphomas and Hodgkin's lymphoma; and the treatment of diseases and defects of the vasculature, such as vascular leak syndrome and aberrant angiogenesis that accompanies tumor growth.

FEATURES OF PROTEIN ENCODED BY GENE NO: 81

The translation product of this gene shares sequence homology with a family of peptide transport genes - particularly the AtPTR2-B gene from *Arabidopsis* - which are thought to be important in the uptake of small peptides.

This gene is expressed in a number of fetal tissues, most notably lung, brain, cochlea, and liver/spleen, and to a lesser extent in osteoclastoma and endometrial tumors.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, osteoclastoma; endometrial tumors; cancer; leukemias. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the bone and endometrium, expression of this gene at significantly higher or lower levels may be

5 routinely detected in certain tissues (e.g., fetal tissue, pulmonary tissue, bone, brain and other tissue of the nervous system, cochlea, liver, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:205 as residues: Lys-186 to Asn-199, Pro-202 to Ala-207.

10 The tissue distribution and homology to peptide transport genes indicates that polynucleotides and polypeptides corresponding to this gene are useful for the control of cell proliferation, owing to its strong expression in fetal tissues undergoing active cell division, as well as its expression in a variety of tumors or cancers of adult tissues. Potentially, it may regulate the uptake of peptides that stimulate cell proliferation. This gene product may also be useful in stimulating the uptake of a variety of peptide-based
15 drug compounds.

FEATURES OF PROTEIN ENCODED BY GENE NO: 82

This gene is expressed in fetal liver and spleen and to a lesser extent in endothelial cells.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer and tumors of a hematopoietic and/or endothelial cell origin; leukemias. Similarly, polypeptides and antibodies directed to these polypeptides are
25 useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and/or vasculature, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, endothelial cells, vascular tissue, and tissue and cells of the immune system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID
30 NO:206 as residues: Met-1 to Asp-9, Arg-66 to Gly-76, Asp-164 to Arg-171.

The tissue distribution indicates that polynucleotides and polypeptides

corresponding to this gene are useful for the treatment of disorders of the immune system. Expression of this gene product in both fetal liver/spleen and endothelial cells indicates that it may be expressed in the hemangioblast, the progenitor cell for both the immune system and the vasculature. Thus, it is most likely expressed in hematopoietic stem cells, and may be useful for the expansion of hematopoietic stem and progenitor cells in conjunction with cancer treatment for a variety of leukemias.

FEATURES OF PROTEIN ENCODED BY GENE NO: 84

The translation product of this gene shares sequence homology with NADH dehydrogenase which is thought to be important in cellular metabolism.

This gene is expressed in fetal dura mater and to a lesser extent in T-cells and hypothalamus.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases affecting cellular metabolism. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., fetal tissue, T-cells and other blood cells, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:208 as residues: Pro-27 to Gln-32, Arg-42 to Glu-51.

The tissue distribution and homology to NADH dehydrogenase indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of diseases involving cellular metabolism.

FEATURES OF PROTEIN ENCODED BY GENE NO: 85

The translation product of this gene shares sequence homology with I-TRAF, a novel TNF receptor associated factor (TRAF)-interacting protein that regulates TNF receptor-mediated signal transduction. This protein is thought to be important in
5 regulating the cellular response to tumor necrosis factor (TNF), which is an important mediator of inflammation.

This gene is expressed in endothelial cells and to a lesser extent in glioblastoma and osteoblastoma.

Therefore, polynucleotides and polypeptides of the invention are useful as
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation; glioblastoma and osteoblastoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of
15 disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endothelial cells, bone, and glial cells and tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from
20 an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:209 as residues: Glu-15 to Thr-22, Glu-46 to Leu-62, Arg-103 to Glu-119, Gln-127 to Glu-132, Asn-152 to Trp-158, Gln-191 to Gln-210, Glu-264 to Thr-271, Tyr-
25 282 to Leu-288, Trp-319 to Thr-331, Glu-335 to Ser-348, Ser-353 to Ser-358, Asp-382 to Asn-392.

The tissue distribution and homology to I-TRAF indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of
30 inflammatory diseases, including rheumatoid arthritis, sepsis, inflammatory bowel disease, and psoriasis, particularly where tumor necrosis factor is known to be involved.

FEATURES OF PROTEIN ENCODED BY GENE NO: 86

This gene has homology with a candidate gene involved in X-linked Retinopathy reported by Wong and colleagues (Genomics 15:467-471 (1993)).

This gene is expressed in a T-cell line.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation and autoimmune diseases; T-cell lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
10 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., T-cells and other blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
15 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of inflammatory
20 disorders such as sepsis, inflammatory bowel disease, psoriasis, and rheumatoid arthritis as well as autoimmune disease such as lupus. It could also be useful in immune modulation and in the process of immune surveillance. The present invention can be used diagnostically and therapeutically to treat X-linked Retinopathy.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 87

This gene is expressed in human brain tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
30 not limited to, brain disorders; neurodegenerative disorders; tumors of a brain origin. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels
35 may be routinely detected in certain tissues (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,

urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID

5 NO:211 as residues: Cys-32 to Tyr-38.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of CNS disorders such as epilepsy, paranoia, depression, Alzheimer's disease, and schizophrenia. It could be useful in the survival and/or proliferation of neurons and could effect neuronal

10 regeneration.

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
1	HAGEW82	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	11	1679	247	1607	353	353	125	1			30
2	HAGFY16	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	12	1830	87	1786	128	128	126	1	26	27	44
2	HBMCF37	xxxxx 03/19/98	pBluescript	98	1487	79	1487	170	170	212	1	44	45	69
2	HFLQB16	209641 02/25/98	Uni-ZAP XR	99	1653	394	1637	413	413	213	1	25	26	81
3	HALAA60	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	13	1212	1	1212	99	99	127	1	24	25	38
4	HAPBL78	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	14	2061	882	2061	900	900	128	1	22	23	22
5	HASAV70	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	15	1412	10	733	103	103	129	1	20	21	109

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
6	HBNAF22	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	16	1052	276	880	538	130	1	17	18	62
7	HBNBL77	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	17	683	1	683	181	131	1			29
8	HCDDR90	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	18	1054	86	1007	86	132	1	23	24	52
9	HCEEF50	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	19	1393	132	1393	192	133	1	17	18	56
10	HCEMU42	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	20	1215	277	1070	401	134	1	18	19	215
11	HCENE16	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	21	2042	614	2011	793	135	1	26	27	48

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
12	HMSJ74	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	22	1872	21	1872	69	69	136	1	23	24	67
13	HCUBF15	97923 03/07/97 209071 05/22/97	ZAP Express	23	289	1	289	89	89	137	1	29	30	51
14	HE2DE47	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	24	3533	2821	3532	808	808	138	1	30	31	539
14	HE2DE47	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	100	1145	435	1115	515	515	214	1	22	23	80
15	HKMLH01	209179 07/24/97	pBluescript	25	1148	171	907	196	196	139	1	26	27	56
15	HE6DGG34	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	101	734	25	734	295	295	215	1	36	37	48
16	HE9DGG49	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	26	717	1	717	70	70	140	1	27	28	200

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
16	HE9DG49	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	102	713	17	713	78	78	216	1	28	29	202
17	HELBA06	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	27	1099	1	1099	38	38	141	1	22	23	215
17	HELBA06	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	103	1080	1	1080	149	149	217	1	25	26	185
18	HSLFM29	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	28	941	171	941	128	128	142	1	42	43	101
19	HELBW38	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	29	756	62	756	294	294	143	1	30	31	111
20	HETHN28	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	30	2100	408	2093	496	496	144	1			19

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
21	HFC DK17	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	31	1448	475	1392	567	567	145	1			29
22	HFEAF41	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	32	456	1	409	21	21	146	1	28	29	98
23	HFKFL13	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	33	1326	1	1322	210	210	147	1			7
24	HFSBG13	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	34	710	1	710	242	242	148	1	16	17	38
25	HFTBE43	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	35	1188	110	1161	178	178	149	1	26	27	130
26	HFTDJ36	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	36	956	1	938	144	144	150	1	21	22	31
27	HKTAC77	97924 03/07/97	Uni-ZAP XR	37	1603	974	1581	1104	1104	151	1			13

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
28	HLHSH36	97924 03/07/97	pBluescript	38	1089	55	1067		209	152	1			7
29	HLHSV96	97924 03/07/97	pBluescript	39	629	1	629	119	119	153	1	32	33	67
30	HLQBQ86	97924 03/07/97	Lambda ZAP II	40	1964	408	1793	581	581	154	1			25
31	HLTBX31	97924 03/07/97	Uni-ZAP XR	41	1522	13	1123	126	126	155	1	32	33	194
32	HLTCI63	97924 03/07/97	Uni-ZAP XR	42	875	1	875	43	43	156	1	18	19	90
33	HMKAH44	97924 03/07/97	pSport1	43	843	1	843	171	171	157	1	30	31	30
34	HMQAJ64	97924 03/07/97	Uni-ZAP XR	44	489	3	489	55	55	158	1	19	20	89
34	HMQAJ64	97924 03/07/97	Uni-ZAP XR	104	489	6	489	58	58	218	1	22	23	89
35	HOABG65	97924 03/07/97	Uni-ZAP XR	45	534	1	534	17	17	159	1	18	19	88
36	HODCL36	97924 03/07/97	Uni-ZAP XR	46	1374	1	1374	15	15	160	1	20	21	173
36	HODCL36	97924 03/07/97	Uni-ZAP XR	105	640	58	640	72	72	219	1	20	21	137
36	HODCL36	97924 03/07/97	Uni-ZAP XR	106	1529	40	1399	54	54	220	1	27	28	47
37	HODCL50	97924 03/07/97	Uni-ZAP XR	47	596	1	596	269	269	161	1	27	28	44

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
38	HODCV74	97924 03/07/97	Uni-ZAP XR	48	851	99	822	170	170	162	1			22
39	HODCZ16	97924 03/07/97	Uni-ZAP XR	49	2020	569	2020	638	638	163	1	17	18	69
40	HTOEU03	97924 03/07/97	Uni-ZAP XR	50	2432	848	2432	99	99	164	1	19	20	322
40	HTOEU03	97924 03/07/97	Uni-ZAP XR	107	2435	849	2435	928	928	221	1	31	32	69
41	HPBCJ74	97924 03/07/97	pBluescript SK-	51	2340	1627	2340	150	150	165	1	60	61	319
41	HPBCJ74	97924 03/07/97	pBluescript SK-	108	805	92	791	239	239	222	1	21	22	82
42	HPMBU33	97924 03/07/97	Uni-ZAP XR	52	601	188	601	432	432	166	1			30
43	HSAUL66	97924 03/07/97	Uni-ZAP XR	53	359	1	337	142	142	167	1	18	19	71
44	HSIDQ18	97924 03/07/97	Uni-ZAP XR	54	1141	1	1141	25	25	168	1	30	31	280
44	HSIDQ18	97924 03/07/97	Uni-ZAP XR	109	1166	21	1166	433	433	223	1	30	31	42
45	HSJBB37	97924 03/07/97	Uni-ZAP XR	55	1560	63	1148	217	217	169	1			22
46	HSJBQ79	97924 03/07/97	Uni-ZAP XR	56	1507	164	608	57	57	170	1	19	20	326
46	HSJBQ79	97924 03/07/97	Uni-ZAP XR	110	586	4	586	35	35	224	1	23	24	183

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
47	HTEGA76	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	57	450	1	450	83	83	171	1	35	36	68
48	HTEJN13	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	58	1147	1	1147	163	163	172	1	15	16	158
48	HTEJN13	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	111	1134	1	1134	155	155	225	1	19	20	70
49	HTHBL86	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	59	777	1	777	115	115	173	1	18	19	122
50	HTSFO71	97958 03/13/97 209072 05/22/97	pBluescript	60	1191	48	598	52	52	174	1	30	31	128
50	HTSFO71	97958 03/13/97 209072 05/22/97	pBluescript	112	1333	594	1333	829	829	226	1			9
51	HAPNO80	209235 09/04/97	Uni-ZAP XR	61	1580	443	1554	114	114	175	1	1	2	371

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
51	HAUCC47	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	113	1015	249	708	244	244	227	1	28	29	137
52	HBMCL41	97958 03/13/97 209072 05/22/97	pBluescript	62	1117	105	1034	182	182	176	1	28	29	215
53	HCFLD84	97958 03/13/97 209072 05/22/97	pSport1	63	361	1	361	97	97	177	1	32	33	54
54	HE8EM69	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	64	1668	1	1638	150	150	178	1	20	21	22
55	HE8EZ48	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	65	1353	35	1303	231	231	179	1	33	34	102
56	HEBGF73	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	66	1011	655	1011	703	703	180	1	38	39	47

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
57	HFEBF41	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	67	1193	267	1090	459	459	181	1	35	36	95
58	HFRBU14	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	68	560	1	560	63	63	182	1	29	30	94
59	HFVGZ79	97958 03/13/97 209072 05/22/97	pBluescript	69	1657	765	1581	839	839	183	1	21	22	26
60	HHGCM76	97958 03/13/97 209072 05/22/97	Lambda ZAP II	70	711	8	711	270	270	184	1			10
61	HHGCO88	97958 03/13/97 209072 05/22/97	Lambda ZAP II	71	935	111	935	272	272	185	1	19	20	64
62	HHGCP52	97958 03/13/97 209072 05/22/97	Lambda ZAP II	72	504	113	484	127	127	186	1	21	22	21

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
63	HHGDB72	97958 03/13/97 209072 05/22/97	Lambda ZAP II	73	620	1	620	96	96	187	1	18	19	131
64	HHGDI71	97958 03/13/97 209072 05/22/97	Lambda ZAP II	74	581	156	581	248	248	188	1	32	33	68
65	HHSDI45	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	75	1843	537	1786	630	630	189	1	27	28	44
66	HHSEB66	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	76	1441	116	800	167	167	190	1	36	37	64
67	HJPAZ83	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	114	1076	398	1076		575	228	1	11	12	22
68	HLDBO49	97958 03/13/97 209072 05/22/97	pCMVSPORT 3.0	78	2776	18	1888	187	187	192	1	14	15	169

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
69	HLDBQ19	97958 03/13/97 209072 05/22/97	pCMVSPORT 3.0	79	1525	401	1480	534	534	193	1	22	23	65
69	HLDBQ19	209226 08/28/97	pCMVSPORT 3.0	115	1487	401	1487	534	534	229	1	22	23	131
70	HMSGT42	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	80	1563	33	1077	40	40	194	1	32	33	91
71	HMWIC78	97957 03/13/97 209073 05/22/97	Uni-Zap XR	81	1020	18	780	238	238	195	1	23	24	175
72	HTTCT79	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	82	770	101	770	286	286	196	1	26	27	69
73	HNGJU84	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	83	481	1	481	58	58	197	1	20	21	24
74	HNTAC73	97957 03/13/97 209073 05/22/97	pCMVSPORT 3.0	84	644	1	623	14	14	198	1	25	26	72

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
75	HOSEI45	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	85	1351	435	1284	98	98	199	1	12	13	288
75	HOSEI45	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	116	1350	428	1283		545	230	1			27
76	HOSFD58	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	86	2527	290	1747	56	56	200	1	30	31	623
76	HOSFD58	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	117	2527	288	1747	477	477	231	1	32	33	60
77	HSAUM95	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	87	2566	1843	2566	251	251	201	1	30	31	648
77	HSAUM95	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	118	1098	375	1098	677	677	232	1	21	22	28

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
78	HSAUR67	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	88	540	1	540	83	83	202	1	32	33	54
79	HSKDI81	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	89	1863	152	1165	188	188	203	1	11	12	265
79	HSKDI81	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	119	1679	152	1166	315	315	233	1			17
80	HSKDW91	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	90	2478	1149	2449	92	92	204	1	19	20	314
81	HTLEX50	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	91	2058	476	2058	414	414	205	1	20	21	206
82	HSKHL65	97957 03/13/97 209073 05/22/97	pBluescript	92	1411	345	1411	157	157	206	1	69	70	194

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
82	HSKHL65	97957 03/13/97 209073 05/22/97	pBluescript	121	1411	345	1411	526	526	235	1	37	38	71
83	HHFGA11	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	93	2187	147	2184	397	397	207	1	30	31	329
83	HHFGA11	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	122	2256	138	2063	228	228	236	1	19	20	95
84	HWTBL40	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	94	757	524	608	445	445	208	1	20	21	57
85	HBXFG80	97957 03/13/97 209073 05/22/97	ZAP Express	95	2394	481	2394	523	523	209	1	1	2	391
86	HCACY32	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	96	672	1	672	117	117	210	1	21	22	25

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
87	HCEDO21	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	97	1419	1	1419	207	207	211	1	20	21	37

Table 1 summarizes the information corresponding to each "Gene No." described above. The nucleotide sequence identified as "NT SEQ ID NO:X" was assembled from partially homologous ("overlapping") sequences obtained from the "cDNA clone ID" identified in Table 1 and, in some cases, from additional related DNA clones. The overlapping sequences were assembled into a single contiguous sequence of high redundancy (usually three to five overlapping sequences at each nucleotide position), resulting in a final sequence identified as SEQ ID NO:X.

The cDNA Clone ID was deposited on the date and given the corresponding deposit number listed in "ATCC Deposit No:Z and Date." Some of the deposits contain multiple different clones corresponding to the same gene. "Vector" refers to the type of vector contained in the cDNA Clone ID.

"Total NT Seq." refers to the total number of nucleotides in the contig identified by "Gene No." The deposited clone may contain all or most of these sequences, reflected by the nucleotide position indicated as "5' NT of Clone Seq." and the "3' NT of Clone Seq." of SEQ ID NO:X. The nucleotide position of SEQ ID NO:X of the putative start codon (methionine) is identified as "5' NT of Start Codon." Similarly, the nucleotide position of SEQ ID NO:X of the predicted signal sequence is identified as "5' NT of First AA of Signal Pep."

The translated amino acid sequence, beginning with the methionine, is identified as "AA SEQ ID NO:Y," although other reading frames can also be easily translated using known molecular biology techniques. The polypeptides produced by these alternative open reading frames are specifically contemplated by the present invention.

The first and last amino acid position of SEQ ID NO:Y of the predicted signal peptide is identified as "First AA of Sig Pep" and "Last AA of Sig Pep." The predicted first amino acid position of SEQ ID NO:Y of the secreted portion is identified as "Predicted First AA of Secreted Portion." Finally, the amino acid position of SEQ ID NO:Y of the last amino acid in the open reading frame is identified as "Last AA of ORF."

SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, SEQ ID NO:X is useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in the deposited clone. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to the secreted proteins encoded by the cDNA clones identified in Table 1.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X and the predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing a human cDNA of the invention deposited with the ATCC, as set forth in Table 1. The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, or the deposited clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are species homologs. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for the desired homologue.

The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below).

It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

- 5 The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified by the one-step method described in Smith and Johnson, *Gene* 67:31-40 (1988). Polypeptides of the invention also can be purified from natural or recombinant sources
- 10 using antibodies of the invention raised against the secreted protein in methods which are well known in the art.

Signal Sequences

- 15 Methods for predicting whether a protein has a signal sequence, as well as the cleavage point for that sequence, are available. For instance, the method of McGeoch, *Virus Res.* 3:271-286 (1985), uses the information from a short N-terminal charged region and a subsequent uncharged region of the complete (uncleaved) protein. The method of von Heinje, *Nucleic Acids Res.* 14:4683-4690 (1986) uses the information from the residues surrounding the cleavage site, typically residues -13 to +2, where +1
- 20 indicates the amino terminus of the secreted protein. The accuracy of predicting the cleavage points of known mammalian secretory proteins for each of these methods is in the range of 75-80%. (von Heinje, *supra*.) However, the two methods do not always produce the same predicted cleavage point(s) for a given protein.

- 25 In the present case, the deduced amino acid sequence of the secreted polypeptide was analyzed by a computer program called SignalP (Henrik Nielsen et al., *Protein Engineering* 10:1-6 (1997)), which predicts the cellular location of a protein based on the amino acid sequence. As part of this computational prediction of localization, the methods of McGeoch and von Heinje are incorporated. The analysis of the amino acid sequences of the secreted proteins described herein by this program provided the results
- 30 shown in Table 1.

- As one of ordinary skill would appreciate, however, cleavage sites sometimes vary from organism to organism and cannot be predicted with absolute certainty. Accordingly, the present invention provides secreted polypeptides having a sequence shown in SEQ ID NO:Y which have an N-terminus beginning within 5 residues (i.e., +
- 35 or - 5 residues) of the predicted cleavage point. Similarly, it is also recognized that in some cases, cleavage of the signal sequence from a secreted protein is not entirely

uniform, resulting in more than one secreted species. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

Moreover, the signal sequence identified by the above analysis may not necessarily predict the naturally occurring signal sequence. For example, the naturally occurring signal sequence may be further upstream from the predicted signal sequence. However, it is likely that the predicted signal sequence will be capable of directing the secreted protein to the ER. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

10 **Polynucleotide and Polypeptide Variants**

"Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

15 By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. The query sequence may be an entire sequence shown in Table 1, the ORF (open reading frame), or any fragment specified as described herein.

25 As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. (1990) 6:237-245). In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are:

35 Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization

Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 bases at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query

amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions,

- 5 interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequences shown in Table 1 or to the amino acid sequence encoded by deposited DNA clone can be
10 determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. (1990) 6:237-245). In a sequence alignment the query and
15 subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window
20 Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity.
25 For subject sequences truncated at the N- and C-termini, relative to the the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of
30 the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are
35 considered for the purposes of manually adjusting the percent identity score. That is, only query residue positions outside the farthest N- and C-terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired
5 residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence.
10 This time the deletions are internal deletions so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query
15 sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or
20 activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in
25 the human mRNA to those preferred by a bacterial host such as *E. coli*).

Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level.
30 Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, one or more amino acids can be
35 deleted from the N-terminus or C-terminus of the secreted protein without substantial loss of biological function. The authors of Ron et al., *J. Biol. Chem.* 268: 2984-2988 (1993), reported variant KGF proteins having heparin binding activity even after

deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

Moreover, ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See, Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

Furthermore, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

Thus, the invention further includes polypeptide variants which show substantial biological activity. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as to have little effect on activity. For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie, J. U. et al., Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham and Wells, Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly.

Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues, where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino acids, such as an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

Polynucleotide and Polypeptide Fragments

In the present invention, a "polynucleotide fragment" refers to a short polynucleotide having a nucleic acid sequence contained in the deposited clone or shown in SEQ ID NO:X. The short nucleotide fragments are preferably at least about
5 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length. A fragment "at least 20 nt in length," for example, is intended to include 20 or more contiguous bases from the cDNA sequence contained in the deposited clone or the nucleotide sequence shown in SEQ ID NO:X. These nucleotide fragments are useful as diagnostic probes and primers
10 as discussed herein. Of course, larger fragments (e.g., 50, 150, 500, 600, 2000 nucleotides) are preferred.

Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments having a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-
15 450, 451-500, 501-550, 551-600, 651-700, or 701 to the end of SEQ ID NO:X or the cDNA contained in the deposited clone. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has biological activity.

In the present invention, a "polypeptide fragment" refers to a short amino acid sequence contained in SEQ ID NO:Y or encoded by the cDNA contained in the deposited clone. Protein fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the
25 invention, include, for example, fragments from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, or 161 to the end of the coding region. Moreover, polypeptide fragments can be about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1)
30 amino acids, at either extreme or at both extremes.

Preferred polypeptide fragments include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or the mature form having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-
35 60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any

combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotide fragments encoding these polypeptide fragments are also preferred.

Also preferred are polypeptide and polynucleotide fragments characterized by structural or functional domains, such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions.

Polypeptide fragments of SEQ ID NO:Y falling within conserved domains are specifically contemplated by the present invention. Moreover, polynucleotide fragments encoding these domains are also contemplated.

Other preferred fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

Epitopes & Antibodies

In the present invention, "epitopes" refer to polypeptide fragments having antigenic or immunogenic activity in an animal, especially in a human. A preferred embodiment of the present invention relates to a polypeptide fragment comprising an epitope, as well as the polynucleotide encoding this fragment. A region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." In contrast, an "immunogenic epitope" is defined as a part of a protein that elicits an antibody response. (See, for instance, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998-4002 (1983).)

Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

In the present invention, antigenic epitopes preferably contain a sequence of at least seven, more preferably at least nine, and most preferably between about 15 to about 30 amino acids. Antigenic epitopes are useful to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. (See, for instance, Wilson et al., Cell 37:767-778 (1984); Sutcliffe, J. G. et al., Science 219:660-666 (1983).)

Similarly, immunogenic epitopes can be used to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., supra; Wilson et al., supra; Chow, M. et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle, F. J. et

al., J. Gen. Virol. 66:2347-2354 (1985).) A preferred immunogenic epitope includes the secreted protein. The immunogenic epitopes may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier. However,
5 immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting.)

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules as well as antibody fragments (such as, for example,
10 Fab and F(ab')₂ fragments) which are capable of specifically binding to protein. Fab and F(ab')₂ fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding than an intact antibody. (Wahl et al., J. Nucl. Med. 24:316-325 (1983).) Thus, these fragments are preferred, as well as the products of a FAB or other immunoglobulin expression library.
15 Moreover, antibodies of the present invention include chimeric, single chain, and humanized antibodies.

Fusion Proteins

Any polypeptide of the present invention can be used to generate fusion
20 proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular locations based on trafficking signals, the polypeptides of the present invention can be
25 used as targeting molecules once fused to other proteins.

Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties may be added to the
35 polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

Moreover, polypeptides of the present invention, including fragments, and specifically epitopes, can be combined with parts of the constant domain of immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life in vivo. One reported example
5 describes chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EP A 394,827; Traunecker et al., Nature 331:84-86 (1988).) Fusion proteins having disulfide-linked dimeric structures (due to the IgG) can also be more efficient in binding and neutralizing other molecules, than the
10 monomeric secreted protein or protein fragment alone. (Fountoulakis et al., J. Biochem. 270:3958-3964 (1995).)

Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a
15 fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP-A 0232 262.) Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified, would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for
20 example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, D. Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol. Chem. 270:9459-9471 (1995).)

Moreover, the polypeptides of the present invention can be fused to marker
25 sequences, such as a peptide which facilitates purification of the fused polypeptide. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for
30 instance, hexa-histidine provides for convenient purification of the fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein. (Wilson et al., Cell 37:767 (1984).)

Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the present invention.

Vectors, Host Cells, and Protein Production

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as E. coli, Streptomyces and Salmonella typhimurium cells; fungal cells, such as yeast cells; insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS, 293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., Basic Methods
5 In Molecular Biology (1986). It is specifically contemplated that the polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography,
10 phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention, and preferably the secreted form, can also
15 be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production
20 procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein
25 after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

30 **Uses of the Polynucleotides**

Each of the polynucleotides identified herein can be used in numerous ways as reagents. The following description should be considered exemplary and utilizes known techniques.

The polynucleotides of the present invention are useful for chromosome
35 identification. There exists an ongoing need to identify new chromosome markers, since few chromosome marking reagents, based on actual sequence data (repeat

polymorphisms), are presently available. Each polynucleotide of the present invention can be used as a chromosome marker.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp) from the sequences shown in SEQ ID NO:X. Primers can be
5 selected using computer analysis so that primers do not span more than one predicted exon in the genomic DNA. These primers are then used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the SEQ ID NO:X will yield an amplified fragment.

Similarly, somatic hybrids provide a rapid method of PCR mapping the
10 polynucleotides to particular chromosomes. Three or more clones can be assigned per day using a single thermal cycler. Moreover, sublocalization of the polynucleotides can be achieved with panels of specific chromosome fragments. Other gene mapping strategies that can be used include in situ hybridization, prescreening with labeled flow-sorted chromosomes, and preselection by hybridization to construct chromosome
15 specific-cDNA libraries.

Precise chromosomal location of the polynucleotides can also be achieved using fluorescence in situ hybridization (FISH) of a metaphase chromosomal spread. This technique uses polynucleotides as short as 500 or 600 bases; however, polynucleotides 2,000-4,000 bp are preferred. For a review of this technique, see Verma et al.,
20 "Human Chromosomes: a Manual of Basic Techniques," Pergamon Press, New York (1988).

For chromosome mapping, the polynucleotides can be used individually (to mark a single chromosome or a single site on that chromosome) or in panels (for marking multiple sites and/or multiple chromosomes). Preferred polynucleotides
25 correspond to the noncoding regions of the cDNAs because the coding sequences are more likely conserved within gene families, thus increasing the chance of cross hybridization during chromosomal mapping.

Once a polynucleotide has been mapped to a precise chromosomal location, the physical position of the polynucleotide can be used in linkage analysis. Linkage
30 analysis establishes coinheritance between a chromosomal location and presentation of a particular disease. (Disease mapping data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library) .) Assuming 1 megabase mapping resolution and one gene per 20 kb, a cDNA precisely localized to a chromosomal region associated with the disease
35 could be one of 50-500 potential causative genes.

Thus, once coinheritance is established, differences in the polynucleotide and the corresponding gene between affected and unaffected individuals can be examined.

First, visible structural alterations in the chromosomes, such as deletions or translocations, are examined in chromosome spreads or by PCR. If no structural alterations exist, the presence of point mutations are ascertained. Mutations observed in some or all affected individuals, but not in normal individuals, indicates that the
5 mutation may cause the disease. However, complete sequencing of the polypeptide and the corresponding gene from several normal individuals is required to distinguish the mutation from a polymorphism. If a new polymorphism is identified, this polymorphic polypeptide can be used for further linkage analysis.

Furthermore, increased or decreased expression of the gene in affected
10 individuals as compared to unaffected individuals can be assessed using polynucleotides of the present invention. Any of these alterations (altered expression, chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

In addition to the foregoing, a polynucleotide can be used to control gene
15 expression through triple helix formation or antisense DNA or RNA. Both methods rely on binding of the polynucleotide to DNA or RNA. For these techniques, preferred polynucleotides are usually 20 to 40 bases in length and complementary to either the region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science
20 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxy-nucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988).) Triple helix formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques are effective in model
25 systems, and the information disclosed herein can be used to design antisense or triple helix polynucleotides in an effort to treat disease.

Polynucleotides of the present invention are also useful in gene therapy. One goal of gene therapy is to insert a normal gene into an organism having a defective gene, in an effort to correct the genetic defect. The polynucleotides disclosed in the
30 present invention offer a means of targeting such genetic defects in a highly accurate manner. Another goal is to insert a new gene that was not present in the host genome, thereby producing a new trait in the host cell.

The polynucleotides are also useful for identifying individuals from minute biological samples. The United States military, for example, is considering the use of
35 restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identifying

personnel. This method does not suffer from the current limitations of "Dog Tags" which can be lost, switched, or stolen, making positive identification difficult. The polynucleotides of the present invention can be used as additional DNA markers for RFLP.

5 The polynucleotides of the present invention can also be used as an alternative to RFLP, by determining the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, individuals can be identified because each individual will have a unique set
10 of DNA sequences. Once an unique ID database is established for an individual, positive identification of that individual, living or dead, can be made from extremely small tissue samples.

 Forensic biology also benefits from using DNA-based identification techniques as disclosed herein. DNA sequences taken from very small biological samples such as
15 tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, etc., can be amplified using PCR. In one prior art technique, gene sequences amplified from polymorphic loci, such as DQa class II HLA gene, are used in forensic biology to identify individuals. (Erich, H., PCR Technology, Freeman and Co. (1992).) Once these specific polymorphic loci are amplified, they are digested with one or more
20 restriction enzymes, yielding an identifying set of bands on a Southern blot probed with DNA corresponding to the DQa class II HLA gene. Similarly, polynucleotides of the present invention can be used as polymorphic markers for forensic purposes.

 There is also a need for reagents capable of identifying the source of a particular tissue. Such need arises, for example, in forensics when presented with tissue of
25 unknown origin. Appropriate reagents can comprise, for example, DNA probes or primers specific to particular tissue prepared from the sequences of the present invention. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

30 In the very least, the polynucleotides of the present invention can be used as molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, as a probe to "subtract-out" known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers for attachment to a "gene chip" or other support, to raise anti-DNA antibodies using
35 DNA immunization techniques, and as an antigen to elicit an immune response.

Uses of the Polypeptides

Each of the polypeptides identified herein can be used in numerous ways. The following description should be considered exemplary and utilizes known techniques.

5 A polypeptide of the present invention can be used to assay protein levels in a biological sample using antibody-based techniques. For example, protein expression in tissues can be studied with classical immunohistological methods. (Jalkanen, M., et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, M., et al., J. Cell . Biol. 105:3087-3096 (1987).) Other antibody-based methods useful for detecting protein gene
10 expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase, and radioisotopes, such as iodine (125I, 121I), carbon (14C), sulfur (35S), tritium (3H), indium (112In), and technetium (99mTc), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

15 In addition to assaying secreted protein levels in a biological sample, proteins can also be detected in vivo by imaging. Antibody labels or markers for in vivo imaging of protein include those detectable by X-radiography, NMR or ESR. For X-radiography, suitable labels include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for
20 NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma.

A protein-specific antibody or antibody fragment which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example, 131I,
25 112In, 99mTc), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously, or intraperitoneally) into the mammal. It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human
30 subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of 99mTc. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments." (Chapter 13 in Tumor Imaging: The
35 Radiochemical Detection of Cancer, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982).)

Thus, the invention provides a diagnostic method of a disorder, which involves (a) assaying the expression of a polypeptide of the present invention in cells or body fluid of an individual; (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a disorder.

Moreover, polypeptides of the present invention can be used to treat disease. For example, patients can be administered a polypeptide of the present invention in an effort to replace absent or decreased levels of the polypeptide (e.g., insulin), to supplement absent or decreased levels of a different polypeptide (e.g., hemoglobin S for hemoglobin B), to inhibit the activity of a polypeptide (e.g., an oncogene), to activate the activity of a polypeptide (e.g., by binding to a receptor), to reduce the activity of a membrane bound receptor by competing with it for free ligand (e.g., soluble TNF receptors used in reducing inflammation), or to bring about a desired response (e.g., blood vessel growth).

Similarly, antibodies directed to a polypeptide of the present invention can also be used to treat disease. For example, administration of an antibody directed to a polypeptide of the present invention can bind and reduce overproduction of the polypeptide. Similarly, administration of an antibody can activate the polypeptide, such as by binding to a polypeptide bound to a membrane (receptor).

At the very least, the polypeptides of the present invention can be used as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art. Polypeptides can also be used to raise antibodies, which in turn are used to measure protein expression from a recombinant cell, as a way of assessing transformation of the host cell. Moreover, the polypeptides of the present invention can be used to test the following biological activities.

Biological Activities

The polynucleotides and polypeptides of the present invention can be used in assays to test for one or more biological activities. If these polynucleotides and polypeptides do exhibit activity in a particular assay, it is likely that these molecules may be involved in the diseases associated with the biological activity. Thus, the polynucleotides and polypeptides could be used to treat the associated disease.

Immune Activity

A polypeptide or polynucleotide of the present invention may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the

proliferation, differentiation, or mobilization (chemotaxis) of immune cells. Immune cells develop through a process called hematopoiesis, producing myeloid (platelets, red blood cells, neutrophils, and macrophages) and lymphoid (B and T lymphocytes) cells from pluripotent stem cells. The etiology of these immune deficiencies or disorders
5 may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or infectious. Moreover, a polynucleotide or polypeptide of the present invention can be used as a marker or detector of a particular immune system disease or disorder.

A polynucleotide or polypeptide of the present invention may be useful in
10 treating or detecting deficiencies or disorders of hematopoietic cells. A polypeptide or polynucleotide of the present invention could be used to increase differentiation and proliferation of hematopoietic cells, including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain (or many) types hematopoietic cells. Examples of immunologic deficiency syndromes include, but are not limited to:
15 blood protein disorders (e.g. agammaglobulinemia, dysgammaglobulinemia), ataxia telangiectasia, common variable immunodeficiency, Digeorge Syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency (SCIDs), Wiskott-Aldrich Disorder, anemia, thrombocytopenia, or hemoglobinuria.

Moreover, a polypeptide or polynucleotide of the present invention could also
20 be used to modulate hemostatic (the stopping of bleeding) or thrombolytic activity (clot formation). For example, by increasing hemostatic or thrombolytic activity, a polynucleotide or polypeptide of the present invention could be used to treat blood coagulation disorders (e.g., afibrinogenemia, factor deficiencies), blood platelet
25 disorders (e.g. thrombocytopenia), or wounds resulting from trauma, surgery, or other causes. Alternatively, a polynucleotide or polypeptide of the present invention that can decrease hemostatic or thrombolytic activity could be used to inhibit or dissolve clotting. These molecules could be important in the treatment of heart attacks (infarction), strokes, or scarring.

A polynucleotide or polypeptide of the present invention may also be useful in
30 treating or detecting autoimmune disorders. Many autoimmune disorders result from inappropriate recognition of self as foreign material by immune cells. This inappropriate recognition results in an immune response leading to the destruction of the host tissue. Therefore, the administration of a polypeptide or polynucleotide of the
35 present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing autoimmune disorders.

Examples of autoimmune disorders that can be treated or detected by the present invention include, but are not limited to: Addison's Disease, hemolytic anemia,

antiphospholipid syndrome, rheumatoid arthritis, dermatitis, allergic encephalomyelitis, glomerulonephritis, Goodpasture's Syndrome, Graves' Disease, Multiple Sclerosis.

5 Myasthenia Gravis, Neuritis, Ophthalmia, Bullous Pemphigoid, Pemphigus, Polyendocrinopathies, Purpura, Reiter's Disease, Stiff-Man Syndrome, Autoimmune Thyroiditis, Systemic Lupus Erythematosus, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitis, and autoimmune inflammatory eye disease.

10 Similarly, allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated by a polypeptide or polynucleotide of the present invention. Moreover, these molecules can be used to treat anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility.

A polynucleotide or polypeptide of the present invention may also be used to
15 treat and/or prevent organ rejection or graft-versus-host disease (GVHD). Organ rejection occurs by host immune cell destruction of the transplanted tissue through an immune response. Similarly, an immune response is also involved in GVHD, but, in this case, the foreign transplanted immune cells destroy the host tissues. The administration of a polypeptide or polynucleotide of the present invention that inhibits
20 an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing organ rejection or GVHD.

Similarly, a polypeptide or polynucleotide of the present invention may also be used to modulate inflammation. For example, the polypeptide or polynucleotide may inhibit the proliferation and differentiation of cells involved in an inflammatory
25 response. These molecules can be used to treat inflammatory conditions, both chronic and acute conditions, including inflammation associated with infection (e.g., septic shock, sepsis, or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel
30 disease, Crohn's disease, or resulting from over production of cytokines (e.g., TNF or IL-1.)

Hyperproliferative Disorders

A polypeptide or polynucleotide can be used to treat or detect hyperproliferative
35 disorders, including neoplasms. A polypeptide or polynucleotide of the present invention may inhibit the proliferation of the disorder through direct or indirect

interactions. Alternatively, a polypeptide or polynucleotide of the present invention may proliferate other cells which can inhibit the hyperproliferative disorder.

For example, by increasing an immune response, particularly increasing antigenic qualities of the hyperproliferative disorder or by proliferating, differentiating, or mobilizing T-cells, hyperproliferative disorders can be treated. This immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, decreasing an immune response may also be a method of treating hyperproliferative disorders, such as a chemotherapeutic agent.

Examples of hyperproliferative disorders that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but are not limited to neoplasms located in the: abdomen, bone, breast, digestive system, liver, pancreas, peritoneum, endocrine glands (adrenal, parathyroid, pituitary, testicles, ovary, thymus, thyroid), eye, head and neck, nervous (central and peripheral), lymphatic system, pelvic, skin, soft tissue, spleen, thoracic, and urogenital.

Similarly, other hyperproliferative disorders can also be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of such hyperproliferative disorders include, but are not limited to: hypergammaglobulinemia, lymphoproliferative disorders, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease, besides neoplasia, located in an organ system listed above.

Infectious Disease

A polypeptide or polynucleotide of the present invention can be used to treat or detect infectious agents. For example, by increasing the immune response, particularly increasing the proliferation and differentiation of B and/or T cells, infectious diseases may be treated. The immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, the polypeptide or polynucleotide of the present invention may also directly inhibit the infectious agent, without necessarily eliciting an immune response.

Viruses are one example of an infectious agent that can cause disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of viruses, include, but are not limited to the following DNA and RNA viral families: Arbovirus, Adenoviridae, Arenaviridae, Arterivirus, Birnaviridae, Bunyaviridae, Caliciviridae, Circoviridae, Coronaviridae, Flaviviridae, Hepadnaviridae (Hepatitis), Herpesviridae (such as, Cytomegalovirus, Herpes

Simplex, Herpes Zoster), Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae), Orthomyxoviridae (e.g., Influenza), Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g., Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g., Rubivirus). Viruses falling within these families can cause a variety of diseases or symptoms, including, but not limited to: arthritis, bronchiollitis, encephalitis, eye infections (e.g., conjunctivitis, keratitis), chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), meningitis, opportunistic infections (e.g., AIDS), pneumonia, Burkitt's Lymphoma, chickenpox, hemorrhagic fever, Measles, Mumps, Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's, warts), and viremia. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Similarly, bacterial or fungal agents that can cause disease or symptoms and that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following Gram-Negative and Gram-positive bacterial families and fungi: Actinomycetales (e.g., Corynebacterium, Mycobacterium, Norcardia), Aspergillosis, Bacillaceae (e.g., Anthrax, Clostridium), Bacteroidaceae, Blastomycosis, Bordetella, Borrelia, Brucellosis, Candidiasis, Campylobacter, Coccidioidomycosis, Cryptococcosis, Dermatocycoses, Enterobacteriaceae (Klebsiella, Salmonella, Serratia, Yersinia), Erysipelothrix, Helicobacter, Legionellosis, Leptospirosis, Listeria, Mycoplasmatales, Neisseriaceae (e.g., Acinetobacter, Gonorrhea, Meningococcal), Pasteurellaceae Infections (e.g., Actinobacillus, Haemophilus, Pasteurella), Pseudomonas, Rickettsiaceae, Chlamydiaceae, Syphilis, and Staphylococcal. These bacterial or fungal families can cause the following diseases or symptoms, including, but not limited to: bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis), gingivitis, opportunistic infections (e.g., AIDS related infections), paronychia, prosthesis-related infections, Reiter's Disease, respiratory tract infections, such as Whooping Cough or Empyema, sepsis, Lyme Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning, Typhoid, pneumonia, Gonorrhea, meningitis, Chlamydia, Syphilis, Diphtheria, Leprosy, Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus, impetigo, Rheumatic Fever, Scarlet Fever, sexually transmitted diseases, skin diseases (e.g., cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Moreover, parasitic agents causing disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following families: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis, Dourine, Ectoparasitic, Giardiasis, Helminthiasis, 5 Leishmaniasis, Theileriasis, Toxoplasmosis, Trypanosomiasis, and Trichomonas. These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), Malaria, pregnancy complications, and toxoplasmosis. A polypeptide or polynucleotide 10 of the present invention can be used to treat or detect any of these symptoms or diseases.

Preferably, treatment using a polypeptide or polynucleotide of the present invention could either be by administering an effective amount of a polypeptide to the patient, or by removing cells from the patient, supplying the cells with a polynucleotide 15 of the present invention, and returning the engineered cells to the patient (ex vivo therapy). Moreover, the polypeptide or polynucleotide of the present invention can be used as an antigen in a vaccine to raise an immune response against infectious disease.

Regeneration

20 A polynucleotide or polypeptide of the present invention can be used to differentiate, proliferate, and attract cells, leading to the regeneration of tissues. (See, Science 276:59-87 (1997).) The regeneration of tissues could be used to repair, replace, or protect tissue damaged by congenital defects, trauma (wounds, burns, incisions, or ulcers), age, disease (e.g. osteoporosis, osteoarthritis, periodontal 25 disease, liver failure), surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, or systemic cytokine damage.

Tissues that could be regenerated using the present invention include organs (e.g., pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac), vascular (including vascular endothelium), nervous, hematopoietic, and 30 skeletal (bone, cartilage, tendon, and ligament) tissue. Preferably, regeneration occurs without or decreased scarring. Regeneration also may include angiogenesis.

Moreover, a polynucleotide or polypeptide of the present invention may increase regeneration of tissues difficult to heal. For example, increased tendon/ligament regeneration would quicken recovery time after damage. A polynucleotide or 35 polypeptide of the present invention could also be used prophylactically in an effort to avoid damage. Specific diseases that could be treated include of tendinitis, carpal tunnel syndrome, and other tendon or ligament defects. A further example of tissue

regeneration of non-healing wounds includes pressure ulcers, ulcers associated with vascular insufficiency, surgical, and traumatic wounds.

Similarly, nerve and brain tissue could also be regenerated by using a polynucleotide or polypeptide of the present invention to proliferate and differentiate nerve cells. Diseases that could be treated using this method include central and peripheral nervous system diseases, neuropathies, or mechanical and traumatic disorders (e.g., spinal cord disorders, head trauma, cerebrovascular disease, and stroke). Specifically, diseases associated with peripheral nerve injuries, peripheral neuropathy (e.g., resulting from chemotherapy or other medical therapies), localized neuropathies, and central nervous system diseases (e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome), could all be treated using the polynucleotide or polypeptide of the present invention.

15 **Chemotaxis**

A polynucleotide or polypeptide of the present invention may have chemotaxis activity. A chemotactic molecule attracts or mobilizes cells (e.g., monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells) to a particular site in the body, such as inflammation, infection, or site of hyperproliferation. The mobilized cells can then fight off and/or heal the particular trauma or abnormality.

A polynucleotide or polypeptide of the present invention may increase chemotactic activity of particular cells. These chemotactic molecules can then be used to treat inflammation, infection, hyperproliferative disorders, or any immune system disorder by increasing the number of cells targeted to a particular location in the body. For example, chemotactic molecules can be used to treat wounds and other trauma to tissues by attracting immune cells to the injured location. Chemotactic molecules of the present invention can also attract fibroblasts, which can be used to treat wounds.

It is also contemplated that a polynucleotide or polypeptide of the present invention may inhibit chemotactic activity. These molecules could also be used to treat disorders. Thus, a polynucleotide or polypeptide of the present invention could be used as an inhibitor of chemotaxis.

Binding Activity

A polypeptide of the present invention may be used to screen for molecules that bind to the polypeptide or for molecules to which the polypeptide binds. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit

(antagonist), or decrease activity of the polypeptide or the molecule bound. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural or functional mimetic. (See, Coligan et al., Current Protocols in Immunology 1(2):Chapter 5 (1991).) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or at least, a fragment of the receptor capable of being bound by the polypeptide (e.g., active site). In either case, the molecule can be rationally designed using known techniques.

Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, *Drosophila*, or *E. coli*. Cells expressing the polypeptide (or cell membrane containing the expressed polypeptide) are then preferably contacted with a test compound potentially containing the molecule to observe binding, stimulation, or inhibition of activity of either the polypeptide or the molecule.

The assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a label, or in an assay involving competition with a labeled competitor. Further, the assay may test whether the candidate compound results in a signal generated by binding to the polypeptide.

Alternatively, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

Preferably, an ELISA assay can measure polypeptide level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The antibody can measure polypeptide level or activity by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptide from suitably manipulated cells or tissues.

Therefore, the invention includes a method of identifying compounds which bind to a polypeptide of the invention comprising the steps of: (a) incubating a candidate binding compound with a polypeptide of the invention; and (b) determining if binding has occurred. Moreover, the invention includes a method of identifying
5 agonists/antagonists comprising the steps of: (a) incubating a candidate compound with a polypeptide of the invention, (b) assaying a biological activity, and (b) determining if a biological activity of the polypeptide has been altered.

Other Activities

10 A polypeptide or polynucleotide of the present invention may also increase or decrease the differentiation or proliferation of embryonic stem cells, besides, as discussed above, hematopoietic lineage.

A polypeptide or polynucleotide of the present invention may also be used to modulate mammalian characteristics, such as body height, weight, hair color, eye color,
15 skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery). Similarly, a polypeptide or polynucleotide of the present invention may be used to modulate mammalian metabolism affecting catabolism, anabolism, processing, utilization, and storage of energy.

A polypeptide or polynucleotide of the present invention may be used to change
20 a mammal's mental state or physical state by influencing biorhythms, circadian rhythms, depression (including depressive disorders), tendency for violence, tolerance for pain, reproductive capabilities (preferably by Activin or Inhibin-like activity), hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities.

25 A polypeptide or polynucleotide of the present invention may also be used as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components.

Other Preferred Embodiments

Other preferred embodiments of the claimed invention include an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 50 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1.

35 Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of

positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Clone Sequence and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous
5 nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Start Codon and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Similarly preferred is a nucleic acid molecule wherein said sequence of
10 contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide
15 sequence which is at least 95% identical to a sequence of at least about 150 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

Further preferred is an isolated nucleic acid molecule comprising a nucleotide
20 sequence which is at least 95% identical to a sequence of at least about 500 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

A further preferred embodiment is a nucleic acid molecule comprising a
nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ
ID NO:X beginning with the nucleotide at about the position of the 5' Nucleotide of the
First Amino Acid of the Signal Peptide and ending with the nucleotide at about the
25 position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in
Table 1.

A further preferred embodiment is an isolated nucleic acid molecule comprising
a nucleotide sequence which is at least 95% identical to the complete nucleotide
sequence of SEQ ID NO:X.

Also preferred is an isolated nucleic acid molecule which hybridizes under
30 stringent hybridization conditions to a nucleic acid molecule, wherein said nucleic acid molecule which hybridizes does not hybridize under stringent hybridization conditions to a nucleic acid molecule having a nucleotide sequence consisting of only A residues or of only T residues.

Also preferred is a composition of matter comprising a DNA molecule which
35 comprises a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the material deposited with the American Type

Culture Collection and given the ATCC Deposit Number shown in Table 1 for said cDNA Clone Identifier.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in the nucleotide sequence of a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the deposit given the ATCC Deposit Number shown in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said sequence of at least 50 contiguous nucleotides is included in the nucleotide sequence of the complete open reading frame sequence encoded by said human cDNA clone.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 150 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 500 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is a method for detecting in a biological sample a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing a nucleotide sequence of at least one nucleic acid molecule in said sample with a sequence selected from said group and determining whether the sequence of said nucleic acid molecule in said sample is at least 95% identical to said selected sequence.

Also preferred is the above method wherein said step of comparing sequences comprises determining the extent of nucleic acid hybridization between nucleic acid molecules in said sample and a nucleic acid molecule comprising said sequence selected from said group. Similarly, also preferred is the above method wherein said step of comparing sequences is performed by comparing the nucleotide sequence determined from a nucleic acid molecule in said sample with said sequence selected from said group. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

A further preferred embodiment is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting nucleic acid molecules in said sample, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for identifying the species, tissue or cell type of a biological sample can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject nucleic acid molecules, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for diagnosing a pathological condition can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1.

Also preferred is a polypeptide, wherein said sequence of contiguous amino acids is included in the amino acid sequence of SEQ ID NO:Y in the range of positions beginning with the residue at about the position of the First Amino Acid of the Secreted Portion and ending with the residue at about the Last Amino Acid of the Open Reading Frame as set forth for SEQ ID NO:Y in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the complete amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is a polypeptide wherein said sequence of contiguous amino acids is included in the amino acid sequence of a secreted portion of the secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in

5 Table 1.

Further preferred is an isolated antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as
10 defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method for detecting in a biological sample a polypeptide comprising an amino acid sequence which is at least 90% identical to a sequence of at
15 least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method
20 comprises a step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group and determining whether the sequence of said polypeptide molecule in said sample is at least 90% identical to said sequence of at least 10 contiguous amino acids.

Also preferred is the above method wherein said step of comparing an amino
25 acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group comprises determining the extent of specific binding of polypeptides in said sample to an antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an
30 amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method wherein said step of comparing sequences is
35 performed by comparing the amino acid sequence determined from a polypeptide molecule in said sample with said sequence selected from said group.

Also preferred is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting polypeptide molecules in said sample, if any, comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method for identifying the species, tissue or cell type of a biological sample, which method comprises a step of detecting polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the above group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

In any of these methods, the step of detecting said polypeptide molecules includes using an antibody.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a nucleotide sequence encoding a polypeptide wherein said polypeptide comprises an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said nucleotide sequence encoding a polypeptide has been optimized for expression of said polypeptide in a prokaryotic host.

Also preferred is an isolated nucleic acid molecule, wherein said polypeptide
5 comprises an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

10 Further preferred is a method of making a recombinant vector comprising inserting any of the above isolated nucleic acid molecule into a vector. Also preferred is the recombinant vector produced by this method. Also preferred is a method of making a recombinant host cell comprising introducing the vector into a host cell, as well as the recombinant host cell produced by this method.

15 Also preferred is a method of making an isolated polypeptide comprising culturing this recombinant host cell under conditions such that said polypeptide is expressed and recovering said polypeptide. Also preferred is this method of making an isolated polypeptide, wherein said recombinant host cell is a eukaryotic cell and said polypeptide is a secreted portion of a human secreted protein comprising an amino acid
20 sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y beginning with the residue at the position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y wherein Y is an integer set forth in Table 1 and said position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y is defined in Table 1; and an amino acid sequence of a secreted portion of a protein encoded by a human
25 cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The isolated polypeptide produced by this method is also preferred.

Also preferred is a method of treatment of an individual in need of an increased level of a secreted protein activity, which method comprises administering to such an
30 individual a pharmaceutical composition comprising an amount of an isolated polypeptide, polynucleotide, or antibody of the claimed invention effective to increase the level of said protein activity in said individual.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of
35 illustration and are not intended as limiting.

Examples

Example 1: Isolation of a Selected cDNA Clone From the Deposited Sample

Each cDNA clone in a cited ATCC deposit is contained in a plasmid vector. Table 1 identifies the vectors used to construct the cDNA library from which each clone was isolated. In many cases, the vector used to construct the library is a phage vector from which a plasmid has been excised. The table immediately below correlates the related plasmid for each phage vector used in constructing the cDNA library. For example, where a particular clone is identified in Table 1 as being isolated in the vector "Lambda Zap," the corresponding deposited clone is in "pBluescript."

	<u>Vector Used to Construct Library</u>	<u>Corresponding Deposited Plasmid</u>
	Lambda Zap	pBluescript (pBS)
	Uni-Zap XR	pBluescript (pBS)
15	Zap Express	pBK
	lafmid BA	plafmid BA
	pSport1	pSport1
	pCMVSPORT 2.0	pCMVSPORT 2.0
	pCMVSPORT 3.0	pCMVSPORT 3.0
20	pCR [®] 2.1	pCR [®] 2.1

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Altling-Mees, M. A. and Short, J. M., Nucleic Acids Res. 17:9494 (1989)) and pBK (Altling-Mees, M. A. et al., Strategies 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Both can be transformed into E. coli strain XL-1 Blue, also available from Stratagene. pBS comes in 4 forms SK+, SK-, KS+ and KS. The S and K refers to the orientation of the polylinker to the T7 and T3 primer sequences which flank the polylinker region ("S" is for SacI and "K" is for KpnI which are the first sites on each respective end of the linker). "+" or "-" refer to the orientation of the f1 origin of replication ("ori"), such that in one orientation, single stranded rescue initiated from the f1 ori generates sense strand DNA and in the other, antisense.

Vectors pSport1, pCMVSPORT 2.0 and pCMVSPORT 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into E. coli strain

DH10B, also available from Life Technologies. (See, for instance, Gruber, C. E., et al., *Focus* 15:59 (1993).) Vector lafmid BA (Bento Soares, Columbia University, NY) contains an ampicillin resistance gene and can be transformed into *E. coli* strain XL-1 Blue. Vector pCR[®]2.1, which is available from Invitrogen, 1600 Faraday Avenue,
5 Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, available from Life Technologies. (See, for instance, Clark, J. M., *Nuc. Acids Res.* 16:9677-9686 (1988) and Mead, D. et al., *Bio/Technology* 9: (1991).) Preferably, a polynucleotide of the present invention does not comprise the phage vector sequences identified for the particular clone in Table 1, as well as the
10 corresponding plasmid vector sequences designated above.

The deposited material in the sample assigned the ATCC Deposit Number cited in Table 1 for any given cDNA clone also may contain one or more additional plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing the same ATCC Deposit Number contain at least a plasmid for each cDNA clone
15 identified in Table 1. Typically, each ATCC deposit sample cited in Table 1 comprises a mixture of approximately equal amounts (by weight) of about 50 plasmid DNAs, each containing a different cDNA clone; but such a deposit sample may include plasmids for more or less than 50 cDNA clones, up to about 500 cDNA clones.

Two approaches can be used to isolate a particular clone from the deposited
20 sample of plasmid DNAs cited for that clone in Table 1. First, a plasmid is directly isolated by screening the clones using a polynucleotide probe corresponding to SEQ ID NO:X.

Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported.
25 The oligonucleotide is labeled, for instance, with ³²P-γ-ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press, Cold Spring, NY (1982).) The plasmid mixture is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as
30 those provided by the vector supplier or in related publications or patents cited above. The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening (e.g., Sambrook et al., *Molecular Cloning: A Laboratory*
35 *Manual*, 2nd Edit., (1989), Cold Spring Harbor Laboratory Press, pages 1.93 to 1.104), or other techniques known to those of skill in the art.

Alternatively, two primers of 17-20 nucleotides derived from both ends of the SEQ ID NO:X (i.e., within the region of SEQ ID NO:X bounded by the 5' NT and the 3' NT of the clone defined in Table 1) are synthesized and used to amplify the desired cDNA using the deposited cDNA plasmid as a template. The polymerase chain reaction is carried out under routine conditions, for instance, in 25 μ l of reaction mixture with 0.5 μ g of the above cDNA template. A convenient reaction mixture is 1.5-5 mM MgCl_2 , 0.01% (w/v) gelatin, 20 μ M each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

Several methods are available for the identification of the 5' or 3' non-coding portions of a gene which may not be present in the deposited clone. These methods include but are not limited to, filter probing, clone enrichment using specific probes, and protocols similar or identical to 5' and 3' "RACE" protocols which are well known in the art. For instance, a method similar to 5' RACE is available for generating the missing 5' end of a desired full-length transcript. (Fromont-Racine et al., *Nucleic Acids Res.* 21(7):1683-1684 (1993).)

Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcripts. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest is used to PCR amplify the 5' portion of the desired full-length gene. This amplified product may then be sequenced and used to generate the full length gene.

This above method starts with total RNA isolated from the desired source, although poly-A+ RNA can be used. The RNA preparation can then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase should then be inactivated and the RNA treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

This modified RNA preparation is used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction is

used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the desired gene.

5

Example 2: Isolation of Genomic Clones Corresponding to a Polynucleotide

A human genomic P1 library (Genomic Systems, Inc.) is screened by PCR using primers selected for the cDNA sequence corresponding to SEQ ID NO:X., according to the method described in Example 1. (See also, Sambrook.)

10

Example 3: Tissue Distribution of Polypeptide

Tissue distribution of mRNA expression of polynucleotides of the present invention is determined using protocols for Northern blot analysis, described by, among others, Sambrook et al. For example, a cDNA probe produced by the method described in Example 1 is labeled with P³² using the rediprime™ DNA labeling system (Amersham Life Science), according to manufacturer's instructions. After labeling, the probe is purified using CHROMA SPIN-100™ column (Clontech Laboratories, Inc.), according to manufacturer's protocol number PT1200-1. The purified labeled probe is then used to examine various human tissues for mRNA expression.

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Multiple Tissue Northern (MTN) blots containing various human tissues (H) or human immune system tissues (IM) (Clontech) are examined with the labeled probe using ExpressHyb™ hybridization solution (Clontech) according to manufacturer's protocol number PT1190-1. Following hybridization and washing, the blots are mounted and exposed to film at -70°C overnight, and the films developed according to standard procedures.

25

Example 4: Chromosomal Mapping of the Polynucleotides

An oligonucleotide primer set is designed according to the sequence at the 5' end of SEQ ID NO:X. This primer preferably spans about 100 nucleotides. This primer set is then used in a polymerase chain reaction under the following set of conditions : 30 seconds, 95°C; 1 minute, 56°C; 1 minute, 70°C. This cycle is repeated 32 times followed by one 5 minute cycle at 70°C. Human, mouse, and hamster DNA is used as template in addition to a somatic cell hybrid panel containing individual chromosomes or chromosome fragments (Bios, Inc). The reactions is analyzed on

30

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either 8% polyacrylamide gels or 3.5 % agarose gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR fragment in the particular somatic cell hybrid.

5 **Example 5: Bacterial Expression of a Polypeptide**

A polynucleotide encoding a polypeptide of the present invention is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 1, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as
10 BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Amp^r), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site
15 (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning sites.

The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the E. coli strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, which expresses
20 the lacI repressor and also confers kanamycin resistance (Kan^r). Transformants are identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis.

Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml).
25 The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells are grown to an optical density 600 (O.D.⁶⁰⁰) of between 0.4 and 0.6. IPTG (Isopropyl-B-D-thiogalacto pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

30 Cells are grown for an extra 3 to 4 hours. Cells are then harvested by centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic agent 6 Molar Guanidine HCl by stirring for 3-4 hours at 4°C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from
35 QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high

affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995) QIAGEN, Inc., *supra*).

5 Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with 6 M guanidine-HCl, pH 5.

10 The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein can be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins are eluted by the addition of 250 mM imidazole. Imidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4° C or frozen at -80° C.

15 In addition to the above expression vector, the present invention further includes an expression vector comprising phage operator and promoter elements operatively linked to a polynucleotide of the present invention, called pHE4a. (ATCC Accession Number 209645, deposited on February 25, 1998.) This vector contains: 1) a 20 neomycinphosphotransferase gene as a selection marker, 2) an E. coli origin of replication, 3) a T5 phage promoter sequence, 4) two lac operator sequences, 5) a Shine-Delgarno sequence, and 6) the lactose operon repressor gene (*lacIq*). The origin of replication (*oriC*) is derived from pUC19 (LTI, Gaithersburg, MD). The promoter sequence and operator sequences are made synthetically.

25 DNA can be inserted into the pHEa by restricting the vector with NdeI and XbaI, BamHI, XhoI, or Asp718, running the restricted product on a gel, and isolating the larger fragment (the stuffer fragment should be about 310 base pairs). The DNA insert is generated according to the PCR protocol described in Example 1, using PCR primers having restriction sites for NdeI (5' primer) and XbaI, BamHI, XhoI, or 30 Asp718 (3' primer). The PCR insert is gel purified and restricted with compatible enzymes. The insert and vector are ligated according to standard protocols.

The engineered vector could easily be substituted in the above protocol to express protein in a bacterial system.

Example 6: Purification of a Polypeptide from an Inclusion Body

The following alternative method can be used to purify a polypeptide expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

- 5 Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50
10 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

- The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by
15 centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

- The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is discarded and the polypeptide containing supernatant is incubated at 4°C
20 overnight to allow further GuHCl extraction.

- Following high speed centrifugation (30,000 xg) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing
25 for 12 hours prior to further purification steps.

- To clarify the refolded polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive
30 Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant polypeptide should exhibit greater than 95% purity after the above refolding and purification steps. No major contaminant bands should be observed from Commassie blue stained 16% SDS-PAGE gel when 5 μ g of purified protein is loaded. The purified protein can also be tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

Example 7: Cloning and Expression of a Polypeptide in a Baculovirus Expression System

In this example, the plasmid shuttle vector pA2 is used to insert a polynucleotide into a baculovirus to express a polypeptide. This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus (AcMNPV) followed by convenient restriction sites such as BamHI, Xba I and Asp718. The polyadenylation site of the simian virus 40 ("SV40") is used for efficient polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene from *E. coli* under control of a weak *Drosophila* promoter in the same orientation, followed by the polyadenylation signal of the polyhedrin gene. The inserted genes are flanked on both sides by viral sequences for cell-mediated homologous recombination with wild-type viral DNA to generate a viable virus that express the cloned polynucleotide.

Many other baculovirus vectors can be used in place of the vector above, such as pAc373, pVL941, and pAcIM1, as one skilled in the art would readily appreciate, as long as the construct provides appropriately located signals for transcription, translation, secretion and the like, including a signal peptide and an in-frame AUG as required. Such vectors are described, for instance, in Luckow et al., *Virology* 170:31-39 (1989).

Specifically, the cDNA sequence contained in the deposited clone, including the AUG initiation codon and the naturally associated leader sequence identified in Table 1, is amplified using the PCR protocol described in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the pA2 vector does not need a second signal peptide. Alternatively, the vector can be modified (pA2 GP) to include a baculovirus leader sequence, using the standard methods described in Summers et al., "A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures," Texas Agricultural Experimental Station Bulletin No. 1555 (1987).

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The plasmid is digested with the corresponding restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("GeneClean" BIO 101 Inc., La Jolla, Ca.).

The fragment and the dephosphorylated plasmid are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing.

Five μ g of a plasmid containing the polynucleotide is co-transfected with 1.0 μ g of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., Proc. Natl. Acad. Sci. USA 84:7413-7417 (1987). One μ g of BaculoGold™ virus DNA and 5 μ g of the plasmid are mixed in a sterile well of a microtiter plate containing 50 μ l of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 μ l Lipofectin plus 90 μ l Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is then incubated for 5 hours at 27° C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27° C for four days.

After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life

Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.)

- 5 After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 µl of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested
10 and then they are stored at 4° C.

- To verify the expression of the polypeptide, Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus containing the polynucleotide at a multiplicity of infection ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is
15 removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc., Rockville, MD). After 42 hours, 5 µCi of ³⁵S-methionine and 5 µCi ³⁵S-cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE
20 followed by autoradiography (if radiolabeled).

Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the produced protein.

Example 8: Expression of a Polypeptide in Mammalian Cells

- The polypeptide of the present invention can be expressed in a mammalian cell.
25 A typical mammalian expression vector contains a promoter element, which mediates the initiation of transcription of mRNA, a protein coding sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription is achieved
30 with the early and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLV, HIV and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter).

- Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden),
35 pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSPORT 2.0, and pCMVSPORT 3.0. Mammalian host cells that could be used

include, human Hela, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the polypeptide can be expressed in stable cell lines containing the polynucleotide integrated into a chromosome. The co-transfection with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that carry several hundred or even several thousand copies of the gene of interest. (See, e.g., Alt, F. W., et al., J. Biol. Chem. 253:1357-1370 (1978); Hamlin, J. L. and Ma, C., Biochem. et Biophys. Acta, 1097:107-143 (1990); Page, M. J. and Sydenham, M. A., Biotechnology 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., Biochem J. 227:277-279 (1991); Bebbington et al., Bio/Technology 10:169-175 (1992). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

Derivatives of the plasmid pSV2-dhfr (ATCC Accession No. 37146), the expression vectors pC4 (ATCC Accession No. 209646) and pC6 (ATCC Accession No.209647) contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen et al., Molecular and Cellular Biology, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart et al., Cell 41:521-530 (1985).) Multiple cloning sites, e.g., with the restriction enzyme cleavage sites BamHI, XbaI and Asp718, facilitate the cloning of the gene of interest. The vectors also contain the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene, and the mouse DHFR gene under control of the SV40 early promoter.

Specifically, the plasmid pC6, for example, is digested with appropriate restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

A polynucleotide of the present invention is amplified according to the protocol outlined in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the vector does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

5 The amplified fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC6 using, for instance, restriction enzyme analysis.

10 Chinese hamster ovary cells lacking an active DHFR gene is used for transfection. Five μ g of the expression plasmid pC6 is cotransfected with 0.5 μ g of the plasmid pSVneo using lipofectin (Felgner et al., *supra*). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are
15 trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of
20 methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μ M, 2 μ M, 5 μ M, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 - 200 μ M. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

25

Example 9: Protein Fusions

The polypeptides of the present invention are preferably fused to other proteins. These fusion proteins can be used for a variety of applications. For example, fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG domains, and maltose
30 binding protein facilitates purification. (See Example 5; see also EP A 394,827; Traunecker, et al., Nature 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and albumin increases the halflife time in vivo. Nuclear localization signals fused to the polypeptides of the present invention can target the protein to a specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the
35 activity of a fusion protein. Fusion proteins can also create chimeric molecules having more than one function. Finally, fusion proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion

proteins described above can be made by modifying the following protocol, which outlines the fusion of a polypeptide to an IgG molecule, or the protocol described in Example 5.

5 Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an expression vector, preferably a mammalian expression vector.

For example, if pC4 (Accession No. 209646) is used, the human Fc portion can be ligated into the BamHI cloning site. Note that the 3' BamHI site should be
10 destroyed. Next, the vector containing the human Fc portion is re-restricted with BamHI, linearizing the vector, and a polynucleotide of the present invention, isolated by the PCR protocol described in Example 1, is ligated into this BamHI site. Note that the polynucleotide is cloned without a stop codon, otherwise a fusion protein will not be produced.

15 If the naturally occurring signal sequence is used to produce the secreted protein, pC4 does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

20 Human IgG Fc region:

GGGATCCGGAGCCCAAATCTTCTGACAAAACTCACACATGCCCACCGTGCC
CAGCACCTGAATTCGAGGGTGCACCGTCAGTCTTCCTCTTCCCCCAAAC
CAAGGACACCCTCATGATCTCCCGGACTCCTGAGGTCACATGCGTGTTGGT
GGACGTAAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACG
25 GCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC
AGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAACCCCC
ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCT
30 GACCTGCCTGGTCAAAGGCTTCTATCCAAGCGACATCGCCGTGGAGTGGGA
GAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTGG
ACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCA
GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGC
ACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGC
35 GACGGCCGCGACTCTAGAGGAT (SEQ ID NO:1)

Example 10: Production of an Antibody from a Polypeptide

The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) For example, cells expressing a polypeptide of the present invention is administered to an animal to induce the production of sera
5 containing polyclonal antibodies. In a preferred method, a preparation of the secreted protein is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

In the most preferred method, the antibodies of the present invention are
10 monoclonal antibodies (or protein binding fragments thereof). Such monoclonal antibodies can be prepared using hybridoma technology. (Köhler et al., Nature 256:495 (1975); Köhler et al., Eur. J. Immunol. 6:511 (1976); Köhler et al., Eur. J. Immunol. 6:292 (1976); Hammerling et al., in: Monoclonal Antibodies and T-Cell Hybridomas, Elsevier, N.Y., pp. 563-681 (1981).) In general, such procedures
15 involve immunizing an animal (preferably a mouse) with polypeptide or, more preferably, with a secreted polypeptide-expressing cell. Such cells may be cultured in any suitable tissue culture medium; however, it is preferable to culture cells in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at about 56°C), and supplemented with about 10 g/l of nonessential amino acids, about
20 1,000 U/ml of penicillin, and about 100 µg/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are
25 selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (Gastroenterology 80:225-232 (1981).) The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide.

Alternatively, additional antibodies capable of binding to the polypeptide can be
30 produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells,
35 and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the protein-specific antibody can be blocked by the polypeptide.

Such antibodies comprise anti-idiotypic antibodies to the protein-specific antibody and can be used to immunize an animal to induce formation of further protein-specific antibodies.

It will be appreciated that Fab and F(ab')₂ and other fragments of the antibodies of the present invention may be used according to the methods disclosed herein. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂ fragments). Alternatively, secreted protein-binding fragments can be produced through the application of recombinant DNA technology or through synthetic chemistry.

For in vivo use of antibodies in humans, it may be preferable to use "humanized" chimeric monoclonal antibodies. Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric antibodies are known in the art. (See, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

Example 11: Production Of Secreted Protein For High-Throughput Screening Assays

The following protocol produces a supernatant containing a polypeptide to be tested. This supernatant can then be used in the Screening Assays described in Examples 13-20.

First, dilute Poly-D-Lysine (644 587 Boehringer-Mannheim) stock solution (1mg/ml in PBS) 1:20 in PBS (w/o calcium or magnesium 17-516F Biowhittaker) for a working solution of 50ug/ml. Add 200 ul of this solution to each well (24 well plates) and incubate at RT for 20 minutes. Be sure to distribute the solution over each well (note: a 12-channel pipetter may be used with tips on every other channel). Aspirate off the Poly-D-Lysine solution and rinse with 1ml PBS (Phosphate Buffered Saline). The PBS should remain in the well until just prior to plating the cells and plates may be poly-lysine coated in advance for up to two weeks.

Plate 293T cells (do not carry cells past P+20) at 2×10^5 cells/well in .5ml DMEM(Dulbecco's Modified Eagle Medium)(with 4.5 G/L glucose and L-glutamine (12-604F Biowhittaker))/10% heat inactivated FBS(14-503F Biowhittaker)/1x Penstrep(17-602E Biowhittaker). Let the cells grow overnight.

The next day, mix together in a sterile solution basin: 300 ul Lipofectamine (18324-012 Gibco/BRL) and 5ml Optimem I (31985070 Gibco/BRL)/96-well plate. With a small volume multi-channel pipetter, aliquot approximately 2ug of an expression vector containing a polynucleotide insert, produced by the methods described in

- 5 Examples 8 or 9, into an appropriately labeled 96-well round bottom plate. With a multi-channel pipetter, add 50ul of the Lipofectamine/Optimem I mixture to each well. Pipette up and down gently to mix. Incubate at RT 15-45 minutes. After about 20 minutes, use a multi-channel pipetter to add 150ul Optimem I to each well. As a control, one plate of vector DNA lacking an insert should be transfected with each set of
- 10 transfections.

- Preferably, the transfection should be performed by tag-teaming the following tasks. By tag-teaming, hands on time is cut in half, and the cells do not spend too much time on PBS. First, person A aspirates off the media from four 24-well plates of cells, and then person B rinses each well with .5-1ml PBS. Person A then aspirates off
- 15 PBS rinse, and person B, using a 12-channel pipetter with tips on every other channel, adds the 200ul of DNA/Lipofectamine/Optimem I complex to the odd wells first, then to the even wells, to each row on the 24-well plates. Incubate at 37°C for 6 hours.

- While cells are incubating, prepare appropriate media, either 1%BSA in DMEM with 1x penstrep, or CHO-5 media (116.6 mg/L of CaCl₂ (anhyd); 0.00130 mg/L
- 20 CuSO₄·5H₂O; 0.050 mg/L of Fe(NO₃)₃·9H₂O; 0.417 mg/L of FeSO₄·7H₂O; 311.80 mg/L of KCl; 28.64 mg/L of MgCl₂; 48.84 mg/L of MgSO₄; 6995.50 mg/L of NaCl; 2400.0 mg/L of NaHCO₃; 62.50 mg/L of NaH₂PO₄·H₂O; 71.02 mg/L of Na₂HPO₄; .4320 mg/L of ZnSO₄·7H₂O; .002 mg/L of Arachidonic Acid ; 1.022 mg/L of Cholesterol; .070 mg/L of DL-alpha-Tocopherol-Acetate; 0.0520 mg/L of Linoleic
- 25 Acid; 0.010 mg/L of Linolenic Acid; 0.010 mg/L of Myristic Acid; 0.010 mg/L of Oleic Acid; 0.010 mg/L of Palmitic Acid; 0.010 mg/L of Palmitic Acid; 100 mg/L of Pluronic F-68; 0.010 mg/L of Stearic Acid; 2.20 mg/L of Tween 80; 4551 mg/L of D-Glucose; 130.85 mg/ml of L- Alanine; 147.50 mg/ml of L-Arginine-HCL; 7.50 mg/ml of L-Asparagine-H₂O; 6.65 mg/ml of L-Aspartic Acid; 29.56 mg/ml of L-Cystine-
- 30 2HCL-H₂O; 31.29 mg/ml of L-Cystine-2HCL; 7.35 mg/ml of L-Glutamic Acid; 365.0 mg/ml of L-Glutamine; 18.75 mg/ml of Glycine; 52.48 mg/ml of L-Histidine-HCL-H₂O; 106.97 mg/ml of L-Isoleucine; 111.45 mg/ml of L-Leucine; 163.75 mg/ml of L-Lysine HCL; 32.34 mg/ml of L-Methionine; 68.48 mg/ml of L-Phenylalanine; 40.0 mg/ml of L-Proline; 26.25 mg/ml of L-Serine; 101.05 mg/ml of L-Threonine; 19.22
- 35 mg/ml of L-Tryptophan; 91.79 mg/ml of L-Tyrosine-2Na-2H₂O; 99.65 mg/ml of L-Valine; 0.0035 mg/L of Biotin; 3.24 mg/L of D-Ca Pantothenate; 11.78 mg/L of

Choline Chloride; 4.65 mg/L of Folic Acid; 15.60 mg/L of i-Inositol; 3.02 mg/L of Niacinamide; 3.00 mg/L of Pyridoxal HCL; 0.031 mg/L of Pyridoxine HCL; 0.319 mg/L of Riboflavin; 3.17 mg/L of Thiamine HCL; 0.365 mg/L of Thymidine; and 0.680 mg/L of Vitamin B₁₂; 25 mM of HEPES Buffer; 2.39 mg/L of Na Hypoxanthine; 5 0.105 mg/L of Lipoic Acid; 0.081 mg/L of Sodium Putrescine-2HCL; 55.0 mg/L of Sodium Pyruvate; 0.0067 mg/L of Sodium Selenite; 20uM of Ethanolamine; 0.122 mg/L of Ferric Citrate; 41.70 mg/L of Methyl-B-Cyclodextrin complexed with Linoleic Acid; 33.33 mg/L of Methyl-B-Cyclodextrin complexed with Oleic Acid; and 10 mg/L of Methyl-B-Cyclodextrin complexed with Retinal) with 2mm glutamine and 1x 10 penstrep. (BSA (81-068-3 Bayer) 100gm dissolved in 1L DMEM for a 10% BSA stock solution). Filter the media and collect 50 ul for endotoxin assay in 15ml polystyrene conical.

The transfection reaction is terminated, preferably by tag-teaming, at the end of the incubation period. Person A aspirates off the transfection media, while person B 15 adds 1.5ml appropriate media to each well. Incubate at 37°C for 45 or 72 hours depending on the media used: 1%BSA for 45 hours or CHO-5 for 72 hours.

On day four, using a 300ul multichannel pipetter, aliquot 600ul in one 1ml deep well plate and the remaining supernatant into a 2ml deep well. The supernatants from each well can then be used in the assays described in Examples 13-20.

20 It is specifically understood that when activity is obtained in any of the assays described below using a supernatant, the activity originates from either the polypeptide directly (e.g., as a secreted protein) or by the polypeptide inducing expression of other proteins, which are then secreted into the supernatant. Thus, the invention further provides a method of identifying the protein in the supernatant characterized by an 25 activity in a particular assay.

Example 12: Construction of GAS Reporter Construct

One signal transduction pathway involved in the differentiation and proliferation of cells is called the Jaks-STATs pathway. Activated proteins in the Jaks-STATs 30 pathway bind to gamma activation site "GAS" elements or interferon-sensitive responsive element ("ISRE"), located in the promoter of many genes. The binding of a protein to these elements alter the expression of the associated gene.

GAS and ISRE elements are recognized by a class of transcription factors called Signal Transducers and Activators of Transcription, or "STATs." There are six 35 members of the STATs family. Stat1 and Stat3 are present in many cell types, as is Stat2 (as response to IFN-alpha is widespread). Stat4 is more restricted and is not in

many cell types though it has been found in T helper class I, cells after treatment with IL-12. Stat5 was originally called mammary growth factor, but has been found at higher concentrations in other cells including myeloid cells. It can be activated in tissue culture cells by many cytokines.

5 The STATs are activated to translocate from the cytoplasm to the nucleus upon tyrosine phosphorylation by a set of kinases known as the Janus Kinase ("Jaks") family. Jaks represent a distinct family of soluble tyrosine kinases and include Tyk2, Jak1, Jak2, and Jak3. These kinases display significant sequence similarity and are generally catalytically inactive in resting cells.

10 The Jaks are activated by a wide range of receptors summarized in the Table below. (Adapted from review by Schidler and Darnell, Ann. Rev. Biochem. 64:621-51 (1995).) A cytokine receptor family, capable of activating Jaks, is divided into two groups: (a) Class 1 includes receptors for IL-2, IL-3, IL-4, IL-6, IL-7, IL-9, IL-11, IL-12, IL-15, Epo, PRL, GH, G-CSF, GM-CSF, LIF, CNTF, and thrombopoietin; and
15 (b) Class 2 includes IFN- α , IFN- γ , and IL-10. The Class 1 receptors share a conserved cysteine motif (a set of four conserved cysteines and one tryptophan) and a WSXWS motif (a membrane proximal region encoding Trp-Ser-Xxx-Trp-Ser (SEQ ID NO:2)).

20 Thus, on binding of a ligand to a receptor, Jaks are activated, which in turn activate STATs, which then translocate and bind to GAS elements. This entire process is encompassed in the Jaks-STATs signal transduction pathway.

 Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the GAS or the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. For example, growth factors and cytokines are
25 known to activate the Jaks-STATs pathway. (See Table below.) Thus, by using GAS elements linked to reporter molecules, activators of the Jaks-STATs pathway can be identified.

	<u>Ligand</u>	<u>tyk2</u>	<u>JAKs</u> <u>Jak1</u>	<u>Jak2</u>	<u>Jak3</u>	<u>STATS</u>	<u>GAS(elements) or ISRE</u>
<u>IFN family</u>							
5	IFN-a/B	+	+	-	-	1,2,3	ISRE
	IFN-g		+	+	-	1	GAS (IRF1>Lys6>IFP)
	Il-10	+	?	?	-	1,3	
<u>gp130 family</u>							
10	IL-6 (Pleiotrohic)	+	+	+	?	1,3	GAS (IRF1>Lys6>IFP)
	Il-11(Pleiotrohic)	?	+	?	?	1,3	
	OnM(Pleiotrohic)	?	+	+	?	1,3	
	LIF(Pleiotrohic)	?	+	+	?	1,3	
	CNTF(Pleiotrohic)	-/+	+	+	?	1,3	
15	G-CSF(Pleiotrohic)	?	+	?	?	1,3	
	IL-12(Pleiotrohic)	+	-	+	+	1,3	
<u>g-C family</u>							
20	IL-2 (lymphocytes)	-	+	-	+	1,3,5	GAS
	IL-4 (lymph/myeloid)	-	+	-	+	6	GAS (IRF1 = IFP >>Ly6)(IgH)
	IL-7 (lymphocytes)	-	+	-	+	5	GAS
	IL-9 (lymphocytes)	-	+	-	+	5	GAS
	IL-13 (lymphocyte)	-	+	?	?	6	GAS
	IL-15	?	+	?	+	5	GAS
25	<u>gp140 family</u>						
	IL-3 (myeloid)	-	-	+	-	5	GAS (IRF1>IFP>>Ly6)
	IL-5 (myeloid)	-	-	+	-	5	GAS
	GM-CSF (myeloid)	-	-	+	-	5	GAS
30	<u>Growth hormone family</u>						
	GH	?	-	+	-	5	
	PRL	?	+/-	+	-	1,3,5	
	EPO	?	-	+	-	5	GAS(B-CAS>IRF1=IFP>>Ly6)
35	<u>Receptor Tyrosine Kinases</u>						
	EGF	?	+	+	-	1,3	GAS (IRF1)
	PDGF	?	+	+	-	1,3	
40	CSF-1	?	+	+	-	1,3	GAS (not IRF1)

To construct a synthetic GAS containing promoter element, which is used in the Biological Assays described in Examples 13-14, a PCR based strategy is employed to generate a GAS-SV40 promoter sequence. The 5' primer contains four tandem copies of the GAS binding site found in the IRF1 promoter and previously demonstrated to
5 bind STATs upon induction with a range of cytokines (Rothman et al., Immunity 1:457-468 (1994).), although other GAS or ISRE elements can be used instead. The 5' primer also contains 18bp of sequence complementary to the SV40 early promoter sequence and is flanked with an XhoI site. The sequence of the 5' primer is:
5':GCGCCTCGAGATTTCCCCGAAATCTAGATTTCCCCGAAATGATTTCCCCG
10 AAATGATTTCCCCGAAATATCTGCCATCTCAATTAG:3' (SEQ ID NO:3)

The downstream primer is complementary to the SV40 promoter and is flanked with a Hind III site: 5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in
15 the B-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI/Hind III and subcloned into BLSK2-. (Stratagene.) Sequencing with forward and reverse primers confirms that the insert contains the following sequence:
5':CTCGAGATTTCCCCGAAATCTAGATTTCCCCGAAATGATTTCCCCGAAATG
20 ATTTCCCCGAAATATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCC
CTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGC
CCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGC
CTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTT
TGCAAAAAGCTT:3' (SEQ ID NO:5)

25 With this GAS promoter element linked to the SV40 promoter, a GAS:SEAP2 reporter construct is next engineered. Here, the reporter molecule is a secreted alkaline phosphatase, or "SEAP." Clearly, however, any reporter molecule can be instead of SEAP, in this or in any of the other Examples. Well known reporter molecules that can be used instead of SEAP include chloramphenicol acetyltransferase (CAT), luciferase,
30 alkaline phosphatase, B-galactosidase, green fluorescent protein (GFP), or any protein detectable by an antibody.

The above sequence confirmed synthetic GAS-SV40 promoter element is subcloned into the pSEAP-Promoter vector obtained from Clontech using HindIII and XhoI, effectively replacing the SV40 promoter with the amplified GAS:SV40 promoter
35 element, to create the GAS-SEAP vector. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

Thus, in order to generate mammalian stable cell lines expressing the GAS-SEAP reporter, the GAS-SEAP cassette is removed from the GAS-SEAP vector using SalI and NotI, and inserted into a backbone vector containing the neomycin resistance gene, such as pGFP-1 (Clontech), using these restriction sites in the multiple cloning site, to create the GAS-SEAP/Neo vector. Once this vector is transfected into mammalian cells, this vector can then be used as a reporter molecule for GAS binding as described in Examples 13-14.

Other constructs can be made using the above description and replacing GAS with a different promoter sequence. For example, construction of reporter molecules containing NFK-B and EGR promoter sequences are described in Examples 15 and 16. However, many other promoters can be substituted using the protocols described in these Examples. For instance, SRE, IL-2, NFAT, or Osteocalcin promoters can be substituted, alone or in combination (e.g., GAS/NF-KB/EGR, GAS/NF-KB, IL-2/NFAT, or NF-KB/GAS). Similarly, other cell lines can be used to test reporter construct activity, such as HELA (epithelial), HUVEC (endothelial), Reh (B-cell), Saos-2 (osteoblast), HUVAC (aortic), or Cardiomyocyte.

Example 13: High-Throughput Screening Assay for T-cell Activity.

The following protocol is used to assess T-cell activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate T-cells. T-cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The T-cell used in this assay is Jurkat T-cells (ATCC Accession No. TIB-152), although Molt-3 cells (ATCC Accession No. CRL-1552) and Molt-4 cells (ATCC Accession No. CRL-1582) cells can also be used.

Jurkat T-cells are lymphoblastic CD4+ Th1 helper cells. In order to generate stable cell lines, approximately 2 million Jurkat cells are transfected with the GAS-SEAP/neo vector using DMRIE-C (Life Technologies)(transfection procedure described below). The transfected cells are seeded to a density of approximately 20,000 cells per well and transfectants resistant to 1 mg/ml gentamicin selected. Resistant colonies are expanded and then tested for their response to increasing concentrations of interferon gamma. The dose response of a selected clone is demonstrated.

Specifically, the following protocol will yield sufficient cells for 75 wells containing 200 ul of cells. Thus, it is either scaled up, or performed in multiple to generate sufficient cells for multiple 96 well plates. Jurkat cells are maintained in RPMI + 10% serum with 1% Pen-Strep. Combine 2.5 mls of OPTI-MEM (Life Technologies)

with 10 ug of plasmid DNA in a T25 flask. Add 2.5 ml OPTI-MEM containing 50 ul of DMRIE-C and incubate at room temperature for 15-45 mins.

- During the incubation period, count cell concentration, spin down the required number of cells (10^7 per transfection), and resuspend in OPTI-MEM to a final
5 concentration of 10^7 cells/ml. Then add 1ml of 1×10^7 cells in OPTI-MEM to T25 flask and incubate at 37°C for 6 hrs. After the incubation, add 10 ml of RPMI + 15% serum.

The Jurkat:GAS-SEAP stable reporter lines are maintained in RPMI + 10% serum, 1 mg/ml Gentamicin, and 1% Pen-Strep. These cells are treated with supernatants containing a polypeptide as produced by the protocol described in Example 11.

- 10 On the day of treatment with the supernatant, the cells should be washed and resuspended in fresh RPMI + 10% serum to a density of 500,000 cells per ml. The exact number of cells required will depend on the number of supernatants being screened. For one 96 well plate, approximately 10 million cells (for 10 plates, 100 million cells) are required.

- 15 Transfer the cells to a triangular reservoir boat, in order to dispense the cells into a 96 well dish, using a 12 channel pipette. Using a 12 channel pipette, transfer 200 ul of cells into each well (therefore adding 100, 000 cells per well).

- After all the plates have been seeded, 50 ul of the supernatants are transferred directly from the 96 well plate containing the supernatants into each well using a 12
20 channel pipette. In addition, a dose of exogenous interferon gamma (0.1, 1.0, 10 ng) is added to wells H9, H10, and H11 to serve as additional positive controls for the assay.

- The 96 well dishes containing Jurkat cells treated with supernatants are placed in an incubator for 48 hrs (note: this time is variable between 48-72 hrs). 35 ul samples
25 from each well are then transferred to an opaque 96 well plate using a 12 channel pipette. The opaque plates should be covered (using sellophene covers) and stored at -20°C until SEAP assays are performed according to Example 17. The plates containing the remaining treated cells are placed at 4°C and serve as a source of material for repeating the assay on a specific well if desired.

- 30 As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate Jurkat T cells. Over 30 fold induction is typically observed in the positive control wells.

Example 14: High-Throughput Screening Assay Identifying Myeloid Activity

The following protocol is used to assess myeloid activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate myeloid cells.

- 5 Myeloid cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The myeloid cell used in this assay is U937, a pre-monocyte cell line, although TF-1, HL60, or KG1 can be used.

- 10 To transiently transfect U937 cells with the GAS/SEAP/Neo construct produced in Example 12, a DEAE-Dextran method (Kharbanda et. al., 1994, Cell Growth & Differentiation, 5:259-265) is used. First, harvest 2×10^7 U937 cells and wash with PBS. The U937 cells are usually grown in RPMI 1640 medium containing 10% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 mg/ml streptomycin.

- 15 Next, suspend the cells in 1 ml of 20 mM Tris-HCl (pH 7.4) buffer containing 0.5 mg/ml DEAE-Dextran, 8 ug GAS-SEAP2 plasmid DNA, 140 mM NaCl, 5 mM KCl, 375 uM $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$, 1 mM MgCl_2 , and 675 uM CaCl_2 . Incubate at 37°C for 45 min.

- 20 Wash the cells with RPMI 1640 medium containing 10% FBS and then resuspend in 10 ml complete medium and incubate at 37°C for 36 hr.

The GAS-SEAP/U937 stable cells are obtained by growing the cells in 400 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 400 ug/ml G418 for couple of passages.

- 25 These cells are tested by harvesting 1×10^8 cells (this is enough for ten 96-well plates assay) and wash with PBS. Suspend the cells in 200 ml above described growth medium, with a final density of 5×10^5 cells/ml. Plate 200 ul cells per well in the 96-well plate (or 1×10^5 cells/well).

- 30 Add 50 ul of the supernatant prepared by the protocol described in Example 11. Incubate at 37°C for 48 to 72 hr. As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate U937 cells. Over 30 fold induction is typically observed in the positive control wells. SEAP assay the supernatant according to the protocol described in Example 17.

Example 15: High-Throughput Screening Assay Identifying Neuronal Activity.

When cells undergo differentiation and proliferation, a group of genes are activated through many different signal transduction pathways. One of these genes, EGR1 (early growth response gene 1), is induced in various tissues and cell types upon activation. The promoter of EGR1 is responsible for such induction. Using the EGR1 promoter linked to reporter molecules, activation of cells can be assessed.

Particularly, the following protocol is used to assess neuronal activity in PC12 cell lines. PC12 cells (rat phenochromocytoma cells) are known to proliferate and/or differentiate by activation with a number of mitogens, such as TPA (tetradecanoyl phorbol acetate), NGF (nerve growth factor), and EGF (epidermal growth factor). The EGR1 gene expression is activated during this treatment. Thus, by stably transfecting PC12 cells with a construct containing an EGR promoter linked to SEAP reporter, activation of PC12 cells can be assessed.

The EGR/SEAP reporter construct can be assembled by the following protocol. The EGR-1 promoter sequence (-633 to +1)(Sakamoto K et al., Oncogene 6:867-871 (1991)) can be PCR amplified from human genomic DNA using the following primers:

5' GCGCTCGAGGGATGACAGCGATAGAACCCCGG -3' (SEQ ID NO:6)

5' GCGAAGCTTCGCGACTCCCCGGATCCGCCTC-3' (SEQ ID NO:7)

Using the GAS:SEAP/Neo vector produced in Example 12, EGR1 amplified product can then be inserted into this vector. Linearize the GAS:SEAP/Neo vector using restriction enzymes XhoI/HindIII, removing the GAS/SV40 stuffer. Restrict the EGR1 amplified product with these same enzymes. Ligate the vector and the EGR1 promoter.

To prepare 96 well-plates for cell culture, two mls of a coating solution (1:30 dilution of collagen type I (Upstate Biotech Inc. Cat#08-115) in 30% ethanol (filter sterilized)) is added per one 10 cm plate or 50 ml per well of the 96-well plate, and allowed to air dry for 2 hr.

PC12 cells are routinely grown in RPMI-1640 medium (Bio Whittaker) containing 10% horse serum (JRH BIOSCIENCES, Cat. # 12449-78P), 5% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 ug/ml streptomycin on a precoated 10 cm tissue culture dish. One to four split is done every three to four days. Cells are removed from the plates by scraping and resuspended with pipetting up and down for more than 15 times.

Transfect the EGR/SEAP/Neo construct into PC12 using the Lipofectamine protocol described in Example 11. EGR-SEAP/PC12 stable cells are obtained by growing the cells in 300 ug/ml G418. The G418-free medium is used for routine

growth but every one to two months, the cells should be re-grown in 300 ug/ml G418 for couple of passages.

To assay for neuronal activity, a 10 cm plate with cells around 70 to 80% confluent is screened by removing the old medium. Wash the cells once with PBS (Phosphate buffered saline). Then starve the cells in low serum medium (RPMI-1640 containing 1% horse serum and 0.5% FBS with antibiotics) overnight.

The next morning, remove the medium and wash the cells with PBS. Scrape off the cells from the plate, suspend the cells well in 2 ml low serum medium. Count the cell number and add more low serum medium to reach final cell density as 5×10^5 cells/ml.

Add 200 ul of the cell suspension to each well of 96-well plate (equivalent to 1×10^5 cells/well). Add 50 ul supernatant produced by Example 11, 37°C for 48 to 72 hr. As a positive control, a growth factor known to activate PC12 cells through EGR can be used, such as 50 ng/ul of Neuronal Growth Factor (NGF). Over fifty-fold induction of SEAP is typically seen in the positive control wells. SEAP assay the supernatant according to Example 17.

Example 16: High-Throughput Screening Assay for T-cell Activity

NF- κ B (Nuclear Factor κ B) is a transcription factor activated by a wide variety of agents including the inflammatory cytokines IL-1 and TNF, CD30 and CD40, lymphotoxin-alpha and lymphotoxin-beta, by exposure to LPS or thrombin, and by expression of certain viral gene products. As a transcription factor, NF- κ B regulates the expression of genes involved in immune cell activation, control of apoptosis (NF- κ B appears to shield cells from apoptosis), B and T-cell development, anti-viral and antimicrobial responses, and multiple stress responses.

In non-stimulated conditions, NF- κ B is retained in the cytoplasm with I- κ B (Inhibitor κ B). However, upon stimulation, I- κ B is phosphorylated and degraded, causing NF- κ B to shuttle to the nucleus, thereby activating transcription of target genes. Target genes activated by NF- κ B include IL-2, IL-6, GM-CSF, ICAM-1 and class I MHC.

Due to its central role and ability to respond to a range of stimuli, reporter constructs utilizing the NF- κ B promoter element are used to screen the supernatants produced in Example 11. Activators or inhibitors of NF- κ B would be useful in treating

diseases. For example, inhibitors of NF- κ B could be used to treat those diseases related to the acute or chronic activation of NF- κ B, such as rheumatoid arthritis.

To construct a vector containing the NF- κ B promoter element, a PCR based strategy is employed. The upstream primer contains four tandem copies of the NF- κ B binding site (GGGGACTTTCCC) (SEQ ID NO:8), 18 bp of sequence complementary to the 5' end of the SV40 early promoter sequence, and is flanked with an XhoI site:
5':GCGGCCTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGAC
TTTCCATCCTGCCATCTCAATTAG:3' (SEQ ID NO:9)

The downstream primer is complementary to the 3' end of the SV40 promoter and is flanked with a Hind III site:

5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in the pB-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI and Hind III and subcloned into BLSK2-. (Stratagene)

Sequencing with the T7 and T3 primers confirms the insert contains the following sequence:

5':CTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGACTTTCC
ATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCCA
TCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACT
AATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTC
CAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTT:
3' (SEQ ID NO:10)

Next, replace the SV40 minimal promoter element present in the pSEAP2- promoter plasmid (Clontech) with this NF- κ B/SV40 fragment using XhoI and HindIII. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

In order to generate stable mammalian cell lines, the NF- κ B/SV40/SEAP cassette is removed from the above NF- κ B/SEAP vector using restriction enzymes SalI and NotI, and inserted into a vector containing neomycin resistance. Particularly, the NF- κ B/SV40/SEAP cassette was inserted into pGFP-1 (Clontech), replacing the GFP gene, after restricting pGFP-1 with SalI and NotI.

Once NF- κ B/SV40/SEAP/Neo vector is created, stable Jurkat T-cells are created and maintained according to the protocol described in Example 13. Similarly, the method for assaying supernatants with these stable Jurkat T-cells is also described in Example 13. As a positive control, exogenous TNF alpha (0.1, 1, 10 ng) is added to wells H9, H10, and H11, with a 5-10 fold activation typically observed.

Example 17: Assay for SEAP Activity

As a reporter molecule for the assays described in Examples 13-16, SEAP activity is assayed using the Tropix Phospho-light Kit (Cat. BP-400) according to the following general procedure. The Tropix Phospho-light Kit supplies the Dilution, Assay, and Reaction Buffers used below.

Prime a dispenser with the 2.5x Dilution Buffer and dispense 15 μ l of 2.5x dilution buffer into Optiplates containing 35 μ l of a supernatant. Seal the plates with a plastic sealer and incubate at 65°C for 30 min. Separate the Optiplates to avoid uneven heating.

Cool the samples to room temperature for 15 minutes. Empty the dispenser and prime with the Assay Buffer. Add 50 μ l Assay Buffer and incubate at room temperature 5 min. Empty the dispenser and prime with the Reaction Buffer (see the table below). Add 50 μ l Reaction Buffer and incubate at room temperature for 20 minutes. Since the intensity of the chemiluminescent signal is time dependent, and it takes about 10 minutes to read 5 plates on luminometer, one should treat 5 plates at each time and start the second set 10 minutes later.

Read the relative light unit in the luminometer. Set H12 as blank, and print the results. An increase in chemiluminescence indicates reporter activity.

Reaction Buffer Formulation:

# of plates	Rxn buffer diluent (ml)	CSPD (ml)
10	60	3
11	65	3.25
12	70	3.5
13	75	3.75
14	80	4
15	85	4.25
16	90	4.5
17	95	4.75
18	100	5
19	105	5.25
20	110	5.5
21	115	5.75
22	120	6

23	125	6.25
24	130	6.5
25	135	6.75
26	140	7
27	145	7.25
28	150	7.5
29	155	7.75
30	160	8
31	165	8.25
32	170	8.5
33	175	8.75
34	180	9
35	185	9.25
36	190	9.5
37	195	9.75
38	200	10
39	205	10.25
40	210	10.5
41	215	10.75
42	220	11
43	225	11.25
44	230	11.5
45	235	11.75
46	240	12
47	245	12.25
48	250	12.5
49	255	12.75
50	260	13

Example 18: High-Throughput Screening Assay Identifying Changes in Small Molecule Concentration and Membrane Permeability

Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium, sodium, and pH, as well as alter membrane potential. These alterations can be measured in an assay to identify supernatants which bind to receptors of a particular cell. Although the following protocol describes an assay for calcium, this protocol can easily be modified to detect changes in potassium, sodium, pH, membrane potential, or any other small molecule which is detectable by a fluorescent probe.

The following assay uses Fluorometric Imaging Plate Reader ("FLIPR") to measure changes in fluorescent molecules (Molecular Probes) that bind small molecules. Clearly, any fluorescent molecule detecting a small molecule can be used instead of the calcium fluorescent molecule, fluo-3, used here.

For adherent cells, seed the cells at 10,000 -20,000 cells/well in a Co-star black 96-well plate with clear bottom. The plate is incubated in a CO₂ incubator for 20 hours. The adherent cells are washed two times in Biotek washer with 200 ul of HBSS (Hank's Balanced Salt Solution) leaving 100 ul of buffer after the final wash.

A stock solution of 1 mg/ml fluo-3 is made in 10% pluronic acid DMSO. To load the cells with fluo-3, 50 ul of 12 ug/ml fluo-3 is added to each well. The plate is incubated at 37°C in a CO₂ incubator for 60 min. The plate is washed four times in the Biotek washer with HBSS leaving 100 ul of buffer.

5 For non-adherent cells, the cells are spun down from culture media. Cells are re-suspended to 2-5x10⁶ cells/ml with HBSS in a 50-ml conical tube. 4 ul of 1 mg/ml fluo-3 solution in 10% pluronic acid DMSO is added to each ml of cell suspension. The tube is then placed in a 37°C water bath for 30-60 min. The cells are washed twice with HBSS, resuspended to 1x10⁶ cells/ml, and dispensed into a microplate, 100
10 ul/well. The plate is centrifuged at 1000 rpm for 5 min. The plate is then washed once in Denley CellWash with 200 ul, followed by an aspiration step to 100 ul final volume.

For a non-cell based assay, each well contains a fluorescent molecule, such as fluo-3. The supernatant is added to the well, and a change in fluorescence is detected.

To measure the fluorescence of intracellular calcium, the FLIPR is set for the
15 following parameters: (1) System gain is 300-800 mW; (2) Exposure time is 0.4 second; (3) Camera F/stop is F/2; (4) Excitation is 488 nm; (5) Emission is 530 nm; and (6) Sample addition is 50 ul. Increased emission at 530 nm indicates an extracellular signaling event which has resulted in an increase in the intracellular Ca⁺⁺ concentration.

Example 19: High-Throughput Screening Assay Identifying Tyrosine Kinase Activity

The Protein Tyrosine Kinases (PTK) represent a diverse group of transmembrane and cytoplasmic kinases. Within the Receptor Protein Tyrosine Kinase
25 RPTK) group are receptors for a range of mitogenic and metabolic growth factors including the PDGF, FGF, EGF, NGF, HGF and Insulin receptor subfamilies. In addition there are a large family of RPTKs for which the corresponding ligand is unknown. Ligands for RPTKs include mainly secreted small proteins, but also membrane-bound and extracellular matrix proteins.

30 Activation of RPTK by ligands involves ligand-mediated receptor dimerization, resulting in transphosphorylation of the receptor subunits and activation of the cytoplasmic tyrosine kinases. The cytoplasmic tyrosine kinases include receptor associated tyrosine kinases of the src-family (e.g., src, yes, lck, lyn, fyn) and non-receptor linked and cytosolic protein tyrosine kinases, such as the Jak family, members
35 of which mediate signal transduction triggered by the cytokine superfamily of receptors (e.g., the Interleukins, Interferons, GM-CSF, and Leptin).

Because of the wide range of known factors capable of stimulating tyrosine kinase activity, the identification of novel human secreted proteins capable of activating tyrosine kinase signal transduction pathways are of interest. Therefore, the following protocol is designed to identify those novel human secreted proteins capable of activating the tyrosine kinase signal transduction pathways.

Seed target cells (e.g., primary keratinocytes) at a density of approximately 25,000 cells per well in a 96 well Loprodyne Silent Screen Plates purchased from Nalge Nunc (Naperville, IL). The plates are sterilized with two 30 minute rinses with 100% ethanol, rinsed with water and dried overnight. Some plates are coated for 2 hr with 100 ml of cell culture grade type I collagen (50 mg/ml), gelatin (2%) or polylysine (50 mg/ml), all of which can be purchased from Sigma Chemicals (St. Louis, MO) or 10% Matrigel purchased from Becton Dickinson (Bedford, MA), or calf serum, rinsed with PBS and stored at 4°C. Cell growth on these plates is assayed by seeding 5,000 cells/well in growth medium and indirect quantitation of cell number through use of alamarBlue as described by the manufacturer Alamar Biosciences, Inc. (Sacramento, CA) after 48 hr. Falcon plate covers #3071 from Becton Dickinson (Bedford, MA) are used to cover the Loprodyne Silent Screen Plates. Falcon Microtest III cell culture plates can also be used in some proliferation experiments.

To prepare extracts, A431 cells are seeded onto the nylon membranes of Loprodyne plates (20,000/200ml/well) and cultured overnight in complete medium. Cells are quiesced by incubation in serum-free basal medium for 24 hr. After 5-20 minutes treatment with EGF (60ng/ml) or 50 ul of the supernatant produced in Example 11, the medium was removed and 100 ml of extraction buffer ((20 mM HEPES pH 7.5, 0.15 M NaCl, 1% Triton X-100, 0.1% SDS, 2 mM Na₃VO₄, 2 mM Na₄P₂O₇ and a cocktail of protease inhibitors (# 1836170) obtained from Boehringer Mannheim (Indianapolis, IN) is added to each well and the plate is shaken on a rotating shaker for 5 minutes at 4°C. The plate is then placed in a vacuum transfer manifold and the extract filtered through the 0.45 mm membrane bottoms of each well using house vacuum. Extracts are collected in a 96-well catch/assay plate in the bottom of the vacuum manifold and immediately placed on ice. To obtain extracts clarified by centrifugation, the content of each well, after detergent solubilization for 5 minutes, is removed and centrifuged for 15 minutes at 4°C at 16,000 x g.

Test the filtered extracts for levels of tyrosine kinase activity. Although many methods of detecting tyrosine kinase activity are known, one method is described here.

Generally, the tyrosine kinase activity of a supernatant is evaluated by determining its ability to phosphorylate a tyrosine residue on a specific substrate (a

biotinylated peptide). Biotinylated peptides that can be used for this purpose include PSK1 (corresponding to amino acids 6-20 of the cell division kinase cdc2-p34) and PSK2 (corresponding to amino acids 1-17 of gastrin). Both peptides are substrates for a range of tyrosine kinases and are available from Boehringer Mannheim.

5 The tyrosine kinase reaction is set up by adding the following components in order. First, add 10ul of 5uM Biotinylated Peptide, then 10ul ATP/Mg₂⁺ (5mM ATP/50mM MgCl₂), then 10ul of 5x Assay Buffer (40mM imidazole hydrochloride, pH7.3, 40 mM beta-glycerophosphate, 1mM EGTA, 100mM MgCl₂, 5 mM MnCl₂, 0.5 mg/ml BSA), then 5ul of Sodium Vanadate(1mM), and then 5ul of water. Mix the
10 components gently and preincubate the reaction mix at 30°C for 2 min. Initiate the reaction by adding 10ul of the control enzyme or the filtered supernatant.

The tyrosine kinase assay reaction is then terminated by adding 10 ul of 120mM EDTA and place the reactions on ice.

Tyrosine kinase activity is determined by transferring 50 ul aliquot of reaction
15 mixture to a microtiter plate (MTP) module and incubating at 37°C for 20 min. This allows the streptavidin coated 96 well plate to associate with the biotinylated peptide. Wash the MTP module with 300ul/well of PBS four times. Next add 75 ul of anti-phosphotyrosine antibody conjugated to horse radish peroxidase(anti-P-Tyr-
20 POD(0.5u/ml)) to each well and incubate at 37°C for one hour. Wash the well as above.

Next add 100ul of peroxidase substrate solution (Boehringer Mannheim) and incubate at room temperature for at least 5 mins (up to 30 min). Measure the absorbance of the sample at 405 nm by using ELISA reader. The level of bound peroxidase activity is quantitated using an ELISA reader and reflects the level of
25 tyrosine kinase activity.

Example 20: High-Throughput Screening Assay Identifying Phosphorylation Activity

As a potential alternative and/or compliment to the assay of protein tyrosine
30 kinase activity described in Example 19, an assay which detects activation (phosphorylation) of major intracellular signal transduction intermediates can also be used. For example, as described below one particular assay can detect tyrosine phosphorylation of the Erk-1 and Erk-2 kinases. However, phosphorylation of other molecules, such as Raf, JNK, p38 MAP, Map kinase kinase (MEK), MEK kinase,
35 Src, Muscle specific kinase (MuSK), IRAK, Tec, and Janus, as well as any other

phosphoserine, phosphotyrosine, or phosphothreonine molecule, can be detected by substituting these molecules for Erk-1 or Erk-2 in the following assay.

Specifically, assay plates are made by coating the wells of a 96-well ELISA plate with 0.1ml of protein G (1ug/ml) for 2 hr at room temp. (RT). The plates are then
5 rinsed with PBS and blocked with 3% BSA/PBS for 1 hr at RT. The protein G plates are then treated with 2 commercial monoclonal antibodies (100ng/well) against Erk-1 and Erk-2 (1 hr at RT) (Santa Cruz Biotechnology). (To detect other molecules, this step can easily be modified by substituting a monoclonal antibody detecting any of the above described molecules.) After 3-5 rinses with PBS, the plates are stored at 4°C
10 until use.

A431 cells are seeded at 20,000/well in a 96-well Loprodyne filterplate and cultured overnight in growth medium. The cells are then starved for 48 hr in basal medium (DMEM) and then treated with EGF (6ng/well) or 50 ul of the supernatants obtained in Example 11 for 5-20 minutes. The cells are then solubilized and extracts
15 filtered directly into the assay plate.

After incubation with the extract for 1 hr at RT, the wells are again rinsed. As a positive control, a commercial preparation of MAP kinase (10ng/well) is used in place of A431 extract. Plates are then treated with a commercial polyclonal (rabbit) antibody (1ug/ml) which specifically recognizes the phosphorylated epitope of the Erk-1 and
20 Erk-2 kinases (1 hr at RT). This antibody is biotinylated by standard procedures. The bound polyclonal antibody is then quantitated by successive incubations with Europium-streptavidin and Europium fluorescence enhancing reagent in the Wallac DELFIA instrument (time-resolved fluorescence). An increased fluorescent signal over background indicates a phosphorylation.

25

Example 21: Method of Determining Alterations in a Gene Corresponding to a Polynucleotide

RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is be isolated. cDNA is then generated from
30 these RNA samples using protocols known in the art. (See, Sambrook.) The cDNA is then used as a template for PCR, employing primers surrounding regions of interest in SEQ ID NO:X. Suggested PCR conditions consist of 35 cycles at 95°C for 30 seconds; 60-120 seconds at 52-58°C; and 60-120 seconds at 70°C, using buffer solutions described in Sidransky, D., et al., Science 252:706 (1991).

35 PCR products are then sequenced using primers labeled at their 5' end with T4 polynucleotide kinase, employing SequiTherm Polymerase. (Epicentre Technologies).

The intron-exon borders of selected exons is also determined and genomic PCR products analyzed to confirm the results. PCR products harboring suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

PCR products is cloned into T-tailed vectors as described in Holton, T.A. and Graham, M.W., Nucleic Acids Research, 19:1156 (1991) and sequenced with T7 polymerase (United States Biochemical). Affected individuals are identified by mutations not present in unaffected individuals.

Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated according to Example 2 are nick-translated with digoxigenindeoxy-uridine 5'-triphosphate (Boehringer Mannheim), and FISH performed as described in Johnson, Cg. et al., Methods Cell Biol. 35:73-99 (1991). Hybridization with the labeled probe is carried out using a vast excess of human cot-1 DNA for specific hybridization to the corresponding genomic locus.

Chromosomes are counterstained with 4,6-diamino-2-phenylidole and propidium iodide, producing a combination of C- and R-bands. Aligned images for precise mapping are obtained using a triple-band filter set (Chroma Technology, Brattleboro, VT) in combination with a cooled charge-coupled device camera (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson, Cv. et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and chromosomal fractional length measurements are performed using the ISee Graphical Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the genomic region hybridized by the probe are identified as insertions, deletions, and translocations. These alterations are used as a diagnostic marker for an associated disease.

Example 22: Method of Detecting Abnormal Levels of a Polypeptide in a Biological Sample

A polypeptide of the present invention can be detected in a biological sample, and if an increased or decreased level of the polypeptide is detected, this polypeptide is a marker for a particular phenotype. Methods of detection are numerous, and thus, it is understood that one skilled in the art can modify the following assay to fit their particular needs.

For example, antibody-sandwich ELISAs are used to detect polypeptides in a sample, preferably a biological sample. Wells of a microtiter plate are coated with specific antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal or polyclonal and are produced by the method described in Example 10.

The wells are blocked so that non-specific binding of the polypeptide to the well is reduced.

The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to validate results. The plates are then washed three times with deionized or distilled water to remove unbounded polypeptide.

Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove unbounded conjugate.

Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate (NPP) substrate solution to each well and incubate 1 hour at room temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale). Interpolate the concentration of the polypeptide in the sample using the standard curve.

Example 23: Formulating a Polypeptide

The secreted polypeptide composition will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the secreted polypeptide alone), the site of delivery, the method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" for purposes herein is thus determined by such considerations.

As a general proposition, the total pharmaceutically effective amount of secreted polypeptide administered parenterally per dose will be in the range of about 1 µg/kg/day to 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01 mg/kg/day, and most preferably for humans between about 0.01 and 1 mg/kg/day for the hormone. If given continuously, the secreted polypeptide is typically administered at a dose rate of about 1 µg/kg/hour to about 50 µg/kg/hour, either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes and the interval following treatment for responses to occur appears to vary depending on the desired effect.

Pharmaceutical compositions containing the secreted protein of the invention are administered orally, rectally, parenterally, intracisternally, intravaginally,

intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

The secreted polypeptide is also suitably administered by sustained-release systems. Suitable examples of sustained-release compositions include semi-permeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules.

Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman, U. et al., Biopolymers 22:547-556 (1983)), poly (2-hydroxyethyl methacrylate) (R. Langer et al., J. Biomed. Mater. Res. 15:167-277 (1981), and R. Langer, Chem. Tech. 12:98-105 (1982)), ethylene vinyl acetate (R. Langer et al.) or poly-D-(-)-3-hydroxybutyric acid (EP 133,988). Sustained-release compositions also include liposomally entrapped polypeptides. Liposomes containing the secreted polypeptide are prepared by methods known per se: DE 3,218,121; Epstein et al., Proc. Natl. Acad. Sci. USA 82:3688-3692 (1985); Hwang et al., Proc. Natl. Acad. Sci. USA 77:4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008; U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the optimal secreted polypeptide therapy.

For parenteral administration, in one embodiment, the secreted polypeptide is formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form (solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. For example, the formulation preferably does not include oxidizing agents and other compounds that are known to be deleterious to polypeptides.

Generally, the formulations are prepared by contacting the polypeptide uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

The carrier suitably contains minor amounts of additives such as substances that enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, manose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, poloxamers, or PEG.

The secreted polypeptide is typically formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of about 3 to 8. It will be understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

Any polypeptide to be used for therapeutic administration can be sterile. Sterility is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). Therapeutic polypeptide compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Polypeptides ordinarily will be stored in unit or multi-dose containers, for example, sealed ampoules or vials, as an aqueous solution or as a lyophilized formulation for reconstitution. As an example of a lyophilized formulation, 10-ml vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous polypeptide solution, and the resulting mixture is lyophilized. The infusion solution is prepared by reconstituting the lyophilized polypeptide using bacteriostatic Water-for-Injection.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the polypeptides of the present invention may be employed in conjunction with other therapeutic compounds.

Example 24: Method of Treating Decreased Levels of the Polypeptide

It will be appreciated that conditions caused by a decrease in the standard or normal expression level of a secreted protein in an individual can be treated by administering the polypeptide of the present invention, preferably in the secreted form. Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a pharmaceutical composition comprising an amount of the polypeptide to increase the activity level of the polypeptide in such an individual.

For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the polypeptide for six consecutive days. Preferably, the polypeptide is in the secreted form. The exact details of the dosing scheme, based on administration and formulation, are provided in Example 23.

Example 25: Method of Treating Increased Levels of the Polypeptide

Antisense technology is used to inhibit production of a polypeptide of the present invention. This technology is one example of a method of decreasing levels of a polypeptide, preferably a secreted form, due to a variety of etiologies, such as cancer.

For example, a patient diagnosed with abnormally increased levels of a polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well tolerated. The formulation of the antisense polynucleotide is provided in Example 23.

Example 26: Method of Treatment Using Gene Therapy

One method of gene therapy transplants fibroblasts, which are capable of expressing a polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and separated into small pieces. Small chunks of the tissue are placed on a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS, penicillin and streptomycin) is added. The flasks are then incubated at 37°C for approximately one week.

At this time, fresh media is added and subsequently changed every several days. After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long
5 terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

The cDNA encoding a polypeptide of the present invention can be amplified using PCR primers which correspond to the 5' and 3' end sequences respectively as set
10 forth in Example 1. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The ligation mixture is then used to
15 transform bacteria HB101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene of interest properly inserted.

The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is
20 then added to the media and the packaging cells transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media,
25 containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is removed and replaced with fresh media. If the titer of virus is high, then virtually all fibroblasts will be infected and no selection is
30 required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine whether protein is produced.

The engineered fibroblasts are then transplanted onto the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

- 5 The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other disclosures) in the Background of the Invention, Detailed Description, and Examples is hereby incorporated herein by reference.

(1) GENERAL INFORMATION:

(i) APPLICANT: Human Genome Sciences, Inc. et al.
(ii) TITLE OF INVENTION: 87 Human Secreted Proteins
(iii) NUMBER OF SEQUENCES: 323
(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
(B) COMPUTER: HP Vectra 486/33
(C) OPERATING SYSTEM: MSDOS version 6.2
(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: March 19, 1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 733 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

164

GGGATCCGGA GCCCAAATCT TCTGACAAAA CTCACACATG CCCACCGTGC CCAGCACCTG 60
 AATTTCGAGGG TGCACCGTCA GTCTTCCTCT TCCCCCAAA ACCCAAGGAC ACCCTCATGA 120
 5 TCTCCCGGAC TCCTGAGGTC ACATGCGTGG TGGTGGACGT AAGCCACGAA GACCCTGAGG 180
 TCAAGTTCAA CTGGTACGTG GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCGCGGG 240
 AGGAGCAGTA CAACAGCACG TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT 300
 10 GGCTGAATGG CAAGGAGTAC AAGTGCAAGG TCTCCAACAA AGCCCTCCCA ACCCCCATCG 360
 AGAAAACCAT CTCAAAGCC AAAGGGCAGC CCCGAGAACC ACAGGTGTAC ACCCTGCCCC 420
 15 CATCCCGGGA TGAGCTGACC AAGAACCAGG TCAGCCTGAC CTGCCTGGTC AAAGGCTTCT 480
 ATCCAAGCGA CATCGCCGTG GAGTGGGAGA GCAATGGGCA GCCGGAGAAC AACTACAAGA 540
 CCACGCCTCC CGTGCTGGAC TCCGACGGCT CCTTCTTCCT CTACAGCAAG CTCACCGTGG 600
 20 ACAAGAGCAG GTGGCAGCAG GGAACGTCT TCTCATGCTC CGTGATGCAT GAGGCTCTGC 660
 ACAACCACTA CACGCAGAAG AGCCTCTCCC TGTCTCCGGG TAAATGAGTG CGACGGCCGC 720
 25 GACTCTAGAG GAT 733

30 (2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Trp Ser Xaa Trp Ser
 1 5

40

45 (2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

55 GCGCCTCGAG ATTTCCCCGA AATCTAGATT TCCCCGAAAT GATTTCCCCG AAATGATTTT 60
 CCCGAAATAT CTGCCATCTC AATTAG 86

60

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GCGGCAAGCT TTTTGCAAAG CCTAGGC

27

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTCGAGATTT CCCCGAAATC TAGATTTCCT CGAAATGATT TCCCCGAAAT GATTTCCTCCG 60
AAATATCTGC CATCTCAATT AGTCAGCAAC CATAGTCCCG CCCCTAACTC CGCCCATCCC 120
GCCCCTAACT CCGCCCAAGT CCGCCCATTC TCCGCCCAT GGCTGACTAA TTTTTTTTAT 180
TTATGCAGAG GCCGAGGCCG CCTCGGCCTC TGAGCTATTC CAGAAGTAGT GAGGAGGCTT 240
TTTTGGAGGC CTAGGCTTTT GCAAAAAGCT T 271

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GCGCTCGAGG GATGACAGCG ATAGAACCCC GG

32

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

5

GCGAAGCTTC GCGACTCCCC GGATCCGCCT C

31

10

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

20

GGGGACTTTC CC

12

25

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

35

GCGGCCTCGA GGGGACTTTC CCGGGGACTT TCCGGGGACT TTCCGGGACT TTCCATCCTG

60

CCATCTCAAT TAG

73

40

(2) INFORMATION FOR SEQ ID NO: 10:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CTCGAGGGGA CTTTCCCGGG GACTTTCCGG GGACTTTCCG GGACTTTCCA TCTGCCATCT

60

55

CAATTAGTCA GCAACCATAG TCCCGCCCCCT AACTCCGCCC ATCCCGCCCC TAACTCCGCC

120

CAGTTCCGCC CATCTCCGC CCCATGGCTG ACTAATTTT TTTATTTATG CAGAGGCCGA

180

GGCCGCCTCG GCCTCTGAGC TATTCCAGAA GTAGTGAGGA GGCTTTTGTG GAGGCCTAGG

240

60

CTTTTGCAAA AAGCTT

256

5

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1679 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

15

GCAGCGCACC CGGGCGATCG CTTCACGGAT GCGGACGACG TAGCCATCCT TACCTACGTG 60

AAGGAAAATG CCCGCTCGCC CAGCTCCGTC ACCGGTAACG CCTTGTGGAA AGCGATGGAG 120

20

AAGAGCTCGC TCACGCAGCA CTCGTGGCAG TCCCTGAAGG ACCGCTACCT CAAGCACCTG 180

CGGGGCCAGG AGCATAAGTA CCTGCTGGGG GACGCGCCGG TGAGCCCCTC CTCCCAGAAG 240

CTCAAGCGGA AGGCGGAGGA GGACCCGGAG GCCGCGGATA GCGGGGAACC ACAGAATAAG 300

25

AGAACTCCAG ATTTGCCTGA AGAAGAGTAT GTGAAGGAAG AAATCCAGGA GAATGAAGAA 360

GCAGTCAAAA AGATGCTTGT GGAAGCCACC CGGGAGTTTG AGGAGGTTGT GGTGGATGAG 420

30

AGCCCTCCTG ATTTTGAAAT ACATATAACT ATGTGTGATG ATGATCCACC CACACCTGAG 480

GAAGACTCAG AAACACAGCC TGATGAGGAG GAAGAAGAAG AAGAAGAAAA AGTTTCTCAA 540

CCAGAGGTGG GAGCTGCCAT TAAGATCATT CGGCAGTTAA TGGAGAAGTT TAACCTGGAT 600

35

CTATCAACAG TTACACAGGC CTTCTAAAAA AATAGTGGTG AGCTGGAGGC TACTTCCGCC 660

TTCTTAGCGT CTGGTCAGAG AGCTGATGGA TATCCCATT TGGTCCGACA AGATGACATA 720

GATTTGCAAA AAGATGATGA GGATACCAGA GAGGCATTGG TCAAAAAATT TGGTGCTCAG 780

AATGTAGCTC GGAGGATTGA ATTTCGAAAG AAATAATTGG CAAGATAATG AGAAAAGAAA 840

AAAGTCATGG TAGGTGAGGT GGTAAAAAAA AATTGTGACC AATGAACTTT AGAGAGTTCT 900

45

TGCATTGGAA CTGGCACTTA TMTCTGACC ATCGCTGCTG TTGCTCTGTG AGTCCTAGAT 960

TTTTGTAGCC AAGCAGAGTT GTAGAGGGGG ATAAAAAGAA AAGAAATTGG ATGTATTTAC 1020

AGCTGTCCTT GAACAAGTAT CAATGTGTTT ATGAAAGGAA GATCTAAATC AGACAGGAGT 1080

TGGTCTACAT AGTAGTAATC CATGTGTGGA ATGGAACCCCT TGCTATAGTA GTGACAAAGT 1140

GAAAGGAAAT TTAGGAGGCA TAGGCCATTT CAGGCAGCAT AAGTAATCTC CTGTCCTTTG 1200

55

GCAGAAGCTC CTTTAGATTG GGATAGATT CAAATAAAGA ATCTAGAAAT AGGAGAAGAT 1260

TTAATTATGA GGCCTTGAAC ACGGATTATC CCCAAACCCT TGTCATTTCC CCCAGTGAGC 1320

60

TCTGATTTCT AGACTGCTTT GAAAATGCTG TATTCATTTT GCTAACTTAG TATTTGGGTA 1380

5 CCCTGCTCTT TGGCTGTCTT TTTTGTGGAG CCCTTCTCAG TCAAGTCTGC CGGATGTCTT 1440
 TCTTTACCTA CCCCTCAGTT TCCCTTAAAA CGCGCACACA ACTCTAGAGA GTGTTAAGAA 1500
 TAATGTTACT TGGTTAATGT GTTATTTATT GAGTATGTGT TGTGCTAAGC ATTGTGTTAG 1560
 ATTTAAAAAA TTAGTGGATT GACTCCACTT TGTGTGTGTG TTTTCATTGT TGAAAATAAA 1620
 10 TATAACTTTG TATTCGAAAA AAAAAAAAAA AAAATNRCTG CGGNCCGACA AGGGAATTC 1679

15 (2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1830 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

25 GCGACCGCGC CCTTCAGCTA GCTCGCTCGC TCGCTCTGCT TCCCTGCTGC CGGCTGCGCA 60
 TGGCTTNGGC GTTGGCGGCG CTGGCGGCGG TCGAGCNGCC TGCGSAGCCG GTACCAGCAG 120
 TTGCAGAATG AAGAAGAGTC TGGAGAACCT GAACAGGCTG CAGGTGATGC TCCTCCACCT 180
 30 TACAGCAGCA TTTCTGCAGA GAGCGCACAT NATTTTGA CTACAAGGATGA GTCTGGGTTT 240
 CCAAAGCCCC CATCTTACAA TGTAGCTACA AACTTGCCCA GTTATGATGA AGCGGAGAGG 300
 35 ACCAAGGCTG AAGCTACTAT CCCTTTGGTT CCTGGGAGAG ATGAGGATTT TGTGGGTCGG 360
 GATGATTTTG ATGATGCTGA CCAGCTGAGG ATAGGAAATG ATGGGATTTT CATGTTAACT 420
 TTTTTCATGG CATTCTCTTT TAACTGGATT GGGTTTCTCC TGTCTTTTGG CCTGACCACT 480
 40 TCAGCTGCAG GAAGGTATGG GGCCATTTC A GATTGCTC TCTCTCTAAT TAAATGGATC 540
 CTGATTGTCA GGTTTTCCAC CTATTTCCCT GGATATTTTG ATGGTCAGTA CTGGCTCTGG 600
 45 TGGGTGTTCC TTGTTTTAGG CTTTCTCCTG TTTCTCAGAG GATTTATCAA TTATGCAAAA 660
 GTTCGGAAGA TGCCAGAAAC TTTCTCAAAT CTCCCCAGGA CCAGAGTTCT CTTTATTTAT 720
 TAAAGATGTT TTCTGGCAAA GGCTTTCCTG CATTTATGAA TTCTCTCTCA AGAAGCAAGA 780
 50 GAACACCTGC AGGAAGTGAA TCAAGATGCA GAACACAGAG GAATAATCAC CTGCTTTAAA 840
 AAAATAAAGT ACTGTTGAAA AGATCATTTT TCTCTATTTG TTCCTAGGTG TAAATTTTAA 900
 55 ATAGTTAATG CAGAATTCTG TAATCATTGA ATCATTAGTG GTTAATGTTT GAAAAAGCTC 960
 TTGCAATCAA GTCTGTGATG TATTAATAAT GCCTTATATA TTGTTTGTAG TCATTTTAAG 1020
 TAGCATGAGC CATGTCCCTG TAGTCGGTAG GGGGCAGTCT TGCTTTATTC ATCCTCCATC 1080
 60

	TCAAAATGAA CTGGAATTA AATATTGTAA GATATGTATA ATGCTGGCCA TTTTAAAGGG	1140
	GTTTCTCAA AAGTTAACT TTTGTTATGA CTGTGTTTTT GCACATAATC CATATTTGCT	1200
5	GTTCAAGTTA ATCTAGAAAT TTATTCAATT CTGTATGAAC ACCTGGAAGC AAAATCATAG	1260
	TGCAAAAATA CATTTAAGGT GTGGTCAAAA ATAAGTCTTT AATTGGTAAA TAATAAGCAT	1320
	TAATTTTTTA TAGCCTGTAT TCACAATTCT GCGGTACCTT ATTGTACCTA AGGGATTCTA	1380
10	AAGGTGTTGT CACTGTATAA AACAGAAAGC ACTAGGATAC AAATGAAGCT TAATTACTAA	1440
	AATGTAATTC TTGACACTCT TTCTATAATT AGCGTTCTTC ACCCCCACCC CCACCCCCAC	1500
15	CCCCCTTATT TTCCTTTTGT CTCCTGGTGA TTAGGCCAAA GTCTGGGAGT AAGGAGAGGA	1560
	TTAGGTACTT AGGAGCAAAG AAAGAAGTAG CTTGGAACCTT TTGAGATGAT CCCTAACATA	1620
	CTGTACTACT TGCTTTTACA ATGTGTTAGC AGAAACCACT GGGTTATAAT GTAGAATGAT	1680
20	GTGCTTTC TG CCAAGTGGT AATTCATCTT GGTTTGCTAT GTTAAACTG TAAATACAAC	1740
	AGAACATTAA TAAATATCTC TTGTGTAGCA CCTTTTAAAA AAAAAAAAAA AAAAAAAAAA	1800
25	AAAAAAAAA AANCCCGGGG GGGGGCCCN	1830

30 (2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

40	TGTTTGAAGT TGTTACTTTT GTTTACAGCA AAGTTTGATG TAGTGTGCAG TAGTGAGCTC	60
	TAGACTGATC TTTTCTAAA TCAGAAAGTG ATTAAAGTAT GCACAACCAA AGGCAGGTTT	120
	TTCTTTTTCA TTTATTCAGC AACTATTTAT TAAGCATCAA CTCGTGCGCA GGCACGTTAC	180
45	TAGCTGCTAC ATACTGTCTG AACATGACAT ACGGTTAAGT AACTTTACAA TTATTATCAA	240
	ATACTTCAAT GTAGATATTT CTTAAGTTGA AATAGCATTA ACTAGGATAA TGCTTTCATG	300
50	TTATTTTATT TGTCTTGTGA TAGAAATTCA ACTTTGTACC ATCTTAAAC TAGGTTGCTA	360
	TAAAAATAGG AGGATGAAGT CAATAAAGTT TATGCCAGTT TAAAACTGG AAGGAAAAGG	420
	TAAGAGCTCT CCATTATAAA ATAGTTGCAT TCGGTTAATT TTTACACATT AGTGCATTGC	480
55	GATATCAAC TGGCCCTCAA TGAAGCATT AAGTGCTTGG AATTTTACTA AACTGACTTT	540
	TTTGCAACTT TGGGAGATTT TTGAGGGGAG TGTGAAAAAT TGCCAAACAC TCACCTCTTA	600
60	CTCAAACTT CAAATAAAAT ACACATTTTC AAGAGGGAGC ACCTTTTATA TTTGATAAGT	660

5 TTTCAATTATA AACCTTATAA TACCAGTCAC AAAGAGGTTG TCTGTCTATG GTTTAGCAAA 720
 CATTGCTTT TCTTTTGGGA AGTGTGATTG CAATGTCAGA ACAGAAAGTG AGAAAACACT 780
 GCCAGCGGTG ATTGCTACTT GAGGTAGTTT TTTACAACATA CCATTTCCCC TCCATGAAAT 840
 TATGTGAAAT TTATTTTATC TTTGGGAAAA GTTGAGAAGA TAGTAAAAGA ATTAGGAATT 900
 10 TAAAATTACA GGGAAAAATA TGTAAGTGAA AAGCAATAAA TATTTTGTTT ACTTTGCTAT 960
 CAAGATGTTT ACTATCAGAT ATTTATTATA TGGCAGCAAT TTATATTTT AATCATTGCC 1020
 15 CATTAATAGA CGCAGTAAAA TATTTTGTGA TCAGACATTT GGGGTTTGTA TGTGCATTAA 1080
 AATTGCTCTT TGTACTGTAA GTTACTGTTA ATTTGAATAT TTTATGAAC TGTCTCCCTG 1140
 TGCCTTTATA ATATAAGTT GTTCTACAA CTTTAATGA TCTTAATAAA GAATACTTTA 1200
 20 AGAAAAAAA AA 1212

25 (2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2061 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

35 GGTTTTCCTC CGACTTCCGG ACATCTCCCT GGGAGTCGCG CAGAGTGGAG TCAAAGGCAA 60
 CCAGTGCTCG CTGCGGTCTC TGGGGATCGG GACCGCGGCG GCGGCCCCG AGCGGGATGT 120
 40 TCCGGGGCTT GAGCAGTTGG TTGGGCTTGC AGCAGCCGGT GGCAGGCGGT GGCAGCCCA 180
 ATGGAGATGC TCCACCCGAG CAGCCGTCCG AGACGGTGGC TGAGTCTGCG GAGGAGGAGC 240
 TGCAGCAAGC GGGAGACCAG GAGCTCCTCC ACCAGGCCAA AGACTTCGGC AACTATTTAT 300
 45 TTAACCTTGC ATCTGCTGCC AAAAAAAGA TAACTGAATC AGTTGCTGAA ACAGCACAAA 360
 CAATAAAGAA ATCCGTAGAA GAAGGAAAAA TAGATGGCAT CATTGACAAG ACAATTATAG 420
 50 GAGATTTTCA GAAGGAACAG AAAAAATTG TTGAAGAGCA ACATACAAAG AAGTCAGAAG 480
 CAGCTGTGCC CCCATGGGTT GACACTAACG ATGAAGAAAC AATTCAACAA CAAATTTTGG 540
 CCTTATCAGC TGACAAGAGG AATTTCTTTC GTGACCCTCC GGCTGGCGTG CAATTTAATT 600
 55 TCGACTTTGA TCAGATGTAC CCCGTGGCCC TGGTCATGCT CCAGGAGGAT GAGCTGCTAR 660
 CAAGATGAGA TTTGCCCTCG TTCTAAACT TGTGAAGGAA GAAGTGTCTT GGAGGAACATA 720
 60 CTTTACC GC GTCTCCCTGA TTAAGCAGTC AGCCAGCTC ACGGCCCTGG CTGCCCCAACA 780

GCAGGCCGCA GGGAAGGGAG GAGAAGAGCA ATGGCAGAGA GCAAGATTG CCGCTGGAGA 840
GGCAGTACGG CCCAAAACGC CACCCGTTGT AATCAAATCT CAGCTTAAAA CTCAAGAGGA 900
5 TGAGGAAGAA ATTTCTACTA GCCCAGGTGT TTCTGAGTTT GTCAGTGATG CCTTCGATGC 960
CTGTAACCTA AATCAGGAAG ATCTAAGGAA AGAAATGGAG CAACTAGTGC TTGACAAAAA 1020
10 GCAAGAGGAG ACAGCCGTAC TGGAAGAGGA TTCTGCAGAT TGGGAAAAAG AACTGCAGCA 1080
GGAACITCAA GAATATGAAG TGGTGACAGA ATCTGAAAAA CGAGATGAAA ACTGGGATAA 1140
GGAAATAGAG AAAATGCTTC AAGAGGAAAA TTAGCTGTTC CTGAAATAGA AGAATAATCC 1200
15 TTAACAGTCT GCAAACCTGAC ATTAAATTCT AGATGTTGAC AATTACTGAA TCAGAAGGCA 1260
TGAAAGAGTA TAATTTTATG AAATTCAAAA TTATTCTTTT TTCAAGTTGA AACTTGCCTC 1320
TTCTACTTTA AAAAAGTATA TAGAACAGTT ACTTCTAATA ATCAGAAAGA GATGTTTTAT 1380
20 AGAACATTTC TTTAATATAA AGTTAGAGAT GTCTTCATAG GCAGTATGGC TATCTTTGCC 1440
ACAGAAACAT AAGTAAATTT TTAGAGTTCT GTTTTCCATG AGGTCAAAAA TATAATTTAT 1500
25 TCCTCAGTCA TGGTTTCTA AATATCTGTA CTCCACATTC CATTTTAATT GATATGAGGG 1560
TGTAAAGTA CCTACTTAAT GGGTTGATTA CTATCAAAAT GACCAAATTA TACCAAAGAA 1620
CTTAAGAGGA AGCACTTTCA GAACTATTC AATTGCCAGGT ATTTTCTAAA ATTCCACCTG 1680
30 AAAGCCAAAA GATAAATAC ATNAGTTGGA TTTTAATGAT ATAAGCATCA CACAATTTTA 1740
CATTAAGAAA TACTGTGCAG CCCATGCGTG GTGGCTCAGG CCTGTAATCC CAGCANTTTG 1800
35 GGAGGCCGAG GTGGGCAGAT CACCGGAGGT CAGGAGTTCG AGACCAGCCT TGCCAACATA 1860
GTGAAACCCT GTCTTTACTA AAAATACAAA AATTAGCCGG GCATGGTGGC AGGCACCTGT 1920
AATCCAGCT ACTAGGGAGG CTTTGAACC CAGGAGGCAG AGGTTGCAGC GAGCTGAGAT 1980
40 CGCGCCACTG CACTCCAGCC TGGGTGATAG AGTGAGATTC AGTCTCAAAA AAAAAAAAAA 2040
AAAAAAAAA AATGACCTCG A 2061

45

(2) INFORMATION FOR SEQ ID NO: 15:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CCCTTCATCT GCGTTGCCAG GAACCCTGTC AGCAGAAACT TCTCAAGCCC CATCCTTGCC 60
60 AGGAAGCTCT GTGAAGGTGC TGCTGATGAC CCAGATTCCT CCATGGTCCT CCTGTGTCTC 120

172

CTGTTGGTGC CCCTCCTGCT CAGTCTCTTT GTACTGGGGC TATTTCTTTG GTTCTGAAG 180
 5 AGAGAGAGAC AAGAAGAGTA CATTGAAGAG AAGAAGAGAG TGGACATTTG TCGGGAAACT 240
 CCTAACATAT GCCCCCATTC TGGAGAGAAC ACAGAGTACG ACACAATCCC TCACACTAAT 300
 AGAACAATCC TAAAGGAAGA TCCAGCAAAT ACGGTTTACT CCACTGTGGA AATACCGAAA 360
 10 AAGATGGAAA ATCCCCACTC ACTGCTCAGC ATGCCAGACA CACCAAGGCT ATTTGCCTAT 420
 GAGAATGTTA TCTAGACAGC AGTGCCTCC CCTAAGTCTC TGCTCAAAAA AAAAAAATT 480
 15 CTCGGCCCAA AGAAAAAAT CAGAAGAATT CACTGATTTG ACTAGAAACA TCAAGGAAGA 540
 ATGAAGAACG TTGACTTTTT TCCAGGATAA ATTATCTCTG ATGCTTCTTT AGATTTAAGA 600
 GTTCATAATT CCATCCACTG CTGAGAAATC TCCTCAAACC CAGAAGGTTT AATCACTTCA 660
 20 TCCCAAAAAT GGGATTTGTA ATGTCAGCAA ACCATAAAAA AAGTGCTTAG AAGTATTCCT 720
 ATAAAAATGT AAATGCAAGG TCACACATAT TAATGACAGC CTGTTGTATT AATGATGGCT 780
 25 CCAGGTCAGT GTCTGGAGTT TCATTCCATC CCAGGGCTTG GATGTCAGGA TTATACCAAG 840
 AGTCTTGCTA CCAGGAGGGC AAGAAGACCA AACAGACAG ACAAGTCCAG CAGAAGCAGA 900
 TGCACCTGAC AAAAATGGAT GTATTAATTG GCTCTATAAA CTATGTGCCC AGCAYTATGC 960
 30 TGAGCTTACA CTAATTGGTC AGACATGCTG TCTGCCCTCA TGAAATTGGC TCCAAATGAW 1020
 TGAAC TACTT TCATGAGCAG TTGTAGCAGG CCTGACCACA GATTCCCAGA GGGCCAGGTG 1080
 35 TGGATCCACA GGACTTGAAG GTCAAAGTTC ACAAAGATGA AGAATCAGGG TAGCTGACCA 1140
 TGTMTGGCAG ATACTATAAT GGAGACACAG AAGTGTGCAT GGCCCAAGGA CAAGGACCTC 1200
 CAGCCAGGCT TCATTTATGC ACTTGTCTGC AAAAGAAAAG TCTAGGTTTT AAGGCTGTGC 1260
 40 CAGAACCCAT CCCAATAAAG AGACCGAGTC TGAAGTCACA TTGTAAATCT AGTGTAGGAG 1320
 ACTTGGAGTC AGGCAGTGAG ACTGGTGGGG CACGGGGGGC ANTGGGTANT GTAAACCTTT 1380
 45 TAAAGATGGT TAATTCNTCA TTAGTGTMTT TT 1412

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1052 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TTCTCTCTCT CTCTCTACCC CTCCTGTCTC TCCTCCCTC CTCTCTCTTC CTCTCTCTC 60

173

TCTCTTCCTC TCCTCTCTCT TCCCTTCCTG TCTCTCTTCC CCTCCTCTCT CTCTTCCTGT 120
 CCTCTATCTC TTCCCCTCCT CTATCTCTTC CTCTCCTCTC TCTCTTCCTC TCCTCTCTCT 180
 5 CTCTTSCCTT CTTCTCTCTC TCCTGTCTCG GCTGTTGTGG GTTGCAGGTT GGGTGCTGCT 240
 GTTGTGGTCC TTCCCAGAAA CTGCCAGTAG AGGGCAGCCT GGGCATCCTA ATGCTTACTC 300
 TGGTTGTTAC ACAAAGAAAA TATGCGGTC ACTGGCGAGC CCACCCACAC TCACCAGAAT 360
 10 CTCCACTGTA GTCCCCCTAA CAAACAGCCC TTCACTTCCT CTCCACTTC AGCAATTTGT 420
 ATTTTGATGC CATTGGCCTC AGATCAGAGT GTTTTAAATC ATCAGCCCT GGCTTATCCC 480
 15 TGGTCGAGCC AGGACACGGG GTGCTTCAGT GGGTCTGTCA CCCTCTCTCC TTGAAGCATG 540
 TTGCTTTTAT TTATTTACTT TTA CTCTCAC CCTGCTCCTG TACCAGCAGG GGCCACTTCA 600
 AAGCCAAGGT ACAGGGTGAT AACTTGTGGT CCAGCATCAG TTTTCTCCAC TTCCTTCTCC 660
 20 CACTCACCCC CAGCAAGGTG CCTGGGGAGA CTTGAGCAGA TGTTCATTT TGGCCTGGCC 720
 AGTGGCTGAA AGCAGGCCTC CAATGCACTG TGACCTCTGG CTTCCTCCAGC AGCTTTCCTCA 780
 25 GAGAGGCAGA GGGGCCTTCC ACAGCCCGG TTCTCCTGCT GCCTCCTGCC TGCATGAGCT 840
 GCAGGCATTC TGAGGGGCAA CGTGGAGGAA GGGCCAGGGA TGCATGGGAT TTTAATTGTT 900
 TCATCACACC TTCCCCGTGG CAAAGAAACA GTCAGTCCTC TTCAGGTGTC TTCTGGATTT 960
 30 CTGGTGATGG ACAGAGAAAT CTTTTTACAG TTCAAATTA TGTTCACAA ATAAAAATTG 1020
 CATTTTTTAT TTTGGAAAAA AAAAAAAAAA AA 1052
 35

(2) INFORMATION FOR SEQ ID NO: 17:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 683 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AATTCCGCAG AGGCACTTAT CATGTACATA TAGCCTGTTT TTAGCATTG TTAGACAAAG 60
 50 TAGGCATATT CCTTCCATC CAAGAACTCA TAACCTAGTA ATTGTAGTTG GCTGATAGCT 120
 CATTGCCCCAT ACACAAGGAT CTAACACAAC CTCTTGAATA AACATCCCCC TTATTCAGAA 180
 ATGCCTTTTC CTATTTCCAT ATTGCAACTT TGCTTACAAA TTTCCAATCT GTCCTTCTGT 240
 55 TTACAGAAGA TATACAAAAT TCCTTTTGTA TGATCTCTTT ATATCTCTTG ATTTTCTTTT 300
 GTGTTTGCTA CCAAAGGGCC TGCACATAGT GAGAAGATTG TGCATGATCT GTGAGCTCTA 360
 60 CCACACCTGG AATTAGGGAT CACCAATATG AGAAAAAAAA TTGGAGGTAC AAATAACATT 420

ATCATATGTW ATTGGCATAT AAATTACAGA TGTWTCATG ACTAAAAACC CTGTGGATAT 480
 WAACCMATG CAGATAAWTW TAATAAAATW TWTAAAAATW TWATCMAATA ATGATAGTGC 540
 5 TATTCAAATA CTTCAAATTT GCACAGTGAT TTATTTCTTA AAATATGTTA ACACATGTGA 600
 GCCAATACAC TGAGGTCACCT GGATAAATAA ACAGATTCTT GCAAAAAAAA AAAAAAAAAA 660
 10 ACTCGAGGGG GGCCCGTACC CTT 683

15 (2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1054 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

25 AAACATCTT AGGTGACACT ATAGAAGGTA CGCCTGCAGG TACCGGTCCG GAATTCCTCGG 60
 GTCGACCCAC GMGNCCGGCG ACAAGATGGC AGCAGCGTGT CGGAGCGTGA AGGGCCTGGT 120
 GGCGGTAATA ACCGGAGGAG CCTCGGGCCT GGGCCTGGCC ACGGCGGACG ACTTGTGGGG 180
 30 CAGGGAGCCT CTGCTGTGCT TCTGGACCTG CCCAACTCGG GTGGGGAGGC CCAAGCCAAG 240
 AAGTTAGGAA ACAACTGCGT TTTCGCCCCA GCCGACGTGA CCTCTGAGAA GGATGTGCAA 300
 35 ACAGCTCTGG CTCTAGCAAA AGGAAAGTTT GGCCGTGTGG ATGTAGCTGT CAACTGTGCA 360
 GGCATCGCGG TGGCTAGCAA GACGTACAAC TTAAAGAAGG GCCAGACCCA TACCTTGGAA 420
 GACTTCCAGC GAGTTCTTGA TGTGAATCTC ATGGGCACCT TCAATGTGAT CCGCCTGGTG 480
 40 GCTGGTGAGA TGGGCCAGAA TGAACCAGAC CAGGGAGGCC AACGTGGGGT CATCATCAAC 540
 ACTGCCAGTG TGGCTGCCTT CGAGGGTCAG GTTGACAAG CTGCATACTC TGCTTCCAAG 600
 45 GGGGAATAG TGGGCATGAC ACTGCCCATT GTCGGGATC TGGCTCCCAT AGGTATCCGG 660
 GTGATGACCA TTGCCCCAGG TCTGTTTGGC ACCCCACTGC TGACCAGCCT CCCAGAGAAA 720
 GTGTGCAACT TCTTGGCCAG CCAAGTGCCC TTCCCTAGCC GACTGGGTGA CCCTGCTGAG 780
 50 TATGCTCACC TCGTACAGGC CATCATCGAG AACCCATTCC TCAATGGAGA GGTCATCCGG 840
 CTGGATGGGG CCATTCTGAT GCAGCCTTGA AGGGAGAAGG CAGAGAAAAC ACACGCTCCT 900
 55 CTGCCCTTCC TTTCCTGGG GTACTACTCT CCAGCTTGGG AGGAAGCCCA GTAGCCATTT 960
 TGTAACTGCC TACCAGTCGC CCTCTGTGCC TAATAAAGTC TCTTTTCTC ACANAAAAA 1020
 60 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA 1054

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1393 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

5	GGACAAGCT GGGATATGTG AGCGTTAAGC TACTCACATC CTTCAAAAAG GTGAAACATC	60
15	TTACACGGGA CTGGAGAACC ACAGCACATG CTTTGAAGTA TTCAGTGGTC CTTGAGTTGA	120
	ATGAGGNCCA CCGGAAGGTG AGGAGGACCA CCCCCGTCCC ACTGTTCCCC AACGAGAACC	180
20	TCCCCAGCAA GATGCTCCTG GTCTATGATC TCTACTTGTY TCCTAAGCTG TGGGCTCTGG	240
	CCACCCCCCA GAAGAATGGG AAGGGTGCAA GARAAGGTGA TGGAACACCT GCTCAAGCTT	300
25	TTTGGGACTT TTGGAGTCAT CTCATCAGTG CGGATCCTCA AACCTGGGAG AGAGCTGCCC	360
	CCTGACATCC GGAGGNTCCA GCAGCCGCTA CAGCTCCTCT GACCCCGAGA GCAACCCAC	420
	ATCCCTATG GCGGGCCGAC GGCACGNGKC CACCAACAAG CTCAGCCCGT CTGGCCACCA	480
30	GAATCTCTTT CTGAGTCCAA ATGCCCTCCCC GTGCACAAGT CCTTGAGCA GCCCCTTGGC	540
	CCAACGCAAA GCGGTTTCCA GAAAGTCCCC ACTGGCGGAG GAAGGTAGAC TGAAGTGCAG	600
35	CACCAGCCCT GAGATCTTCC GCAAGTGTAT GGATTATTCC TCTGACAGCA GCGTCACTCC	660
	CTCTGGCAGC CCCTGGGTCC GGAGGCGTCG CCAAGCCGAG ATGGGGACCC AGGAGAAAAG	720
	CCCCGGTACG AGTCCCCTGC TCTCCCGGAA GATGCAGACT GCAGATGGGS TACCCGTAGG	780
40	TNGCTTGAGG TTGCCCAGGG GTCCTGACAA CACCAGAGGA TTTCATGGCC ATGAGAGGAG	840
	CAGGGCCTGT GTATAAATAC CTTCTATTTT TAATACAAGC TCCACTGAAA ACCACCTTCG	900
45	TTTTCAAGGT TCTGACAAAC ACCTGGCATG ACAGAATGGA ATTCGTTCCC CTTTGAGAGA	960
	TTTTTTTATC ATGTAGACCT CTTAATTTAT CTATCTGTAA TATACATAAA TCGGTACGCC	1020
	ATGGTTTGAA GACCACCTTC TAGTTCAGGA CTCCTGTTCT TCCCAGCATG GCCACTATTT	1080
50	TGATGATGGC TGATGTGTGT GAGTGTGATG GCCCTGAAGG GCTGTAGGAC GGAGGTTCCC	1140
	TGGGGGAAGT CTGTTCTTTG GTATGGAATT TTTCTCTCTT CTTTGGTATG GAATTTTTC	1200
55	CTTCAGTGAC TGAGCTGTCC TCGATAGGCC ATGCAAGGCG TTCCTGAGAG TTCAGGAAAG	1260
	TTCTCTTGTC CAACAGCAAG TAGCTAAGCC TATAGCATGG TGTCTGTAG GACCAAATCG	1320
	ATGTTACCTG TCAAGTAAAT AAATAATAAA ACACCCAACCT GGGAGTGCCTG AAAAAAANA	1380
60	ANNAAAAAAC TCG	1393

5 (2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1215 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

15 AGGAAAAGTT TTCCNAATTG GAAAGCGGGC AGTGAGCGCA ACGCAATTAA TGTGAGTTAG 60
 NTCANTCATT AGGCACCCCA GGCTTTACAC TTTATGCTTC CGGNTCGTAT GTTGTGTGGA 120
 20 ATTGTGAGCG GATAACAATT TCACACAGGA AACAGCTATG ACCATGATTA CGCCAAGCTN 180
 TAATACGACT CACTATAGGG AAAGCTGGTA CGCCTGCAGG TACCGGTCCG GAATTCCCGG 240
 GTCGACCCAC GCGTCCGCCC ACGCGTCCGT GAAAATCCGA AGTGCCGCGG AAAGTGAGG 300
 25 TGAGGGCCGC CCGCCCTAGA GGTGCCCCTC CGAGAGGCAG AGCTGACAAG GAAGGTTTCG 360
 AGCGTTTTCG TGGCAAAGGG ATTTCTTACA ACCTCCAGGC ATGCGTCTTT CTGCCCTGCT 420
 30 GGCTTTGGCA TCCAAGGTCA CTCTGCCCCC CCATTACCGC TATGGGATGA GCCCCCAGG 480
 CTCTGTGTGA GACAAGAGGA AGAACCCCCC ATGGATCAGG CGGCGCCCAG TGGTTGTGGA 540
 ACCCATCTCT GATGAAGACT GGTATCTGTT CTGTGGGGAC ACGGTGGAGA TCTTGAAGG 600
 35 CAAGGATGCC GGAAGCAGG GCAAAGTGGT TCAAGTTATC CGGCAGCGAA ACTCGGTGGT 660
 CGTGGGAGGG CTGAACACAC ATTACCGCTA CATTGGCAAG ACCATGGATT ACCGGGGAAC 720
 40 CATGATCCCT AGTGAAGCCC CCTTGCTCCA CCGCCAGGTC AAAGTTGTGG ATCCTATGGA 780
 CAGGAAACCC ACTGAGATCG AGTGGAGATT TACTGAAGCA GGAGAGCGGG TACGAGTCTC 840
 CACACGATCA GGGAGAAATTA TCCCTAAACC CGAATTTCCC AGAGCTGATG GCATCGTCCC 900
 45 TGAAACGTGG ATTGATGGCC CCAAAGACAC ATCAGTGGAA GATGCTTTAG AAAGAACCTA 960
 TGTGCCCTGT CTAAAGACAC TGCAGGAGGA GGTGATGGAG GCCATGGGGA TCAAGGAGAC 1020
 50 CCGGAAATAC AAGAAGGTCT ATTGGTATTG AGCCTGGGGC AGAGCAGCTC CTCCCCAACT 1080
 TCTGTCCCAG CCTTGAAGGC TGAGGCACTT CTTTTCAGCA TGCCAATAAA GAGCACTTTA 1140
 TGAGTCCTCC AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1200
 55 AAAAGGGCCG GCCGC 1215

60 (2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2042 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

10 CTGCATCCAG GCGCAGAATA ACCTGGGTAT CTTGTGGTCT GAAAGAGAGA AATTGAAACT 60
GCACAGGCTT ACCTAGAGTC ATCAGAAGCA CTATATAATC AGTATATGAA AGAGGTTGGG 120
AGTCCTCCTC TTGATCCTAC TGAGCGTTTT CTTCTGAAGA AGAGAACTT ACTGAACAAG 180
15 AGAGATCAAA AAGATTTGAA AAGGTTTATA CTCATAACCT ATATTACCTA GCTCAAGTCT 240
ACCAGCATCT GGAAATGTTT GAGAAGGCTG CTCACTATTG CCATAGTACA CTAAAACGCC 300
20 AGCTTGAGCA CAATGCCTAC CATCCTATAG AGTGGGCTAT CAATGCTGCT ACCTTGTCAC 360
AGTTTACAT CAATAAGCTA TGCTTTATGG AGGCCAGGCA CTGTTTATCA GCTGCTAATG 420
TCATTTTGG TCAAACCTGA AAGATCTCAG CCACAGAAGA CACTCCTGAA GCTGAAGGAG 480
25 AAGTGCCAGA GCTTTATCAT CAAAGAAAGG GGGAAATAGC AAGGTGCTGG ATCAAATACT 540
GTTTGACTCT CATGCAGAAT GCCCAACTCT CCATGCAGGA CAACATAGGA GAGCTTGATC 600
30 TTGATAACA GTCTGAACCT AGAGCTTTAA GGAAAAAGA ACTAGATGAG GAGGAAAGCA 660
TTCGGAAAA AGCTGTGCAG TTTGGAACCG GTGAACTGTG TGATGCCATC TCTGCAGTAG 720
AAGAGAAAGT GAGCTACTTG AGACCTTTAG ATTTTGAAGA AGCCAGAGAA CTTTTCTTAT 780
35 TGGGTCAGCA CTATGTCTTT GAGGCAAAAG AGTTCTTTCA GATTGATGGT TATGTCACTG 840
ACCATATTGA AGTTGTCCAA GACCACAGTG CTCTGTTTAA GGTGCTTGCA TTCTTTGAAA 900
40 CTGACATGGA GAGACGGTGC AAGATGCATA AACGCRGAAT AGCCATGCTA GAGCCCCTAA 960
CTGTAGACCT GAATCCACAG TATTATCTGT TGGTCAACAG ACAGATCCAG TTTGAAATTG 1020
CACATGCTTA CTATGATATG ATGGATTTGA AGGTTGCCAT TGCTGACAGG CTAAGGGATC 1080
45 CTGATTCACA CATTGTAAAA AAAATAAATA ATCTTAATAA GTCAGCACTG AAGTACTACC 1140
AGCTCTTCTT AGACTCCCTG AGAGACCCAA ATAAAGTATT CCCTGAGCAT ATAGGGGAAG 1200
50 ATGTTCTTCG CCCTGCCATG TTAGCTAAGT TTCGAGTTGC CCGTCTCTAT GGCAAAATCA 1260
TTACTGCAGA TCCCAAGAAA GAGCTGGAAG ATTTGGCAAC ATCATTGGGA ACATTACAAA 1320
TTTATTGTTG ATTACTGTGA AAAGCATCCT GAGGCCGCCC AGGAAATAGA AGTTGAGCTA 1380
55 GAACTTAGTA AAGAGATGGT TAGTCTTCTC CCAACAAAAA TGGAGAGATT CAGAACCAAG 1440
ATGGCCCTGA CTTAATCCTT GTTTTAAAG AAAGGAAATG TGCAATATTG AAGTGATCTT 1500
60 TTCCCTAGT CAGACAGGCC CAATTCCATT GTGATGTTTA CCTTTATAGC CAGGTGAGTG 1560

CAGTTTGAAC TTGAGATACA GTCAACTGAG TGTTCGCTAG GATCCTAAGG AACATAAAGT 1620
 5 TAATTAATAA CTTACACCTA ATTATGTAAA TTGCCTTGTT AAAGACATGT GATTGTGATT 1680
 TTAGATGCTT GTTTCCTATT AAAATACAGA CATTTCTACC CTCAGTTTCT AAATGTAGAC 1740
 TATTTGTTGG CTAGTACTTG ATAGATTCCT TGTAAGAAAA AATGCTGGGT AATGTACCTG 1800
 10 GTAACAAGCC TGTTAATATA TTAAGATTGA AAAAGTAACT TCTATAGTTA CTCCTTCTAA 1860
 AATATTTGAC TTCCTACATT CCCCCACCC AAAATCTTTC CCTTTTGAAA ATACTAAAAA 1920
 15 CTAAGTTATG TTATTATAAA GTGTAAATG GTTTGTCTTA ATTATAGGAG AAAAAGGCCT 1980
 TGTTAGAAAT AAAATAAACT GACTTATTTT ACTAATGAAA AAAAAAAAAA AAAAAAAAAA 2040
 TT 2042

(2) INFORMATION FOR SEQ ID NO: 22:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1872 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GGGTCGACCC ACGCGTCCGA TTGGCCTAGA GCTCCTGTGA CCGAGAGCGC CACGGAAGCC 60
 35 TGGGGATGAT GTCGGGCAGC TTTATTCTTT GCTTGGCTTT GGTAAGTAGG TGGTCCCCTC 120
 AAGCATCCTC AGTTCCTCTT GCTGTTTATG AATCTAAGAC AAGGAAGTCC TATAGAAGCC 180
 40 AAAGGGACAG GGACGGAAAG GACAGGTCCC AAGGGATGGG GCTGTCTTTA CTGTGGGAAA 240
 CCAGGAAATT GCTCCTCTCA GCCAACCAAG GTTGACCACA CACCACCTT CCGGAGCAGC 300
 TCAGTCAGCC CTCGGGGACG RGAAACCACA AGCGCAGAGA CGCTGAGGCC CAGGCAGGTG 360
 45 AAGAGGAAGT GGCTTTGGGT TTTTAAAGTA GGTGAGCGTG ACCTCTCTGA CTGCTTCTTC 420
 CCCGGGGGGG ACTGCAAACC GCTCAGGGTT GCGGCAGAGC CATGGACTTC CGGTCCCTGC 480
 50 AACGGGTGAC CTAAGCGTGG TGCACCCATC AGTCACGCAG GAGGACTGAC TTGACAGACG 540
 AAAGACAAGC CCGGATGACA CAGGGTGAGA AGAGTCAGGG CCGCACCTCT GTCCCTGCAA 600
 ACCAACAGGT GCATGGTGAG TGTGGCAGTC CCCACAGCTC CACAATGGGC TCCCCGCCA 660
 55 ACGGGGACGA CAGGGATCTT CAGGAACTTC TGACCTCACC AAGTCAAGTG GACCACTCTC 720
 CACTCCACGA GGATGTGAAA CGGTTCTTTA AAATGGGATT TTAGAGCCTC GGGAAATGCAT 780
 60 GTGCGTCGCA TCTTTCATAT TATGGGTCAG GATAGATTCA TTTCTTGCAA CATAGTGAA 840

	AAGATATAAG CTGCAGTAAT TTGCTCTTTG AATGACCGTC ACCCCCAGTA TAGGATATGC	900
	TTGTATCCCC CCGTCACTCC TCCGCCTGTT TTTTAAACTT TTCCACCACC TCGTCCAAA	960
5	AAGAATGTTA TAGCGAGTGC TCTTAAATGT TGAACCTGGG TGTTGCTTCC GGGCCAGTCT	1020
	GCGTGGCTCC ATGAAAAGCT CACTGCTGCC CCAGCCGGGC TTCTTAGAGG AGGTCAGTTG	1080
10	TCCTATGTAT CATCATTTAC TCTGGGAATC CTACTGTGAA ATCATGTCTG TATTTTCTG	1140
	GAGCAGTTCA CATAGAGTAG AATGTGGAAT TTCCCGTGAA CGTCTCCTTC CTCCCCGTA	1200
	TCTGCCGCTT GTCACCTCGC CACCGTGCTA GAATACTGTT GTGTTGTAAG ATGACTAATT	1260
15	TTAAAGAAC CTGCCCTGAA AAGTTCTTAG AAACGCAATG AAAGGGAGGA ACTTGTCTTT	1320
	TACCCAGTTT TTCTTTTGTA GGATGGGAAA GTATAAAAAG GCACAGAAGG TTGTCATGGG	1380
20	CTGTTCTCTG GGGGTTTTTA TCCTGCTCAC CGTGGAGATA AGCCTGCGGC TTGTCTAACC	1440
	AGCGCAGCGM AAAGGTCTCA ATGCCTTTTG GTAACATCCG TCATTGCAGA AGAAAGTTTA	1500
	CACGACGTCA AAAAGTGACG TTCATGCTAA GTGTTTTTCC AGAAATATG GTTTCATGTT	1560
25	TCTTATKGC TCTGCCTCCT GTGCTTATAT CATCCAAAAA CTTTTTAAAA AGGTCCAGAA	1620
	TTCTATTTTA ACCTGATGTT GAGCACCTTT AAAACGTTCC TATGTGTGTT GACTAATTC	1680
30	TAAACTTTGG AGGCATTTTG CTGTGTGAGG CCGATCGCCA CTGTAAAGGT CCTAGAGTTG	1740
	CCTGTTTGTC TCTGGAGATG GAATTAACC AAATAAGAG CTCCACTGG AGGCTGTAT	1800
	TGACCTTGTA ACTATATGTT AATCTCGTGT TAAAATAAAA TATAACTTGT GAAAAAAAAA	1860
35	AAAAAAAAAC NT	1872

40 (2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

50	CATTTACCCA CCTATCAACA TGTTTGCTTT CTCTTTGTGTT GGTGAGAATG AGTGGCTTCT	60
	TGCTCCTAGC TAGAGCCAGT CCTTCCATAT GTGCTTTAGA TTCTTCTGT TTTGTTCAAG	120
	AATATTGCTC AAGCTATTCT TCCTCCTGTT TCCTGCATCA GCATTTCCCC TCTCTACTAG	180
55	ATCATCTCTG TCAGTAAATG AACATGTTGT TGTTTCTCCT AGAAGTACTG TTTCTATATC	240
	TAGATAGTAC TCTAGCTAGA GTTAAAAAAA AAAAAAAAAA CCTNNGGGG	289

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(2) INFORMATION FOR SEQ ID NO: 24:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3533 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

	TTTTATTTAC TTCAAATTAA CTGTACTTTA CTCAAATAGA AAANGAATAA TTTTCACATT	60
15	ATGAAGCTAC ACAATTCCAA AATACACATG CTGAGGCTCT TTTTAAGTCC GAATTGTCTA	120
	GTAATTACAA AAAAGTGAAG AGTTTACAGA TATACAAGGA AATAAAGGCG AATTATTGCA	180
20	AAGAAAACAA GTTTAATTTT ACTTTGAATG ACAACGATTT TTCTGGAAAG CAGATACTTC	240
	ACTCCTTTAA GTTTCACCCC AAGCCACAAT AATTTCAAAC GGTCTTGCGG ATGACCCAGC	300
	TGGTCACTCT TGTTTATGTG GGGACTGGAG GTAATGAGAG CCAAAAAAAG TGCTATAAAC	360
25	CTAATTTGGC TAGAGCAAGT TCACACGACA CGACCGTGCT TTAAAAACTT GCTCTCCATT	420
	ATGTACTTCC TTCCATCAGG TTGGGGAAAA AAAAATGGTG GGGATGGTGA GTAAACACAC	480
30	CAGTGGTTTC ATCAGAGGGG AACTCACTAC TCAGGAGGTG ACGGTGACGT GGTGCCGGTC	540
	CCTGAAGTAC GCGCACAAAGC TCCGGAGGTT GCGGGAGCTT CCGCTGCCGC CTGGAGGGAA	600
	GCCGGAGCGA CCGGGGTCAC GGCGGCGGTC AGAGGGTAAA GGTCTTGCTC CCAGCAGCCT	660
35	CCGCGGTGGA TACGTCGCCA TCTTGATCC GCGGGACAAG AAAATTCTATG CGAGGGAGAC	720
	GTGGTGGGCG GTCCTTCCTG TGACACGACC CTTGAGTGAC AGTTCTATTT GATTGCCTCC	780
40	GGTACTGTGA GGAAAGGACA CGACTCTATG GTGAGGACTG ATGGACATAC ATTATCTGAG	840
	AAAAGAACT ACCAGGTGAC AAACAGCATG TTTGGTGCTT CAAGAAAGAA GTTTGTAGAG	900
	GGGGTCGACA GTGACTACCA TGACGAAAAC ATGTACTACA GCCAGTCTTC TATGTTTCCA	960
45	CATCGGTCAG AAAAAGATAT GCTGGCATCA CCATCTACAT CAGGTCAGCT GTCTCAGTTT	1020
	GGGGCAAGTT TATACGGGCA ACAAAGTGCA CTAGGCCTTC CAATGAGGGG GATGAGCAAC	1080
50	AATACCCCTC AGTTAAATCG CAGCTTATCA CAAGGCACTC AGTTACCGAG CCACGTCACG	1140
	CCAACAACAG GGGTACCAAC AATGTCACTT CACACGCCCT CATCTCCAAG CAGGGGTATT	1200
	TGCTCTATGA ATCTARGAA TATGATGAAC CACTCCCAGG TTGGTCAGGG CATTGGAATT	1260
55	CCTAGCAGGA CAAATAGCAT GAGCAGTTCA GGGTTAGGTA GCCCAACAG AAGCTCGCCA	1320
	AGCATAATAT GTATGCCAAA GCAGCAGCCT TCTCGACAGC CTTTACTGT GAACAGTATG	1380
60	TCTGGATTTG GAATGAACAG GAATCAGGCA TTTGGAATGA ATAACCTCTT ATCAAGTAAC	1440

	ATTTTAAATG GAACAGACGG AAGTGAAAAT GTGACAGGAT TGGACCTTTC AGATTTCCTCA	1500
	GCATTAGCAG ACCGAAACAG GAGGGAAGGA AGTGGTAACC CAACTCCATT AATAAACCCC	1560
5	TTGGCTGGAA GAGCTCCTTA TGTGGAATG GTAACAAAAC CAGCAAATGA ACAATCCCAG	1620
	GACTTCTCAA TACACAATGA AGATTTTCCA GCATTACCAG GCTCCAGCTA TAAAGATCCA	1680
10	ACATCAAGTA ATGATGACAG TAAATCTAAT TTGAATACAT CTGGCAAGAC AACTTCAAGT	1740
	ACAGATGGAC CCAAATTCCT TGGAGATAAA AGTTCAACAA CACAAAATAA TAACCAGCAG	1800
	AAAAAAGGGA TCCAGGTGTT ACCTGATGGT CGGGTTACTA ACATTCTCTA AGGGATGGTG	1860
15	ACGGACCAAT TTGGAATGAT TGGCCTGTTA ACATTTATCA GGGCAGCAGA GACAGACCCA	1920
	GGAATGGTAC ATCTTGCAAT AGGAAGTGAC TTAACAACAT TAGGCCTCAA TCTGAACTCT	1980
20	CCTGAAAATC TCTACCCCAA ATTTGCGTCA CCCTGGGCAT CTTACCTTG TCGACCTCAA	2040
	GACATAGACT TCCATGTTCC ATCTGAGTAC TTAACGAACA TTCACATTAG GGATAAGCTG	2100
	GCTGCAATAA AACTTGGCCG ATATGGTGAA GACCTTCTCT TCTATCTCTA TTACATGAAT	2160
25	GGAGGAGACG TATTACAACCT TTTAGCTGCA GTGGAGCTTT TTAACCGTGA TTGGAGATAC	2220
	CACAAAGAAG AACGAGTATG GATTACCAGG GCACCAGGCA TGGAGCCAAC AATGAAAACC	2280
30	AATACCTATG AGAGGGGAAC ATATTACTTC TTTGACTGTC TTAACGGAG GAAAGTAGCT	2340
	AAGGAGTTCC ATCTGGAATA TGACAAATTA GAAGAACGGC CTCACCTGCC ATCCACCTTC	2400
	AACTACAACC CTGCTCAGCA AGCCTTCTAA AAAAAAAAAA AAAAAAAAAA AAAAAGACTT	2460
35	CCCTTTTCTT GGGGTATGGC TGTCTCAGCA CAATACTCAA CATAACTGCA GAACTGATGT	2520
	GGCTCAGGCA CCCTGGTTTT AATTCCCTGA GGATCTGGCA ATTGGCTTAC GCAAAAGGTC	2580
40	ACCATTGAG GTCCTGCCTT ACTAATTATG TGCTGCCCAA CAACTAAATT TGTAATTTGT	2640
	TTTTCTCTAG TTTGAGCAGG GTCTGAATTT TTTCAATTTAT TTCCTTTTTT GCCAGCAGAC	2700
	AGACTTGAGT CTGTAAAGAC AAGCAAATAC ACTGACAGAA GTTTACCATA GTTTCTAAAA	2760
45	TGTAAAAAAG AAAACCCCCA AAAGACTCAA GAAAATTAGA CCACAAATTT TGCATTGTTC	2820
	ATTGTAGCAC TATTGGTAAT AAAATAACAA ATGTTTGTGC ATTTTTATGT GAAGATCCTT	2880
50	CTCGTATTTT ATTTGGAAAG ATGAGCAAGA GGTCTGCTTC CTTCAATTTA CTTCCCTTC	2940
	TGTTTTTTGAA AGGCAGTTTC GCCAAGCTTA ATGCAAGAAT ATCTGACTGT TTAGAAGAAA	3000
	GATATTGCCA CAATCTCTGG ATGGTTTTCC AGGGTTGTGT TATTACTGAG CTTCACTTTT	3060
55	CCAGAATGAG CAAAACACTG TCCAGTCTTT GTTACGATTT TGTAATAAAT GTGTACATTT	3120
	TTTTTAAATT TTTGACATC ACATGAATAA AGGTATGTAT GTACGAATGT GTATATATTA	3180
60	TATATATGAC ATCTATTTTG GAAAATGTTT GCCCTGCTGT ACCTCATTTT TAGGAGGTGT	3240

GCATGGATGC AATATATGAA AATGGGACAT TCTGGAAC TGCTGTCAGGG GACTTTGTCTG 3300
 CCCTGTGCAC TAAAAGGGCC AGATTTTCAG CAGCCAAGGA CATCCATACC CAAGTGAATG 3360
 5 TGATGGGACT TAAAAGAAGT GAACTGAGAC AATTCACTCT GGCTGTTTGA ACAGCAGCGT 3420
 TTCATAGGAA GAGAAAAAAA GATCAATCTT GTATTTTCTG ACCACATAAA GGCTTCTTCT 3480
 CTTTGTAATA AAGTAGAAAA GCTCTCCTCA AAAAAAAAAA AAAAAAACTC GAG 3533
 10

(2) INFORMATION FOR SEQ ID NO: 25:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1148 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ACCCACGCGT CCGCAAATTA TACTTCCTCA TTCATATTAT GTTGATACAA AAGACCTTGG 60
 25 CAGCCATTTC TCCCAGCAGT TTTAAAGGAT GAACATTGGA TTTCATGCCA TCCCATAGAA 120
 AACCTGTTTT AAAATTTTAG GGATCTTTAC TTGGTCATAC ATGAAAAGTA CACTGCTTAG 180
 30 AAATTATAGA CTATTATGAT CTGTCCACAG TGCCCATTTG CACTTCTTTG TCTCATTTCT 240
 TCCCTTTGTT CCTTAGTCAT CCAAATAAGC CTGAAAACCA TAAGAGATAT TACTTTATTG 300
 AATATGGTTG GCATTAAATT TAGCATTTCA TTATCTAACA AAATTAATAT AAATTCCAGG 360
 35 ACATGGTAAA ATGTGTTTTA ATAACCCCA GACCCAAATG AAAATTTCAA AGTCAATACC 420
 AGCAGATTCA TGAAAGTAAA TTTAGTCCTA TAATTTTCAG CTTAATTATA AACAAAGGAA 480
 40 CAAATAAGTG GAAGGGCAGC TATTACCATT CGCTTAGTCA AAACATTCGG TTAGTCCCT 540
 TTAATACACT CCTATCATCA GCACTTCAC CATGTATTAC AAGTCTTGAC CCATCCCTGT 600
 CGTAACTCCA GTAAAAGTTA CTGTTACTAG AAAATTTTTA TCAATTAACT GACAAATAGT 660
 45 TTCTTTTTAA AGTAGTTTCT TCCATCTTTA TTCTGACTAG CTTCCAAAT GTGTTCCCTT 720
 TTTGAATCGA GGTTTTTTTG TTTTGTTTTG TTTTCTGAAA AAATCATACA ACTTTGTGCT 780
 50 TCTATTGCTT TTTTGTGTTT TGTTAAGCAT GTCCCTTGGC CCAAATGGAA GAGGAAATGT 840
 TTAATTAATG CTTTTTAGTT TAAATAAATT GAATCATTTA TAATAATCAG TGTTAACAAT 900
 TTAGTGACCC TTGGTAGGTT AAAGGTTGCA TTATTTATAC TTGAGATTTT TTTCCCTAA 960
 55 CTATTCTGTT TTTTGTACTT TAAACTATG GGGGAAATAT CACTGGTCTG TCAAGAAACA 1020
 GCAGTAATTA TTAGTGAGTT AAATTGAAAA GTCCAGTGGG CCAGGCATTT CTTATATAAA 1080
 60 TAAAATTGGT GGTACTAATG TGAAAAAAA AAAAAAAAAA AACTCGAGGG GGGCCCGGTA 1140

CCCTATTA

1148

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(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GGCACGAGCT AGCTGCCGCC ACCCGAACAG CCTGTCCTGG TGCCCCGGCT CCCTGCCCCG	60
CGCCCACTCA TGACCCTGCG CCCCTCACTC CTCCCCTCC ATCTGCTGCT GCTGCTGCTG	120
CTCAGTGCGG CGGTGTGCCG GGCTGAGGCT GGGCTCGAAA CCGAAAGTCC CGTCCGGACC	180
CTCCAAGTGG AGACCCTGGT GGAGCCCCCA GAACCATGTG CCGAGCCCGC TGCTTTTGGA	240
GACACGCTTC ACATACACTA CACGGAAGC TTGGTAGATG GACGTATTAT TGACACCTCC	300
CTGACCAGAG ACCCTCTGGT TATAGAACTT GGCCAAAAGC AGGTGATGCC AGGTCTGGAG	360
CAGAGTCTTC TCGACATGTG TGTGGGAGAG AAGCGAAGGG CAATCATGCC TTCTCACTTG	420
GCCTATGGAA AACGGGGATT TCCACCATCT GTCCCAGCGG ATGCAGTGCT GCAGTATGAC	480
GTGGAGCTGA TTGCACTAAT CCGAGCCAAC TACTGGCTAA AGCTGGTGAA GGGCATTTTG	540
CCTCTGGTAG GGATGGCCAT GGTGCCAGCC CTCCTGGGCC TCATTGGGTA TCACCTATAC	600
AGAAAGGCCA ATAGACCCAA AGTCTCCAAA AAGAAGCTCA AGGAAGAGAA ACGAAACAAG	660
AGCAAAAAGA AATAATAAAT AATAAATTTT AAAAAAAAAA AAAAAAAAAA AAAAAAA	717

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(2) INFORMATION FOR SEQ ID NO: 27:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GGCACGAGCC GATGTGGACA TCATCCTGTC TATCCCCATG TTCCTGCGCC TGTACCTGAT	60
CGCCCGAGTC ATGCTGCTGC ACAGCAAGCT CTTCACCGAT GCCTCGTCCC GCAGCATCGG	120
GGCCCTCAAC AAGATCAACT TCAACACCCG CTTTGTTCATG AAGACGCTCA TGACCATCTG	180
CCCTGGCACT GTGCTGCTCG TGTTACAGCAT CTCTCTGTGG ATCATGCTG CCTGGACCGT	240

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	CCGTGCTCTGT GAAAGTCCTG AATCACCAGC CCAGCCTTCT GGCTCATCAC TTCCTGCTTG	300
5	GTACCATGAC CAGCAGGACG TAACTAGTAA CTTTCTGGGT GCCATGTGGC TCATCTCCAT	360
	CACATTCCCTT TCCATTGGTT ATGGGGACAT GGTGCCCCAC ACATACTGTG GGAAAGGTGT	420
	CTGTCTCCTC ACTGGCATCA TGGGTGCAGG CTGCACTGCC CTTGTGGTGG CCGTGGTGGC	480
10	CCGAAAGCTG GAACTCACCA AAGCGGAGAA GCACGTTTCAT AACTTCATGA TGGACACTCA	540
	GCTCACCAAG CGGATCAAGA ATGCTGCAGC CAATGTCCTT CGGGAAACAT GGTTAATCTA	600
15	TAAACACACA AAGCTGCTAA AGAAGATTGA CCATGCCAAA GTGAGGAAAC ACCAGAGGAA	660
	GTTCCTCCCA AGCTATCCAC CAGTTTGAGG AGCGTCCCAG ATGGAACAGA GGAAAGCTGA	720
	GTGACCAAGC CAACACTCTG GTGGACCTTT CCAAGATGCA GAATGTCATG TATGACTTAA	780
20	TCACAGAACT CAATGACCGG AGCGAAGACC TGGAGAAGCA GATTGGCAGC CTGGAGTCGA	840
	AGCTGGAGCA TCTCACCGCC AGCTTCAACT CCCTGCCGCT GCTCATCGCC GACACCCTGC	900
25	GCCAGCAGCA GCAGCAGCTC CTGTCTGCCA TCATCGAGGC CCGGGGTGTC AGCGTGGCAG	960
	TGGGCACCAC CCACACCCCA ATCTCCGATA GCCCCATTGG GGTGAGCTCC ACCTCCTTCC	1020
	CGACCCCGTN CACAAGTTCA AGCAGTTGCT AAATAAATCT CCCCCTCCA GAAGCATTAA	1080
30	AAAAAAAAA AAAAAAAAAA	1099

35 (2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 941 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

45	AATTCGGCAG AGAGCCAACC GAGGGCGTTC CTGTCGGGGC TGCAGCGGCG GGAGGGAGCC	60
	CAGTGGAGGC GCCCTCCCGA AGCGCCACTG CCCATGCTGA CCACCCAGCC CTCCGGCTGC	120
50	TGATGTCATG AGTAACACCA CTGTGCCCAA TGCCCCCAG GCCAACAGCG ACTCCATGGT	180
	GGGCTATGTG TTGGGGCCCT TCTTCCTCAT CACCCTGGTC GGGGTGGTGG TGGCTGTGGT	240
	AATGTATGTA CAGAAGAAAA AGCGGGTGGA CCGGCTGCGC CATCACCTGC TCCCCATGTA	300
55	CAGCTATGAC CCAGCTGAGG AACTGCATGA GGCTGAGCAG GAGCTGCTCT CTGACATGGG	360
	AGACCCCAAG GTGGTACATG GCTGGCAGAG TGGCTACCAG CACAAGCGGA TGCCACTGCT	420
60	GGATGTCAAG ACGTGACCTG ACCCCCTTGC CCCACCCTTC AGAGCCTGGG GTYCTGGACT	480

GCCTGGGGCC CTGCCATCTG CTTCCCTGCG TGTCACCTGG STCCCCCTGC TGGGTGCTGG 540
GTCTCCATTT CTCCCTCCAC CCACCCTCAG CAGCATCTGC TTCCCATGCC CTCACCATCA 600
5 CCTCACTGCC CCCAGGCCTT CTGCCCTTTG TGGGTGTTGA GCTCACC GCC CACCCACAGG 660
CACTCATGGG AAGAGGCTTT CTTCTGCGGA TGGCGGCGGC TGGTAGACAC CTTTGCTTTTC 720
TCTAGCCCTC CTGGGCTGGG CTTGGGCACA AATCCCCAGG CAGGCTTTGG AGTTGTTTCC 780
10 ATGGTGATGG GGCCAGATGT ATAGTATTC A GTATATATTT TGTAAATAAA ATGTTTGTG 840
GCTAAAAAAA AAAAAAAAAA ATCNAAGGGG GGGCCGGTAC CCAAATTCCT CCTATANTGA 900
15 ATTCTATTATTA ACAATTCCT TGGGGCCGTC CTTTAAANAA C 941

20 (2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 756 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

30 GGCACGAGGA AGCTGGAGCG GGCCGGCGGT GCAGTCACGG GGGAGCGAGG CCTGCTGGGC 60
TTGGCAACGA GGGACTCGGC CTCGGAGGCG ACCCAGACCA CACAGACACT GGGTCAAGGA 120
GTAAGCAGAG GATAACAAC TGGAAGGAGA GCAAGCACAA AGTCATCATG GCTTCAGCGT 180
35 CTGCTCGTGG AAACCAAGAT AAAGATGCCC ATTTTCCACC ACCAAGCAAG CAGAGCCTGT 240
TGTTTTGTCC AAAATCAAAA CTGCACATCC ACAGAGCAGA GATCTCAAAG ATTATGCGAG 300
40 AATGTCAGGA AGAAAGTTTC TGGAAGAGAG CTCTGCCTTT TTCTCTTGTA AGCATGCTTG 360
TCACCCAGGG ACTAGTCTAC CAAGGTATT TGGCAGCTAA TTCTAGATTT GGATCATTGC 420
CCAAAGTTGC ACTTGCTGGT CTCTTGGGAT TTGGCCTTGG AAAGGTATCA TACATAGGAG 480
45 TATGCCAGAG TAAATTCCAT TTTTGAAG ATCAGCTCCG TGGGGCTGGT TTTGGTCCAC 540
AGCATAACAG GCACTGCCTC CTTACCTGTG AGGAATGCAA AATAAAGCAT GGATTAAAGT 600
50 AGAAGGGAGA CTCTCAGCCT TCAGCTTCCT AAATCTGTG TCTGTGACTT TCGAAGTTTT 660
TTAAACCTCT GAATTTGTAC ACATTTAAAA TTCAAGTGT ACTTTAAAAT AAAATACTTC 720
TAATGGAAAA AAAAAAAAAA AAAAAAAAAA ACTCGA 756
55

(2) INFORMATION FOR SEQ ID NO: 30:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

5	NCCAGAGGCA GAAAGTCCTG CTTCTGGGGC GTAACCTACA GGATATCCTT GGAACAGAAG	60
10	ATCTTATTTGT GGAAGTRACT TCCAATGATG CTGTGAGATT TTATCCCTGG ACCATTGATA	120
	ATAAATACTA TTCAGCAGAC ATCAATCTAT GTGTGGTGCC AAACAAATTT CTGTGTACTG	180
15	CAGAGATTGC AGAATCTGTC CAAGCATTTG TGGTTTACTT TGACAGCACA CAAAAATCGG	240
	GCCTTGATAG TGTCTCCTCA TGGCTTCCAC TGGCAAAAGC ATGGTTACCY GAGGTGATGA	300
20	TCTTGGTCTG CGATAGAGTG TCTGAAGATG GTATAAACCG AAAAAAGCT CAAGAATGGT	360
	GCATCCAAAC ATGGCTTTGA ATTGGTAGAA CTTAGTCCAG AGGAGTTGCC TGAGGAGGAT	420
	GATGACTTCC CAGAATCTAC AGGAGTAAAG CGAATTGTCC AAGCCCTGAA TGCCAATGTG	480
25	TGGTCCAATG TAGTGATGAA GAATGATAGG AACCAAGGCT TTAGCTTGCT GCAACTCATT	540
	GA CTGGAACA AACCATAGCA TTGGGTCAGC AGATCCCTGT CACCCAGAGC AACCCCATTT	600
30	GCCAGCAGCA GATAGTACTG AATCCCTCTC TGATCATCGG GGTGGTGCAT CTAACACAAC	660
	AGATGCCCAG GTTGATAGCA TTGTGGATCC CATGTTAGAT CTGGATATTC AAGAATTAGC	720
	CAGTCTTACC ACTGGAGGAG GAGATGTGGA GAATTTTGAA AGACTCTTTT CAAAGTTAAA	780
35	GGAAATGAAA GACAAGGCTG CGACGCTTCC TCATGAGCAA AGAAAAGTGC ATGCAGAAAA	840
	GGTGGCCAAA GCATTCTGGA TGGCAATCGG GGGAGACAGA GATGAAATTG AAGGCCTTTC	900
40	ATCTGATGAA GAGCACTGAA TTATTCATAC TAGGGTTTGA CCAACAAAGA TGCTAGCTGT	960
	CTCTGAGATA CCTCTCTACT CAGCCCAGTC ATATTTTGCC AAAATTGCCC TTATCATGTT	1020
	GGCTGCCTGA CTTGTTTATA GGGTCCCCTT AATTTTAGTT TTTAGTAGGA GGTTAAGGAG	1080
45	AAATCTTTT TTTCTCAGT ATATTGTAAG AGAGTGAGGA ATACAGTGAT AGTAATGAGT	1140
	GAGGATTTCT TAAATRTACT TTTTTTTTGT TCTAGGAATG AGGGTAGGAT AAATCTCAGA	1200
50	GGTCTGTGTG ATTTACTCAA GTTGAAGACA ACCTCCAGGC CATTCCTGGT CAACCTTTTA	1260
	AGTAGCATTT CCAGCATTC AACTTGATAC TGCACATCAG GAGTTGTGTC ACCTTTCCTG	1320
	GGTGATTTGG GTTTTCTCCA TTCAAGGAGC TTGTAGCTCT GAAGCTATGA TGCTTTTATT	1380
55	GGGAGGAAAG GAGGCAGCTG CAGAATTGAT GTGAGCTATG TGGGGCCGAA GTCTCAGCCC	1440
	GCAGCTAAGT CTCTACCTAA GAAAATGCCT CTGGGCATTC TTTTGAAGTA TAGTGTCTGA	1500
60	GCTCATGCTA GAAAGAATCA AAAAGCCAGT GTGGATTTTT AGACTGTAAT AAATGAGGCA	1560

AAGGATTTCT ATTCCAGTGG GAAGRAAACC TCTCTACTGA GTTGTGGGGG ATATGTTGTA 1620
 TGTTAGAGAG AACCTTAAGG AGTCCTTGTA TGGGCCATGG AGACAGTATG TGATAACATA 1680
 5 CCGTGATTTT CATGAAGAAA TTCTTCTGTC TTAGAGTTCT CCCCTGCTGC TTGAGATGCC 1740
 AGAGCTGTGT TGTGTCACAC CTGCAAAACA AGGCACATTT CCCCTTTTCT CTTTAAAGCC 1800
 AAAGAGAGAT CACTGCCAAA GTGGGAGCAC TAAGGGGTGG GTGGGGAAGT GAAATGTTAG 1860
 10 GCGATGAATT CCTGAGCACC TTGTTTTTCT TCCAAGGTC GTAGCTCCTC TCTGCCCTTC 1920
 CAAGCCTGTA ACCTCGGAGG ACTATCTTTT GTTCTTTATC CTTTGTCTTG TTTGAGTGGG 1980
 15 TCAGCCCCAG AGGAACTGAT AAGCAAATGG CAAGTTTTTA AAGGAAGAGT GGAAAGTACT 2040
 GCAAATAAAA ATCCTTATTT GTTTTTGTAG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAAG 2100

20

(2) INFORMATION FOR SEQ ID NO: 31:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1448 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AAAAAAAAAA AAAGCCCACC TGAAAGCCTG TCTCTTTCCA CTTTGTGGC CCTTCCAGTG 60
 GGATTATCGA GCATGTTGTT TTTTCATAGT GCCTTTTTC TATTTC AAG GGTGCTTCT 120
 35 GAGTGGTGTT TTTTTTTTTT TTAATTTGTT TTGTTTTAAA ATAAGTTAAA GACAGTCCAG 180
 AGCTTTTCAG CCAATTTGTC TCCTACTCTG TGTAATATTT TTTCCCTCCG GGCAGGGGAG 240
 40 CCAGGGTAGA GCAAAGGAGA CAAGCAGGAG TGGAAGGTGA GCGTTCCTCC TGCTTGTA CT 300
 AAGCCAGGAG STTTAAGCTC CAGCTTTAAG GGTGTGAGC CCCTTGGGGT TCAGGGA ACT 360
 GCTTGCC CAG GGTG CAGTGT GATG GGCCACC GGG GCAAGAGGGA AGGTGACCGC 420
 45 CCAGCTCTCC CACATCCCAC TGGATCTGGC TTACAGGGGG GTCGGAAGCC TGTCTCACC 480
 GTCTCGGGGG TTGTGGCCCC CGCCCCCTCC CTATATGCAC CCCTGGAACC AGCAAGTCCC 540
 50 AGACAAGGAG AGCGGAGGAG GAAGTCATGG GAACGCAGCC TCCAGTTGTA GCAGGTTTCA 600
 CTATTCCTAT GCTGGGGTAC ACAGTGAGAG TACTCACTTT TCACTTGTCT TGCTCTTAGA 660
 TTGGGCCATG GCTTTCATCC TGTGTCCCCT GACCTGTCCA GGTGAGTGTG AGGGCAGCAC 720
 55 TGGGAAGCTG GAGTGTGCT TGTGCCTCCC TTCCCAGTGG GCTGTGTTGA CTGCTGCTCC 780
 CCACCCCTAC CGATGGTCCC AGGAAGCAGG GAGAGTTGGG GAAGGCAAGA TTGGAAAGAC 840
 60 AGGAAGACCA AGGCCTCGGC AGAACTCTCT GTCTTCTCTC CACTTCTGGT CCCCTGTGGT 900

5 GATGTGCCTG TAATCTTTT CTCCACCCAA ACCCCTTCCC ACGACAAAA CAAGACTGCC 960
 TCCCTCTCTT CCGGGAGCTG GTGACAGCCT TGGGCCTTTC AGTCCCAAAG CGGCCGATGG 1020
 GAGTCTCCCT CCGACTCCAG ATATGAACAG GGGCCAGGCC TGGAGCGTTT GCTGTGCCAG 1080
 GAGGCGGCAG CTCTTCTGGG CAGAGCCTGT CCCCCTTTC CCTCACTCTT CCTCATCTG 1140
 10 CTCTCTTTT CCTCGCAGAT GATAAAAGGA ATCTGGCATT CTACACCTGG ACCATTTGAT 1200
 TGTMTTATTT TGGAATTGGT GTATATCATG AAGCCTTGCT GAACTAAGTT TTGTGTGTAT 1260
 ATATTTAAAA AAAAAATCAG TGTTTAAATA AAGACCTATG TACTTAATCC TTAACTCTG 1320
 15 CGGATAGCAT TTGGTAGGTA GTGATTAAT GTGAATAATA AATACACAAT GAATTCTTMA 1380
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAACCCCGGG GGGGGCCCCG GGCCCCAATT 1440
 20 CCCCCCAA 1448

25 (2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 456 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

35 GGCACAGCAA ACTTGACGCC ATGAAGATCC CGGTCTTCC TGCCGTGGTG CTCCTCTCCC 60
 TCCTGGTGCT CCACTCTGCC CAGGGAGCCA CCCTGGGTGG TCCTGAGGAA GAAAGCACCA 120
 TTGAGAATTA TGCCTCACGA CCCGAGGCCT TTAACACCCC GTTCTTGAAC ATCGACAAAT 180
 40 TGGGATCTGC GTTTAAGGCT GATGAGTTCC TGAAGTGGCA CGCCCTCTTT GAGTCTATCA 240
 AAAGGAACT TCCTTTCCTC AACTGGGATG CCTTTCCTAA GCTGAAAGGA CTGAGGAGCG 300
 45 CAACTCCTGA TGCCCAGTGA CCATGACCTC CACTGGAAGA GGGGGCTAGC GTGAGCGCTG 360
 ATTCTCAACC TACCATAACT CTTTCTTGCC TCAGGAAGTC CAATAAACA TTTTCCATCC 420
 AAAAAAAAAA AAAAAAAAC CCCNGGGGGG GCCCGG 456
 50

55 (2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 1326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

5	GGCACGAGTG CAGGCCCAGA GAGGACTCAT TGAAAGGACT GAAAGGGGAG GTGGCGTMTT	60
	CTTCCTACCC AAACCTTACCC CTGTGAGCTG GACAGCTTGG TAGCACCTGC CTGGACTTAG	120
	ATGGTGCTAG CCAAGAAGAC TGACATTTTA GGGAACAGGA CGGGGAGGAG AAGGCTCTGG	180
10	CACACACACA TGTGTCCATA TGTCTGCAA TGGTCTGGGG ACTATTGCTA GGCTAGGAGC	240
	CCTAAGTGTC TTCTTCCTCA TGTCTMTTCT CCCCTGTSTC ATGGGCCCTA AGTCTCTTT	300
	CACTGGGCCT GCCTCAATGA ACGTGTGCC CAGCTACCCC GAAACACGGC ANCTGCCGGC	360
15	TATCAATGCC CCAGCTGCAA TGGCCCATCT TCCCCAACC AACCTGGCTG GGCCCGTGGG	420
	CTCCGCACTG AGARARAAAS TTGGCACART CAACTGGGCC CGGGCAGGAC TGGGCCYCCC	480
20	TCTGATCGAT GAAGKTGGTG ARCCCAGAGC CCGAGCCCCT CAACACGTCT GACTTCTCTG	540
	ACTGGTCTAG TTTTAATGCC AGCAGTACCC CTGGACCAGA GGAGGTAGAC AGCGCCTCTG	600
	CTGCCCCAGC CTCTACAGC CGAGCCCCC GGCCCCAGC TTCCCCAGGC CGGCCGAGC	660
25	AGCACACAGT GATCCACATG GGCAATCCTG AGCCCTTGAC TCACGCCCT AGGAAGGTGT	720
	ATGATACGCG GGATGATGAC CGGACACCAG GCCTCCATGG AGACTGTGAC GATGACAAGT	780
30	ACCGACGTCG GCCGGCCTTG GGTGGCTGG CCCGGCTGCT AAGGAGCCGG GCTGGGTCTC	840
	GGAAGCGRCC GCTGACCCTG CTCCAGCGGG CGGGGCTGCT GCTACTCTTG GACTGCTGG	900
	GCTTCCTGGC CTTCTTGCC CTCATGTCTC GCCTAGGCCG GGCCGAGCT GACAGCGATC	960
35	CCAACCTGGA CCCACTCATG AACCTCACA TCCGCGTGGG CCCCTCCTGA GCCCCTTGC	1020
	TTGTGGCTAG GCCAGCCTAG GATGTGGGTT CTGTGGAGGA GAGGCGGGT AATGGGGAGG	1080
40	CTGAGGGCAC CTCTTCACTG CCCCTCTCCC TCAAGCCTAA GACACTAAGA CCCAGACCC	1140
	AAAGCCAAGT CCACCAGAGT GGCTGCAGGC CAGGCCTGGA GTCCCCGTGG GTCAAGCATT	1200
	TGTCTTGACT TGCTTTCCTC CCGGTYTCC AGCCTCCGAC CCCTCGCCCC ATGAAGGAGC	1260
45	TGGCAGGTGG AAATAAACAA CAACTTTATT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1320
	AAANAA	1326
50		

(2) INFORMATION FOR SEQ ID NO: 34:

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 710 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

5 GCGAAAGAGA AAAAGGCTGG AGCTCCCGCC CCCGGGGCTG TCAGATGGCT TGGGTTCCTG 60
 CGACGCGATT GGCTCGCGGA GGGCAGAAAT TACTCAGCAA ACATGACTAT TATTAGCTGC 120
 TTAGCAACAG CTCACCAAAG TAGAGAGACC ACCCAGGTAG GCAACCCAGT GTGTGCATCC 180
 10 TCGGCTTCGG GGCAGCCTCT GAGAGCGCCA ACCTTCTCGC ATGCAATACT TCCATTAAGG 240
 AATGCTCCCC CTCCTTCTC TCTTATTCCT TTTCTTTTCA ACAGTGTCTT CTTTTGTGG 300
 GATGCCTTTG CGCGCACACA CGCGCGCGCA SGCACACACA CGAACATTG CCTCGCGGTA 360
 15 GACACGGGGG GAAATGTWAT ATTTTTTTAA GCGCTTAAAC AATTTCTGAA ATTCCTCAAA 420
 GAAAAGCCTT TCAGARGCAC CTGGCCTCA AGCTGCAACA AATACTGGGA RGTCCGGCTC 480
 20 GCATTCCTCAG GCCTGCACCA ATAATGACAG CGTGCTGGAT ARTGCGCCAG TGTGTGCCAG 540
 ATTTTTTTTT CCTCTTCTCT TTTCTTTTAT AACTAAAGG AAGACTTAGG CTCTTGCAGG 600
 GAACAACGCC TCGCATTAAG ATAAACAGAA TGGAAAGTTA AAGAGGAAAG CAAGGACGTT 660
 25 GGGAAAAGCC ATCTTTCTTA AAATCCGTCT GCCCCCAGC CGCTTTCTCC 710

30 (2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1188 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

40 GATGGCTTTT ATATCTATTA TCGACCCACA GACAGTGACA ATGATAGTGA CTACAAGAAG 60
 GATATGGTGG AAGGGGACAA GTACTGGCAC TCCATCAGCC ACCTGCAGCC AGAGACCTCC 120
 45 TACGACATTA AGATGCAGTG CTTCAATGAA GGAGGGGAGA GCGAGTTCAG CAACGTGATG 180
 ATCTGTGAGA CCAAAGCTCG GAAGTCTTCT GGCCAGCCTG GTCGACTGCC ACCCCCAACT 240
 CTGGCCCCAC CACAGCCGCC CCTTCCTGAA ACCATAGAGC GGCCGGTGGG CACTGGGGCC 300
 50 ATGGTGGCTC GCTCCAGCGA CCTGCCCTAT CTGATGTGCG GGGTCGTCCT GGGCTCCATC 360
 GTTCTCATCA TCGTCACCTT CATCCCCTTC TGCTTGTGGA GGGCCTGGTC TAAGCAAAAA 420
 55 CATACAACAG ACCTGGGTTT TCCTCGAAGT GCCCTTCCAC CCTCCTGCCC GTATACTATG 480
 GTGCCATTGG GAGGACTCCC AGGCCACCAG GCAGTGGACA GCCCTACCTC AGTGGCATCA 540
 GTGGACGGGC CTGTGCTAAT GGGATCCACA TGAATAGGGG CTGCCCCCTG GCTGCAGTGG 600
 60 GCTACCCGGG CATGAAGCCC CAGCAGCACT GCCCAGGCGA GCTTCAGCAG CAGAGTGACA 660

CCAGCAGCCT GCTGAGGCAG ACCCATCTTG GCAATGGATA TGACCCCAA AGTCACCAGA 720
 TCACGAGGGG TCCCAAGTCT AGCCCGGACG AGGGCTCTTT CTTATACACA CTGCCCAGC 780
 5 ACTCCACTCA CCAGCTGCTG CAGCCCCATC ACGACTGCTG CCAACGCCAG GAGCAGCCTG 840
 CTGSTGTGGG CCAGTCAGGG GTGAGGAGAG CCCCCGACAG TCCTGTCCTG GAAGCAGTGT 900
 10 GGGACCCTCC ATTTCACTCA GGGCCCCCAT GCTGCTTGGG CCTGTGCCA GTTGAAGAGG 960
 TGGACAGTCC TGACTCCTGC CAAGTGAGTG GAGGAGACTG GTGTCCCCAG CACCCCGTAG 1020
 GGGCCTACGT AGGACAGGAA CCTGGAATGC AGCTCTCCCC GGGGCCACTG GTGCGTGTGT 1080
 15 CTTTTGAAAC ACCACCTCTC ACAATTTAGG CAGAAGCTGA TATCCAGAA AGACTATATA 1140
 TTGTTMTTTT TTAAAAAAA AAAAAAAAAA AWCYCGGGG GGGGCCCC 1188
 20

(2) INFORMATION FOR SEQ ID NO: 36:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 956 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GGCAGAGCAG TGAAAATGCA TCCTAAAAAT TCAATGTTTA TACCAGGCTC ATGACACTAA 60
 35 GATGTGACAT CTGGACACGA GGGGTGAGCC ACGTGGATAC ATCCCTCCCA GATTGCATCT 120
 CCAGGAATCA CTCTGCTAGC AGAATGGGCG CCCCATCCCT TACTATGCTG CTCTCCTCA 180
 AAGTGCAGCC CAGAAGGACC CAGGCCTTTG ATGCACATTG GGTGGGTCTC CCACTACTTT 240
 40 AGTTGAAATG GGAGCATGCT GGAGTCGGCG TTCTGTTGCT TCTGGTGAGA AGGACATCCC 300
 ATTGACCCCT GGCCACCAGG TCCAGTATTC CATCCTTCCT TCTGTCCCAG CCTATCGCCC 360
 45 TCCCCACYAG GCCCACCCCC ACAACTTCTC CTCAAGGGAG GTTNTCCCGC AGCTGGAGGG 420
 CTTGCACAGA CCAGCAGTCA CAGAAATCAT TCTTCCTGCT GTACTGGGCC TTAAGTGCCT 480
 GCAAATGTCC GAGCACTACT GCATAGGATG CCAGAGCCAC CGAAGATAAA CACAGCCAAG 540
 50 TTTAATAATA ATAAAAGGAA AAATCTCAGC CTGCAGAACT CTGGTTTGA CCCACCATCG 600
 GCCAGATGCA CATCTTCAGG GCCTGTTGAG CACCTTCTGA AAAGCAGGGC TCGTAATAGA 660
 55 CTCCAGCACA TTCCATCAGA GTCAGGAAAA CTGCGGTGAG TCCCAGAGAA TCTAGGGTGC 720
 AGGGCAGGGA GCAGGAGTCA TAAGGAGTGA TAACCTAAAC TGTGTGTAGT CAGCGGGGAG 780
 GGTCTTATGT TATCAGGTGA AATGAGAGCC AGTAAGTTAG TTGATCCTGT CACAGATATA 840
 60

ACCCTGATAA CACCCCATAG ATACGCGACA CGTGTGTCCT GCCCCTGCTT TCCCCATCCA 900
 ACATGGTCTT TCTGTTCCAC AGACATTAAA GGGGCTTTCT GCAATTACTT AAAAAA 956

5

(2) INFORMATION FOR SEQ ID NO: 37:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1603 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

TCGACCCACG CGTCCGCTCT GCCAGGAATC TGGTCTTTCT GTAGACCCAA GTCAGAAAGA 60
 20 ACCATTTGTG GAGTTAAATC GAATATTAGA RGCATTAAAR GTCAGAGTTC TGAGACCTGC 120
 TCTGGAATGG GCAGTTTCAA ACCGAGAGAT GCTTATAGCC CAAAACAGCT CCTTGAATT 180
 25 TAAACTACAC AGACTGTATT TTATTAGCTT RTTAATGGGT GGAACACAAA TCAGCGAGAR 240
 GCATTACAAT ATGCTAAAAA TTTTCAGCCA TTTGCCCTAA ATCATCAAAA AGACATTCAG 300
 GTTTTGATGG GAAGCCTTGT GTACCTGAGA CAAGGGATTG AGAACTCACC ATATGTTTAC 360
 30 CTACTTGATG CAAACCAAGT GGCTGATATC TGTGACATCT TTACACGGGA TGCTTGTGCC 420
 CTCCTGGGGC TCTCCGTGGA GTCCCTCTC AGTGTCACTT TCTCAGCAGG TTGTGTGGCG 480
 35 CTGCCAGCTT TAATTAACAT CAAAGCCGTG ATTGAACAGA GGCAGTGTAC TGGAGTTTGG 540
 AACCAGAAAG ATGAATTACC TATGAAGTG GACCTTGGTA AAAAGTGCTG GTATCACTCT 600
 ATATTTGCCT GCCCATTTCT TCGTCAGCAA ACAACAGATA ACAATCCACC CATGAAATTG 660
 40 GTCTGTGGTC ATATTATATC AAGAGATGCC CTGAATAAAA TGTTTAATGG TAGCAAATTA 720
 AAATGTCCCT ACTGTCCAAT GGAACAAAGT CCAGGAGATG CCAAACAGAT ATTTTCTGA 780
 45 AGAGATAACT TTAGTTTGCA ATTTGTAAGT GAAACTGAAT CGTGGGTGCA TTTCAGAAGA 840
 GAACGTTCCA TATAATGCAG CTAACCAAGG ACTCCTGTGT TTCTATAAGC TAATGCTCCA 900
 GAAACTTTGC CAACCTGTTA GTGTACACAC ACTGAGGGGA GTGCTCCCGG TGAATATTAT 960
 50 CATAGGGCTT TATTATATTC TTGGTCTTCA TTTCTGATCA AGTAAATACA CCAGCAGTTG 1020
 TCATTCAATG CAGGTTTTTG TACTTAATTA TATGGTGATT TTTTACTTTT TTAAGAGCAG 1080
 55 AAACGGAAAT TGACCTCCCC GCCATGTGTT TAATATTCCT CCTGCTTTTA CTTTGTGCAT 1140
 TTTCTTGATA ATCGTAAGCC TTGAGAGTGT TTGTGAAAAA GTTTTATTTC CTGTTATGTA 1200
 TACATAATTA AATGAAAATT CTTCAGAAAA AGTTTGATAA ATTGAATTGT GGTATGAAA 1260
 60 CTAATTTGCA TTTTATTTG CTTAAGAAAG AAAGCTGTGA TAGATTCCAG ATATGCTTTT 1320

5 TGATGTTTTTCTCTGCTCCA GCTCCAAGAA GTCAGCACAC CTGCATTTTA GCTCTGCATG 1380
 CAGCCCCAGC AGGCTGCGTG TTTAAGAATT TCATTGTTTA ACTGGCTGGT GTGAGAAGTC 1440
 TTCCGTTAGC ATAGAGTGA AGGAGTACTA TTGTTTGGTT GGGTTTTTGT TTGTTTGTTC 1500
 TTTGTTTTTG CTTTTATTGC CAAGAGGTGC TTGTTTTTAA AGTATGTTTA ATAAAATGAA 1560
 10 ATTCTAAAGT TAARAAGTGT TCTTAAAGTT GATATTTAAC TCT 1603

15 (2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1089 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

25 GGCACGAGCT ACCTTTCTGC CTGCTTTGCT GGCTGCAACA GCACGAATCT CACGGGCTGT 60
 GCGTGCCTCA CCACCGTCCC TGCTGAGAAC GCAACCGTGG TTCCTGGAAA ATGCCCCAGT 120
 CCTGGGTGCC AAGAGGCCTT CCTCACTTTC CTCTGTGTGA TGTGTATCTG CAGCCTGATC 180
 30 GGTGCCATGG CAAGACACCC TCAGTCATCA TCCTCATCAG GACAGTCAGC CCTGAACTCA 240
 AGTCTTACGC TTTGGGAGTT CTTTTTCTCC TCCTTCGTTT GTTGGGCTTC ATCCCTCCAC 300
 35 CCCTCATCTT CGGGGCTGGC ATCGACTCCA CCTGCCTGTT CTGGAGCACG TTCTGTGGGG 360
 AGCAAGGCGC CTGCGTCTTC TACGACAATG TGGTCTACCG ATACCTGTAT GTCAGCATCG 420
 CCATCGCGCT CAAATCCTTC GCCTTCATCC TGTACACCAC CACGTGGCAG TGCTGAGGAA 480
 40 AAATATAAA CGCTACATCA AAAACCACGA GGGCGGGCTG AGCACCAGTG AGTTCTTTGC 540
 CTCTACTCTG ACCCTAGACA ACCTGGGGAG GGACCCTGTG CCCGCAAACC AGACACATAG 600
 45 GACAAAGTTT ATCTATAACC TGGAAGACCA TGAGTGGTGT GAAAACATGG AGTCCGTTTT 660
 ATAGTGACTA AAGGAGGGCT GAACTCTGTA TTAGTAATCC AAGGGTCATT TTTTTCTTAA 720
 AAAAAGAAAA AAAGGTTCCA AAAAAACCA AAACCTAGTA CACACACACA GGCACAGATG 780
 50 CACACACAG CAGACAGACA CACCGACTTT GTCCTTTTTC TCAGCATCAG AGCCAGACAG 840
 GATTTCAGAA AAGGAGAGAA TGACATCGTG CGGCAGGGTC CTGGAGGCCA CTCGCGCGGC 900
 55 TGGGCCACAG AGTCTACTTT GAAGGCACCT CATGGTTTTT AGGATGCTGA CAGCTGCAAG 960
 CAACAGGCAC TGCCAAATTC AGGGAACAGT GGTGGCCAGC TTGGAGGATG GACATTTCTG 1020
 60 GATACACATA CACATACAAA ACAGAAAACA TTTTITAAAA GAAGTTTCCT AAAATAAAAA 1080

AAAAAAAAA

1089

5

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 629 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

15

AGCTCAGTTC CCTAGAAAT GAAATTTTAA ATGACACTAC CAGGTAAGCC ACTGAGACCA 60

GTGGAGGTGA TAGCTAAGAA CATAAGGAAT TAAGAATTTT TAATGGAGAA AGGAGGTAAT 120

20

GAATACCAGT TACATCCTAA GACTCACTGT AGTGGTGAGT GTTGTAATTT ATCTCGCTAT 180

CCATCCTCTT TTAAGTTTTT CCTTAGAAAG TCCTCTATTG GTACCTTGGA GGGACTGCTG 240

25

TCAAAATATA TGGAAAAGTG GGCTGTGTGT GTACAAGAGG TGGACTTTGC CACACATGGA 300

AGTTTGCTGC CAAGATCTTC ACTAATGAAA GAAATCACCA GTGAGCTGCA CAGATTAGCC 360

AAATACTGAG CTCATTAGAA CTACTAAGGC CTGGACATTT CTGCCTAATC CAGGACTCCT 420

30

GTAATTATCA GTCCTTGCTT TGGAGCTTCC CATGTGTGTAG CTGARAATTT GTCATATCTG 480

CATTATAATC TAAGGCTCCA CATACTTAAT CCTGCTTCTC CCCCTTTTTT TTTCCCTTTC 540

35

CCAGCGGTCA GCTCTGCTGC ATAGTCTGAA GACTTTCCTT GCCCAATCCT GATAAAATTC 600

TTGCACTCGT AACCCCATCT CAGTGTCTG 629

40

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1964 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

50

AAGAAGACAT GGAAATTGCT GAAGGATGTT TCAGGCATAT TAAGAAAATC TTTACGCAGC 60

TTGAGGAATT CAGAGCCTCT GAATTGCTTC GAAGTGGACT GGACAGATCT AAATACCTTT 120

55

TAGTGAAAGA AGCCAAAATT ATTGCTATGA CCTGTACTCA TGCTGCCTTA AAACGACATG 180

ACTTGGTCAA GCTAGGTTTC AAGTATGACA ACATTTTGAT GGAAGAGGCT GCTCAGATTC 240

60

TGGAGATAGA AACTTTTATC CCTCTTCTTC TACAGAATCC TCAGGATGGA TTTAGCCGAC 300

	TAAAACGATG GATTATGATT GGCGATCATC ACCAGTTACC TCCAGTTATT AANGAACATG	360
	GCCTTTCAAA AGTACTCAAA CATGGAGCAG TCTCTCTTCA CTCGCTTTGT TCGCGTTGGA	420
5	GTTCCGACTG TTGACCTTGA TGCTCAAGGG AGAGCCAGAG CAAGCTTGTG CAMCTNCTAC	480
	AACTGGCGAT ACAAGAATCT AGGAAACTTA CCCCATGTGC AGCTCTTGCC AGAGTTTAGT	540
10	ACAGCAAATG CTGGCTTACT GTATGACTTC CAGCTCATTA ATGTTGAAGA TTTTCAAGGA	600
	GTGGGAGAAT CTGAACCTAA TCCTTACTTC TATCAGAATC TTGGAGAGGC AGAATATGTA	660
	GTAGCACTTT TTATGTACAT GTGTTTACTT GGTTACCCTG CTGACAAAAT CAGTATTCTA	720
15	ACAACATATA ATGGCCAAAA GCATCTTATT CGCGACATCA TCAATAGACG ATGTGGAAAC	780
	AATCCATTGA TTGGAAGACC AAACAAGGTG ACAACTGTTG ATAGATTTCA AGGTCAACAG	840
20	AATGACTATA TTCTTCTTTC TCTGGTACGA ACCAGGGCAG TGGGCCATCT GAGGGATGTC	900
	CGTCGCTTGG TAGTGGCCAT GTCTAGAGCC AGACTTGGAC TTTATATCTT CGCCAGAGTA	960
	TCCCTCTTCC AAAACTGTTT TGAAGTACT CCAGCTTTCA GTCAGCTCAC AGCTCGCCCC	1020
25	CTTCATTTGC ATATAATTCC AACAGAACCT TTCCCAACTA CTAGAAAGAA TGGAGAGAGA	1080
	CCATCTCATG AAGTACAAAT AATAAAAAAT ATGCCCCAGA TGGCAAACCT TGTATACAAC	1140
30	ATGTACATGC ATTTGATACA GACTACACAT CATTATCATC AGACTTTATT ACAACTACCA	1200
	CCTGCTATGG TAGAAGAGGG TGAGGAAGTT CAAAATCAAG AAACAGAATT GGAAACAGAA	1260
	GAAGAGGCCA TGACTGTTCA AGCTGACATC ATACCCAGTC CAACAGACAC CAGCTGCCGT	1320
35	CAAGAACTC CAGCCTTTCA AACTGACACC ACCCCCAGTG AGACAGGAGC CACTTCCACT	1380
	CCAGAAGCCA TCCCTGCTTT ATCTGAGACC ACCCTACTG TGGTAGGAGC TGTATCTGCA	1440
40	CCGGCAGAAG CTAACACACC TCAGGATGCC ACATCTGCCC CAGAAGAGAC CAAGTAGCCA	1500
	AACTGTAGTC CTCTAAAGG AGGACATGGC AGTCAAAAAG TCTGAGTAAA GCTGTTTTTT	1560
	GTATTTTATA TTTGCTTCTG CCATTTTACT GTCACATAAT AATGTTTAGT TCTTATATTT	1620
45	GTAACTGAT TTCGGTGTCT TGAATATATT TTTTAAATT ATGTGTATGA ACAATTCTAG	1680
	TTTCATTTGT TCAATCAGAA GAGCAAATAA CCATTCCTTT CATGTTTGA TCACTGAGTG	1740
50	TGTCTGTAAT CATACCTACA TTAAAATCAT TTTCTATGAA TATATAATAT ATACTTCACA	1800
	TTTTTAGTGA ACTTCTCTAA AGAAGAGGAC AGAATATACT GGACTTAACC ACGAATACCC	1860
	TTGAGTGTCC AAATGGGAA GGAACKGTT TCTTCYGTTA TACTAYCAAA TGCTTAAATT	1920
55	CKGTTTCCTT TTTCTTACC TTTGTTGCT GTCTTTATGT AAAG	1964

60 (2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1522 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

10	CGTGTCCGCG CGCCTGGGAG ACGCTGCCTC GGCCCGGACG CGCCCGCGCC CCCGCGGCTG	60
	GAGG3TGGTC GCCACTGGGA CACTGTGAAC CAGGAGTRAG TCGGAGCTGC CGCGCTGCCC	120
	AGGCCATGGA CTGTGAGGTC AACAAACGGTT CCAGCCTCAG GGATGAGTGC ATCACAAACC	180
15	TACTGGTGTT TGGCTTCCTC CAAAGCTGTT CTGACAACAG CTTCCGCAGA GAGCTGGACG	240
	CACTGGGCCA CGAGCTGCCA GTGCTGGCTC CCCAGTGGGA GGGCTACGAT GAGCTGCAGA	300
20	CTGATGGCAA CCGCAGCAGC CACTCCCGCT TGGGAAGAAT AGAGGCAGAT TCTGAAAGTC	360
	AAGAAGACAT CATCCGAAT ATTGCCAGGC ACCTCGCCCA GGTCGGGGAC AGCATGGACC	420
	GTAGCATCCC TCCGGGCCTG GTGAACGGCC TGGCCCTGCA GCTCAGGAAC ACCAGCCGGT	480
25	CGGAGGAGGA CCGGAACAGG GACCTGGCCA CTGCCCTGGA GCAGCTGCTG CAGGCCTACC	540
	CTAGAGACAT GGAGAAGGAG AAGACCATGC TGGTGCTGGC CCTGTGCTG GCCAAGAAGG	600
30	TGGCCAGTCA CACGCCGTCC TTGCTCCGTG ATGTCTTTCA CACAACAGTG AATTTTATTA	660
	ACCAGAACCT ACGCACCTAC GTGAGGAGCT TAGCCAGAAA TGGGATGGAC TGAACGGACA	720
	GTTCAGAAAG TGTGACTGGC TAAAGCTCGA TGTGGTCACA GCTGTATAGC TGCTTCCAGT	780
35	GTAGACGGAG CCCTGGCATG TCAACAGCGT TCCTAGAGAA GACAGGCTGG AAGATAGCTG	840
	TGACTTCTAT TTAAAGACA ATGTTAACT TATAACCCAC TTAAATATAT CTACATTAAT	900
40	ATACTTGAAT GAAATGTCC ATTTACACGT ATTTGAATGG CCTTCATATC ATCCACACAT	960
	GAATCTGCAC ATCTGTAAAT CTACACACGG TGCCTTTATT TCCACTGTGC AGGTTCACCAC	1020
	TTAAAAATTA AATTGGAAAG CAGGTTTCAA GGAAGTAGAA ACAAATACA ATTTTTTTGG	1080
45	TAAAAAATAA TTACTGTTTA TTAAAGTACA ACCATAGAGG ATGGTCTTAC AGCAGGCAGT	1140
	ATCCTGTTTG AGGAAAGCAA GAATCAGAGA AGGAACATAC CCCTTACAAA TGAAAAATTC	1200
50	CACTCAAAAT AGGGAATATC YATCTTAATA CTAAGGAACC AACAACTTC CTGTTTAAAA	1260
	AACCACATGG CACAGAGATT CNGAACTAAA GTGCTGCACT CAAATGATGG GAAGTCCCGG	1320
	CCCCAGTACA CCAGGGGCTT TGGACTTTTT TCAACTTCGT TTCTTTTGT TTGGANTCCA	1380
55	AAAGAACCAC TTTGTGGTTC TTAAAAGGGT GTGAAGGTGA TTAAAGGGC CCAGGTCAGC	1440
	CACTGGTTGG TTTACAAAT CNGGGTAACT AACTGCATAC AACTTTTTCC CNFTTCCATG	1500
60	NCATCAGGAC TTTGCTAAAG AC	1522

5 (2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 875 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

15 TGGGATTTCCT CTTTATCATG GAGGCCTTGT CCCACTTCCT CTATGTCCCT TTCCTTGGTG 60
TCTGTGTCTG TGGGGCCATC TACACTGGCC TGTTCTTCC TGAGACCAA GGCAAGACCT 120
TCCAAGAGAT CTCCGAGGAA TTACACAGAC TCAACTTCCC CAGGCGGGCC CAGGGCCCCA 180
20 CGTGGAGGAG CCTGGAGGTT ATCCAGTCAA CAGAACTCTA GTCCCAAAGG GGTGGCCGTA 240
GCCAAAGCCA GCTACCGTCC TGTCTCTGC TTCCTGCCAG GGCCCTGGTC CTCAMTYCCT 300
25 YCTGCATTCC TCATTTAAGG AGTGTTTATT GAGCACCTT TGTGTGCAGA CATGGCTCCA 360
GGTGCTTAGC AATCAWTGGT GAGCGTGGTA TCCAGGCTAA AGGTAATTAA CTGACAGRAA 420
ATCAGTAACA ACATAATTAC AGGYTGGTTG TGGCAGYTCA TGA CTGTAAT CCCAGCACTT 480
30 TTGGGAGCCA AGGTGGGARG ATCAATTGAG GCCAGAGTTT GAAAMCAGCT AGGTAACATA 540
GTGAGACCCC CTATCTCTAC AAAAAATTTT AAACATTAGC TGGGCATGGT GGTATGTGCT 600
35 AACAGCTCTA GCTACTCAGG AGGCTGAGGC AGCAGGATCA CTGAGTCCA AGAGTTCAAG 660
GTAGCAGTAA GCTACAATCA CACCACTGCA TGCCAGACTG GGTGACAGAG GGAGACTTCA 720
TCTCTTTAAA ACATAATAAT AATAATTACA GACTCAGGAA ATGCAGTGAA AGAAAAATAC 780
40 AGGTTGGCCA GGTGAGGTGG CTGATGCCTG TAATCCCAGC ACTTTGGGAG GCCAAGATGG 840
GAAGATGCT TTGAGACCAG AAGTTTGAGA CCAGC 875

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(2) INFORMATION FOR SEQ ID NO: 43:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CCCACGCGGT CCGNATCGTC CTTCCCTCAC TTCAGAGGGT GGCCAGAGCT GAATACCCAG 60
60 AGAGGGACAA GTAAGGTCC AGTTCCAAA CATCATGAGG ATGTATCATC CCACGTGTCT 120

CACCTGACAG TTACAGAGGA AACCCGCACC CAGAATGCAC GTGCTGTCCTT ATGGGAACAC 180
 5 TCAGCGCAGA GTGCTCAGGT CCGGCCACAC TCGGGCTGTG CTTGGTCGTG CCATGGAATT 240
 CCTCAGGACT TTCTCAGCCT CCCTAATGGC AGAAGCCCCT TTACAGCAAG ACATTTACCG 300
 TTTGTCTGAA AATAGCCGAA CTGAGCTTTT CTTCAGGCTA TATGAGAAGT CTCTAGACAG 360
 10 TGGGCACCGT CAGAAAGCCC AGAGCCTTGT GATAGCTCCC ACCCTGCCTG GCTCAGATCT 420
 TCCCATTTTT TTCTCTCTGG CACTAACCTC ACCTTTTGTT TTTTGTGTT TGTGTTTGTT 480
 15 TTTGTTTMTG CAGAGTTGGA TTACAGAAAC TCCTATGAAA TTGAATATAT GGAGAAAATT 540
 GGCTCCTCCT TACCTGTAAG TTCGTCTGCC TCGGGCCACT TAGGGGACTC GCTTTCCTGC 600
 CTTCAGGGGC CTCTCCCTT GTGCAGAGTG TCTCTGGGAG CTCAGACCCC AAATCGAGTG 660
 20 TTTTCTGTGT ACACAGCTTC CCGGGTGCAC AGCAATGATG GACTGGGGCT GGGGGGTGA 720
 GGTTTGTACT CAATCCACTT CGTTTGACAT TTTCAGGGAG AAAATGATAG AATACAATTA 780
 25 GACGTCCTGC AGAATTACTT TCCTAGACTG AGAAAGAGCT AGAGATTTCT TTAACAAAAA 840
 AAA 843

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(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 489 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

40

CTCTTAGGCT TTGAAGCATT TTTGTCTGTG CTCCCTGATC TTCAGGTCAC CACCATGAAG 60
 TTCTTAGCAG TCCTGGTACT CTTGGGAGTT TCCATCTTTC TGGTCTCTGC CCAGAATCCG 120
 45 ACAACAGCTG CTCCAGCTGA CACGTATCCA GCTACTGGTC CTGCTGATGA TGAAGCCCCT 180
 GATGCTGAAA CCACTGCTGC TGCAACCACT GCGACCACTG CTGCTCCTAC CACTGCAACC 240
 ACCGCTGCTT CTACCACTGC TCGTAAAGAC ATTCCAGTTT TACCCAAATG GGTGGGGAT 300
 50 CTCCCGAATG GTAGAGTGTG TCCCTGAGAT GGAATCAGCT TGAGTCTTCT GCAATTGGTC 360
 ACAACTATTC ATGCTTCCTG TGATTTTCATC CAACTACTTA CCTGCTCTAC GATATCCCCT 420
 55 TTATCTCTAA TCAGTTTATT TTCTTTCAA TAAAAAATAA CTATGAGCAA CAAAAAATAA 480
 AAAAAAATAA 489

60

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 534 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GAAGCAGTGT GTATCTATGA TTATATCTCT GTTCATCTAT ATATTTTGA CATGTAGCAA 60
CACCTCTCCA TCTTATCAAG GAACTCAACT CGGTCTGGGT CTCCCCAGTG CCCAGTGGTG 120
15 GCCTTTGACA GGTAGGAGGA TGCAGTGCTG CAGGCTATTT TGTMTTGTGT TACAAAAC TG 180
TCTTTTCCCT TTTCCCTCC ACCTGATTCA GCATGATCCC TGTGAGCTGG TTCTCACAAT 240
20 CTCTGGGAC TGGGCTGAGG CAGGGGCTTC GCTCTATTCT CCCTAACCAT ACTGTCTTCC 300
TTTCCCTTG CCACTTAGCA GTTATCCCC CAGCTATGCC TTCTCCCTCC CTCCCTTGCC 360
CTGGCATATA TTGTGCCTTA TTTATGCTGC AAATATAACA TTAAACTATC AAGTGAAAAA 420
25 AAAAAAAAAA AAAACTCCAA GGGGGGCGG GTACCCAATT CCCCTATAN TGAGTCNTAT 480
TACAATTAC TGGGCCGTCG TTTTACAACG TCGTGAATGG GAAAACCTGG GCGT 534
30

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GGCACCAGTC CGGGATGAGC TCAGCCGCGG CCGACCACTG GGCGTGGTTG CTGGTGCTCA 60
45 GCTTCGTGTT TGGATGCAAT GTTCTTAGGA TCCTCCTCCC GTCCTTCTCA TCCTTCATGT 120
CCAGGGTGCT GCAGAAGGAC GCGGAGCAGG AGTCACAGAT GAGAGCGGAG ATCCAGGACA 180
TGAAGCAGGA GCTCTCCACA GTCAACATGA TGGACGAGTT TGCCAGATAT GCCAGGCTGG 240
50 AAAGAAAGAT CAACAAGATG ACGGATAAGC TCAAAACCCA TGTGAAAGCT CGGACAGCTC 300
AATTAGCCAA GATAAAATGG GTGATAAGTG TCGCTTTCTA CGTATTGCAG GCTGCCCTGA 360
55 TGATCTCACT CATTTGGAAG TATTATTCTG TCCCTGTGGC TGTGCTGCCG AGTAAATGGA 420
TAACCCCTCT AGACCGCCTG GTAGCCTTTC CTACTAGAGT AGCAGGTGGT GTTGGGAATTA 480
CCTGTTGGAT TTTAGTCTGT AACAAAGTTG TCGCTATTGT GCTTCATCCG TTCAGCTGAA 540
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200

CAGGAGGATG GATACAGCCG CGAGGCTAAA AACCGGATTT CCTCTTCCTA GCTTAAAATC 600
 TGATTTACAC TGTMTTGT TTAAAGAAAC AAAAGTGCAT AGTTTAGATT TTTTMTTTTG 660
 5 TTGAATATGT TTGTCTTGG ACTTTATGAG AGACTCTTAT AAGAATCACG ATTTTCTACA 720
 CCTGTCATTG AGCCAAGAAA GTCCAGTTTA TGACACGTAT GTACTAGTGA ACACCGTCCT 780
 10 CGATCTGTAC GAAATGTGAA ATGTTTAGGG ACATCTCCAT GCTGTCACTT GTGATTGACC 840
 CTCTTATGTA TTTTGTCAT ATTGCCAACT GGAAAGTCAA AATTTCTAA CAACTTTAAG 900
 TAAGTTCTTT GAAGACTTAG TGCTGTTTTT AATCCAGTTT AGAAAGTAAC TTAATTTTAA 960
 15 TACCACTACT AAAAATTCGA AAATTTCTTC TTAAATCACA TTCAATATGG TTAAAAGAAC 1020
 AACACTAATT GACATGCGT GGGCTTTTTC TCCCTTTGTT TAAAATGTCA TTTGTTGAGC 1080
 AAGAGTTGTA TAGTATTATC TACTTACTTG AGGCTGTTAA TTTTTCATTA CAGTGTTTTG 1140
 20 TAAATGTATC CACGAGACCA TGATGCATTG TTTGTGCTC AACTTGTTT TGTATTTAA 1200
 AGCATTTTGA ATGAAGTGTA TTTTATAAGC ATTTAATATT TATGCTCTTT AGAATGGAAC 1260
 25 ACAGAAAACA AACCTTATAA GTCCTGATTA ATCTGAACCA ATAACCTGTG TGGCCTACAA 1320
 AGTATAATTC TATTAAATGT TCCTTAAAAC AAAAAAAAAA AAAAAAAAAA AAAA 1374

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(2) INFORMATION FOR SEQ ID NO: 47:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 596 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GAATTCGNCA CGAGATTACT TGGACATGAA AGAACTCAGG TTCAAGTTTA TTCATTTACT 60
 AAGTTAGTTA AATCATGTGC CTTCCATGAG CCTTCATTTG GTAACCTGGA AAATGGAAAT 120
 45 AATAACACTA GTCATATATA TTCTACACTG CTACCATATG GACCAAAGGG ATTATAGATT 180
 ACAATCACCA TCATTCCTGC TGACAGGTAT ATAGAAAACA ATTTCAATTGA AGAAAAGTCC 240
 50 TTACATTTAT CCTTTTCCTA ATATCTGCAT GGGTAAACTA ATAAATATAG TCATTAGAAA 300
 ACCCTTATTA TTATATTAG TTCAATGTGA GAACTGCTGC AGAAAAATA TGCTTTATAA 360
 TATTTTCTTG AATATACATA ATATTCATAA ATTTCAAAT CATTGAAAAT TACCTTAAAA 420
 55 TTGGAAAAAA TGTGCATTTT TACTCATATA ACAGTATAAA ATTCCTATGT CAATCTCTTT 480
 TTTTMTTTT TGTMTTGTAGT TGGAGTCTCG CTCTGTCGCC CAGGCTGGGC AACAGAGCAG 540
 60 GACCCTGTCT TAATTAAAAA AAAAAAAAAA AAACCTCGAGG GGGGCCCGGT ACCCTA 596

5 (2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 851 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

15 CACATGAAGA CACACAGTGG TGAGAAGCCC TTCCGCTGCG CCCGCTGTCC TTATGCCTCT 60
CCTCATCTGG ATAACCTGAA ACGGCACCAG CGCGTCCATA CAGGAGAGAA GCCCTACAAG 120
TGCCCCCTCT GCCCTTATGC CTGTGGCAAT CTGGCCAACC TCAAGCGTCA TGGTCGCATC 180
20 CACTCTGGTG ACAAACCTTT TCGGTGTAGC CTTTGCAACT ACAGCTGCAA CCAGAGCATG 240
AACCTCAAAC GTCACATGCT GCGGCACACA GGCAGAGAAGC CTTCCGCTGT GCCACCTGCG 300
25 CCTATACCAC GGGCCACTGG GACAACTACA AGCGCCACCA GAAGGTGCAT GGCCACGGTG 360
GGGCAGGAGG GCCTGGTCTC TCTGCCTCTG AGGGCTGGGC CCCACCTCAT AGCCCACCCT 420
CTGTTTTGAG CTCTCGGGGC CCACCAGCCC TGGGGACTGC TGGCAGCCGG GCTGTCCACA 480
30 CAGACTCATC CTGAACTAGG TCCTTCTTCC CCATGTTTTA TACAGACGGA CCAGAAGCCA 540
CCTTTTCTC CCCCCTGGC CAGGGGCTCC ACACAGACTA ACGTAGGCAC TATAAGGACC 600
35 AGCCCAACCC CATGGGCGGG GGGGCCATA TGGACCAGG GACCTTGCCT TGA CTGAGGC 660
ACTTCACGAG CTCAGTGAGA AGGGCCCTGT ATTCACCTCC ACTGCCCCCA GGGGCTGTGG 720
ACAAACCGGC TGGGGGACTG CCCAGCCTCC CACCTGTTTA TTAACTTAT TTCAGTGCTT 780
40 TATAATAAAG GAAACACTAA CAAAGCCATG TCTATGCTGA ATTGGCAATG GCAGGCAATT 840
TGGCCTTACC C 851

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(2) INFORMATION FOR SEQ ID NO: 49:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2020 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GTGAAATGAA AACAGTCTTT TTATAGCCTT TAGCTGTGA GTTTGGAAGT TTGGGGGTC 60
60 TTATGTTTGT TTGCCTCTT CTGTTTCTTG GAGGAGAGTT GAGGCTTTTC TTAGGTGCAT 120

	ACACAGACCC AGGTGAACAC GCTGACTGTG AACCTGCCCT GTATCCGGAG CTGTGCTGGG	180
5	CACTGAGGGG ATGCAACAAA ATTAGGAGAG GWTCCTTGCT CCCAACGTCT ACTTCTCCTA	240
	CCTCAACAGG GGTCCAGGGT GCAGTGAAC T CAGTTCTTGG CCCTTGGGTG AGGATTTCATG	300
	GATGAATGAA AGCTAGACCT GATGGGGAGG CATTATGACT AAATAGGCCC AGCCTCCTTC	360
10	CCTTCCAGCT CTGTCCCTAGG AGCATAGGCG GGAAATCTGA GTAGAGTCTG ACTGCAGTTT	420
	TTGCTTATGA TTTGTAAAAG CCGTCATGGG GTCAATAAGA AAATAGGGGT GATGGAGGGG	480
15	GAGAAGCCCA GGA CTGGGAG AATCGCACGT GCCCCAGGGG TTTTCACCAA GGATTTTCAA	540
	GACAAACTGG AGTAAGAATT AAAGCCCCAG AGGATTTAAT TATCCTGGTT TGCAAAAGAG	600
	CCTCCCATGC CAGTACCGCC CAGCCTTGGA GGCCGGAATG CTCATGCCCC CTGTGGTCTG	660
20	CTGTCTCTTC AGCCCATGCC CAGCAGATAC CTCCTGACT GGAGACGGGC TCAAAGCTGG	720
	ATTAGAAAGG GGAGMGGCAC TTGTGACTTT GTTTGACTCT GTGACTCACT TCCTCGCTCA	780
25	CACCTTGTTT GAACTACTGG ACTTTCAACT GGCTTCTCTT AGGTCAGGCA AGCAGACAGC	840
	TCCCCACTGA AGAGGTCTGT ACAGTGACAA CCCGGGCCGG CAGCAAGGAC ACAGATGCAG	900
	CCACAGTAAG GCTCCATCAG GACTGGGTCA GTGATGGCAA CAGGATGGCC AAGGATGGCT	960
30	CTAGAACAYT CTGTCCATGC GTCACCTCCC CCAGTTTTRT TTTTAGCTTT GGCTTCAGGG	1020
	AGTGACAGCC ATCACAAATA GCCACATTCT GCTCTACTCT CCAACATACC AGATTSTACA	1080
35	CTGTTGTTAT TTCATGAGAC GTGAATGTTG CAGAGAGTGG GGGGATCTTG GTTGTTAAGG	1140
	AACCTTACACT GGGGAGCTTT ACTCTTCCGT GTCAACAATG TGA CTACATG TTCTCCAGAT	1200
	TAGCCACACA TGCAAAATC AGTGTCCTTC TAGCTTTANC CGAGAAAGAA ACCAGTCCCA	1260
40	GGGAATGAAT GGTGGTCTCC CCACTCCCGG CAGCACTTTA GGCAGCCCAT AAGCTATGCG	1320
	AGAATGTGAA CGCTCACCTT GCTCCGTCAC GGTCTGACC TACCACATAA ACAGGAAGAA	1380
45	GCCAGTGACC GGAACAGCTC TAGGAATAAC AAGTCAGAAT AGAAGTGTC TTTATATTAC	1440
	CAGAAAATAT GGGCTTGGCC TAAGTCGCTG TCTCCTAACC TGCCGGGGTC ATTCCCCACC	1500
	AAACACCCCA TACTAAGGAG CCATGAGCCA CCTGGACATT CACCTTTTCT TTGACCATCT	1560
50	GGAGTCTGGG GCAACTTAAG GAAGGCNCCA CACAGTGGTG CAGGCACATT TCCAAGCGTA	1620
	GGTGTCCCTG GCTTTTGTGG CCAAAGCTAG TGTATGGTC AACACAGGC CAGGGTCTGT	1680
55	GGGGCACTGA CCTTGAAAGT GGCAAAATGG AGGTTTCACA GGCTGTGCGG GAGCAGGACG	1740
	GCTTGCTTCA TCTAACAATC TCAGTTTCCT TTAATAAAG AAAGAAAGGA AAAGATTTC	1800
	TAAGCAGGTG TCAGTGGACA GTTTAAGYAC TTAACCATTT CTCTTCTTCT TTATGGATGT	1860
60	GAAGTGTGCT GTGGATAAAT CATTTGTATT TCTTGAATGT TCTCTATGAC TAACAGTTAT	1920

TAAGTCGGTT GTGTATATGT GTAACATAATG TAACTGCCTT TTAATAATTC ATTACAATAA 1980
AAATGACTTT GCTCTGAAMA AAAAAAAAAA AAAAATCTGA 2020

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(2) INFORMATION FOR SEQ ID NO: 50:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2432 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

ATGAAGGGTC GTTGGTGGGA AAGATGGCGG CGACTCTGGG ACCCCTTGGG TCGTGGCAGC 60
AGTGGCGGCG ATGTTTGTTCG GCTCGGGATG GGTCCAGGAT GTTACTCCTT CTTCTTTTGT 120
TGGGTCTTGG GCAGGGGCCA CAGCAAGTCG GGGCGGGTCA AACGTTTCGAG TACTTGAAAC 180
GGGAGCACTC GCTGTCGAAG CCCTACCAGG GTGTGGGCAC AGGCAGTTCC TCACTGTGGA 240
ATCTGATGGG CAATGCCATG GTGATGACCC AGTATATCCG CCTTACCCCA GATATGCAAA 300
GTAAACAGGG TGCTTTGTGG AACCGGGTGC CATGTTTCCT GAGAGACTGG GAGTTGCAGG 360
TGCACTTCAA AATCCATGGA CAAGGAAAGA AGAATCTGCA TGGGGATGGC TTGGCAATCT 420
GGTACACAAG GAATCGGATG CAGCCAGGGC CTGTGTTTGG AAACATGGAC AAATTTGTGG 480
GGCTGGGAGT ATTTGTAGAC ACCTACCCCA ATGAGGAGAA GCAGCAAGAG CGGGTATTCC 540
CCTACATCTC AGCCATGGTG AACAACGGCT CCCTCAGCTA TGATCATGAG CGGGATGGGC 600
GGCCTACAGA GCTGGGAGGC TGCACAGCCA TTGTCCGCAA TCTTCATTAC GACACCTTCC 660
TGGTGATTCTG CTACGTCAAG AGGCATTGTA CGATAATGAT GGATATTGAT GGCAAGCATG 720
AGTGGAGGGA CTGCATTGAA GTGCCCGGAG TCCGCTGCC CCGCGCTAC TACTTCGGCA 780
CCTCCTCCAT CACTGGGGAT CTCTCAGATA ATCATGATGT CATTTCTCTG AAGTTGTGTTG 840
AACTGACAGT GGAGAGAACC CCAGAAGAGG AAAAGCTCCA TCGAGATGTG TTCTTGCCCT 900
CAGTGGACAA TATGAAGCTG CCTGAGATGA CAGCTCCACT GCCGCCCTG AGTGGCCTGG 960
CCCTCTTCTT CATCGTCTTT TTCTCCCTGG TGTTTCTGT ATTTGCCATA GTCATTGGTA 1020
TCATACTCTA CAACAAATGG CAGGAACAGA GCCGAAAGCG CTTCTACTGA GCCCTCCTGC 1080
TGCCACCACT TTTGTGACTG TCACCCATGA GGTATGGAAG GAGCAGGCAC TGGCCTGAGC 1140
ATGCAGCCTG GAGAGTGTTC TTGTCTCTAG CAGCTGGTTG GGGACTATAT TCTGTCACTG 1200
GAGTTTGTGAA TGCAGGGACC CCGCATTCCC ATGGTTGTGC ATGGGGACAT CTAACCTCTG 1260

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	TCTGGGAAGC CACCCACCCC AGGGCAATGC TGCTGTGATG TGCCTTTCCC TGCAGTCCTT	1320
	CCATGTGGGA GCAGAGGTGT GAAGAGAATT TACGTGGTTG TGATGCCAAA ATCACAGAAC	1380
5	AGAATTCAT AGCCCAGGCT GCCGTGTTGT TTGACTCAGA AGGCCCTTCT ACTTCAGTTT	1440
	TGAATCCACA AAGAATTAAA AACTGGTAAC ACCACAGGCT TTCTGACCAT CCATTCGTTG	1500
10	GGTTTGCAT TTGACCCAAC CCTCTGCCTA CCTGAGGAGC TTTCTTTGGA AACCAGGATG	1560
	GAAACTTCTT CCCTGCCTTA CCTTCCTTTC ACTCCATTCA TTGTCCTCTC TGTGTGCAAC	1620
	CTGAGCTGGG AAAGGCATTT GGATGCCTCT CTGTTGGGGC CTGGGGCTGC AGAACACACC	1680
15	TGCGTTTCAC TGGCCTTCAT TAGGTGGCCC TAGGGAGATG GCTTCTCTGCT TTGGATCACT	1740
	GTTCCCTAGC ATGGGTCTTG GGTCTATTGG CATGTCCATG GCCTTCCCAA TCAAGTCTCT	1800
20	TCAGGCCCTC ACTGAAGTTT GGCTAAAGGT TGGTGTAAAA ATCAAGAGAA GCCTGGAAGA	1860
	CATCATGGAT GCCATGGATT AGCTGTGCAA CTGACCAGCT CCAGGTTTGA TCAAACCAAA	1920
	AGCAACATTT GTCATGTGGT CTGACCATGT GGAGATGTTT CTGGACTTGC TAGAGCCTGC	1980
25	TTAGCTGCAT GTTTTGTAGT TACGATTTTT GGAATCCAC TTGAGTGCT GAAAGTGTA	2040
	GGAAGCTTTC TTCTTACACC TTGGGCTTGG ATATTGCCCA GAGAAGAAAT TTGGCTTTTT	2100
30	TTTTCTTAAT GGACAAGAGA CAGTTGCTGT TCTCATGTTT CAAGTCTGAG AGCAACAGAC	2160
	CCTCATCATC TGTGCCTGGA AGAGTTCAC TGCATTGAGC AGCACAGCCT GAGTGCTGGC	2220
	CTCTGTCAAC CCTTATTCCA CTGCCTTATT TGACAAGGGG TTACATGCTG CTCACCTTAC	2280
35	TGCCCTGGGA TTAAATCAGT TACAGGCCAG AGTCTCCTTG GAGGGCCTGG AACTCTGAGT	2340
	CCTCCTATGA ACCTCTGTAG CCTAAATGAA ATTCTTAAAA TCACCGATGG AACCACAAAA	2400
40	AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA	2432

- 45 (2) INFORMATION FOR SEQ ID NO: 51:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 50 (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

55	GACGCTGGGG GCGGGTGGGG GCGCGGGGTA CCGGGCTGGA CGGCCGGCCG GCGCCCCCTC	60
	ATTAGTATGC GGACGAAGCG GCGGGCTGCG CGGAGNGACG TCCCCTGCAG CCGCGGACCG	120
	AGGCAGCGGC GGCACCTGCC GGCCGAGCAA TGCCAAGTGA GTACACCTAT GTRAAACTGA	180
60	GAAGTGATTG CTCGAGGCCT TCCCTGCAAT GGTACACCCG AGCTCAAAGC AAGATGAGAA	240

	GGCCCAGCTT GTTATTAAAA GACATCCTCA AATGTACATT GCTTGTGTTT GGAGTGTGGA	300
	TCCTTTATAT CCTCAAGTTA AATTATACTA CTGAAGAATG TGACATGAAA AAAATGCATT	360
5	ATGTGGACCC TGACCATGTA AAGAGAGCTC AGAAATATGC TCAGCAAGTC TTGCAGAAGG	420
	AATGTCGTCC CAAGTTTGCC AAGACATCAA TGGCGCTGTT ATTTGAGCAC AGGTATAGCG	480
10	TGGACTTACT CCTTTTGTG CAGAAGGSCC CCAAAGACAG TGAAGCTGAG TCCAAGTACG	540
	ATCCTCCTTT TGGGTTCGG AAGTTCTCCA GTAAAGTCCA GACCCTCTTG GAACTCTTGC	600
	CAGAGCACGA CCTCCCTGAA CACTTGAAAG CCAAGACCTG TCGGCGCTGT GTGGTTATTG	660
15	GAAGCGGAGG AATACTGCAC GGATTAGAAC TGGGCCACAC CCTGAACCAG TTCGATGTTG	720
	TGATAAGGTT AAACAGTGCA CCAGTTGAGG GATATTCAGA ACATGTTGGA AATAAACTA	780
20	CTATAAGGAT GACTTATCCA GAGGGCGCAC CACTGTCTGA CCTTGAATAT TATTCCAATG	840
	ACTTATTTGT TGCTGTTTTA TTAAAGAGTG TTGATTTCAA CTGGCTTCAA GCAATGGTAA	900
	AAAAGGAAAC CCTGCCATTC TGGGTACGAC TCTTCTTTTG GAAGCAGGTG GCAGAAAAAA	960
25	TCCCAC TGCA GCCAAAACAT TTCAGGATTT TGAATCCAGT TATCATCAAA GAGACTGCCT	1020
	TTGRACATCC TTCAGTACTC AGAGCCTCAG TCAAGGTCTT GGGGGCCGAG ATAAGAACGT	1080
30	CCCCACAATC GGTGTCATTG CCGTTGTCTT AGCCACACAT CTGTGCGATG AAGTCAGTTT	1140
	GGCGGGTTTT GGATATGACC TCAATCAACC CAGAACACCT TTGCACTACT TCGACAGTCA	1200
	ATGCATGGCT GCTATGAACT TTCAGACCAT GCATAATGTG ACAACGGAAA CCAAGTTCCT	1260
35	CTTAAAGCTG GTCAAAGAGG GAGTGGTGAA AGATCTCAGT GGAGGCATTG ATCGTGAATT	1320
	TTGAACACAG AAAACCTCAG TTGAAAATGC AACTCTAACT CTGAGAGCTG TTTTGTACAG	1380
40	CCTTCTTGAT GTATTTCTCC ATCCTGCAGA TACTTTGAAG TGCAGCTCAT GTTTTAACT	1440
	TTTAATTTAA AAACACAAAA AAAATTTTAG CTCTTCCCAC TTTTTTTTTC CTATTTATTT	1500
	GAGGTCAGTG TTTGTTTTTG CACACCATTT TGTAAATGAA ACTTAAGAAT TGAATTGGAA	1560
45	AGACTTCTCA AAGAGAATTG TATGTAACGA TGTGTWTTG ATTTTAAAGA AAGTAATTTA	1620
	ATTTGTAAAA CTCTGCTCG TTTACACTGC ACATTGAATA CAGGTAAC TAATTGGAAGGA	1680
50	GAGGGGAGGT CACTCTTTTG ATGGTGGCCC TGAACCTCAT TCTGGTTCCT TGCTGCGCTG	1740
	CTTGGTGTGA CCCACGGAGG ATCCACTCCC AGGATGACGT GCTCCGTAGC TCTGCTGCTG	1800
	ATACTGGGTC TGCGATGCAG CGGCGTGAGG CCTGGGCTGG TTGGAGAAGG TCACAACCCT	1860
55	TCTCTGTGG TCTGCCTTCT GCTGAAAGAC TCGAGAACCA ACCAGGGAAG CTGTCTCTGGA	1920
	GGTCCCTGGT CGGAGAGGGA CATAGAATCT GTGACCTCTG ACAACTGTGA AGCCACCCTG	1980
60	GGCTACAGAA ACCACAGTCT TCCCAGCAAT TATTACAATT CTTGAATTCC TTGGGGATTT	2040

TTTACTGCCC TTTCAAAGCA CTTAAGTGTT AGATCTAACG TGTTCAGTG TCTGTCTGAG 2100
 GTGACTTAAA AAATCAGAAC AAAACTTCTA TTATCCAGAG TCATGGGAGA GTACACCCCTT 2160
 5 TCCAGGAATA ATGTTTTGGG AAACACTGAA ATGAAATCTT CCCAGTATTA TAAATTGTGT 2220
 ATTTAAAAAA AAGAACTTT TCTGAATGCC TACTGGCGGT GTATACCAGG CAGTGTGCCA 2280
 10 GTTTAAAAAG ATGAAAAAGA ATAAAACTT TTAGGAAMA AAAAAAAAAA AAAAAGTCGA 2340

15 (2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 601 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

25 AGTAGGGGAG ACTGAGACTG ACCGGTAGCC AGGCAGGCGG ACGACGCACG CCCGGACAGA 60
 CTGAGCAGGC GCCGGAGAAC CACTCACAGG TTCCCCCGC CTTTCCCTTT GAAANCTAGG 120
 CTTTTCCTTT TCCCGTGGCG CCCGAGAGAG AATGCTGGAC TCTGCCGACT TCAGCGCAAC 180
 30 TAANGATTTC TCAAGCTAGG GGACAAACGA TCAGCCCAAT CCTGAGAAGG GGGGAACCAA 240
 GCACCCCGTC CCCATCCCCC TCCCCTCCCC CGACTAAACT CGGGCGCCAA ACCCAGCCCT 300
 35 TCTCTAACCA CCCTACTTCC TCCTCTCCTT TCTAGCATGG TGGCTGTATG GACAGTCTGA 360
 CAGAACAGAG ACTGACATCT CCCAATCTGC CGGCCCCCA CCTGGAACAC TACAGTGTTT 420
 TGCATTGCAC CATGACCCTG GATGTGCAAA CTGTAGTCGT TTTTGCCGTG ATTGTAGTCC 480
 40 TCCTGCTTGT CAATGTCATA CTCATGTTTT TCCTGGGAAC GCGCTGAATG GAGTCCAGNC 540
 ACCTGAGCTG TCGCGAATC TCGCTTGAT TTCATCCCGA GAGCCACCGA GAAGAAAAAA 600
 45 A 601

50 (2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

60 CTCGTGCCGA ATTCGGCACG AGAGATGGTA CTTTTAAGAG GTAATTAGGT TGCTAAGATG 60

5 GATTAACATC TTTCTCTTGA CACTGAGACT GGGTCTCCT GGAATGGTT AGTTCCCAAG 120
AGAGTGAGTT GTTATAAAAC AATGCTGCCT CTTCTATTTT GCGCTTTTGT TTTGCACAAA 180
CTCGGTCCCC TTCTGTTTCT CTACGATGTT TTGATGCRGC ATGAGGCAGT CATGAGAACC 240
CACCAGATAC AGCTGCCTGA TCCTGAATTT CCCAGCCAAC AGAACCAAGT GCTAAATAAA 300
10 ACTCTTTTTA ATAAGTTAAA AAAAAAAAAA AAAAAAAAAA AANAAANANA AAAAAAAAAA 359

15 (2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1141 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

25 GGCACGAGCT GCTGAGGCGT GAGAATGGCG TCCCGCGGCC GCGTCCGGA GCATGGCGGA 60
CCCCCAGAGC TGTTTATGA CGAGACAGAA GCCCGGAAAT ACGTTCGCAA CTCACGGATG 120
ATTGATATCC AGACCAGGAT GGCTGGGCGA GCATTGGAGC TTCTTTATCT GCCAGAGAAT 180
30 AAGCCCTGTT ACCTGCTGGA TATTGGCTGT GGCAGTGGC TGAGTGAAG TTATCTGTCA 240
GATGAAGGCG ACTATTGGGT GGGCCTGGAT ATCAGCCCTG CCATGCTGGA TGAGGCTGTG 300
35 GACCGAGAGA TAGAGGGAGA CCTGCTGCTG GGGGATATGG GCCAGGGCAT CCCATTCAAG 360
CCAGGCACAT TTGATGGTTG CATCAGCATT TCTGCTGTGC AGTGGCTCTG TAATGCTAAC 420
AAGAAGTCTG AAAACCCTGC CAAGCGCCTG TACTGCTTTT TTGCTTCTCT TTTTCTGT 480
40 CTCGTCCGGG GATCCCGAGC TGTCTGCAG CTGTACCCTG AGAACTCAGA GCAGTTGGAG 540
CTGATCACAA CCCAGGCCAC AAAGGCAGGC TTCTCCGGTG GCATGGTGGT AGACTACCCT 600
45 AACAGTGCCA AAGCAAAGAA ATTCTACCTC TGCTTGTTTT CTGGGCCTTC GACCTTTATA 660
CCAGAGGGGC TGAGTGAAAA TCAGGATGAA GTTGAACCCA GGGAGTCTGT GTTCACCAAT 720
GAGAGGTTC CATTAAAGGAT GTCGAGGCGG GGAATGGTGA GGAAGAGTCG GGCATGGGTG 780
50 CTGGAGAAGA AGGAGCGGCA CAGGCGCCAG GGCAGGGAAG TCAGACCTGA CACCCAGTAC 840
ACCGGCCGCA AGCGCAAGCC CCGCTTCTAA GTCACCACGC GGTTCCTGGAA AGGCACTTGC 900
55 CTCTGCACTT TTCTATATTG TTCAGCTGAC AAAGTAGTAT TTTAGAAAAG TTCTAAAGTT 960
ATAAAAAATGT TTTCTGCAGT AAAAAAAAAA TTCTCTGGGC CGGGCGTGGT GGCTCACACC 1020
TGTAATCCCA GCACCTTGGG AGGCTGAGGT GGGAGGATCA TTTGAGGCCA GGAGTTTGAG 1080
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ACCTGCCTGG GCAACATAAT GAAACTTCCT TTCCAGGGAG AAAAAAAAAA AAAAAAAAAA 1140

A 1141

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(2) INFORMATION FOR SEQ ID NO: 55:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1560 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

	TCCTTCTCTG GGGCGGTCGC GTTGGCAGCG GATGCGGGAA GCCGGACTCT GGGCGTCATG	60
20	TACTACAAGT TTAGTGGCTT CACGCAGAAG TTGGCAGGAG CATGGGCTTC GGAGGCCTAT	120
	AGCCCGCAGA TTNAAGCCT GTGGTTTCCA CAGAAGCACC ACCTATCATA TTTGCCACAC	180
25	CAACTAACT GACCTCCGAT TCCACAGTGT ATGATTATGC TGGGAAAAC AAAGTTCCAG	240
	AGCTACAAAA GTTTTCCAG AAAGCTGATG GTGTGCCCCG CTACCTGAAA CGAGGCCTGC	300
	CTGACCAAAT GCTTTACCGG ACCACCATGG CGCTGACTGT GGGAGGGACC ATCTACTGCC	360
30	TGATCGCCCT CTACATGGCT TCGCAGCCCA AAAACAAATG AGTTAGGCTG CAGAGGACTG	420
	GTTTGTTTTT TGGCATAAAC CCTTTGAAGT TCCTTTTTCA TTGTTAAATT AAAATTTTTT	480
35	TTTTTACTTG GATGGCTTAA CATTTTGTCA AGAAAAATAG GAAGATATGA AGATGATGTT	540
	TTGGTTTGTT TATGAAATGC ATATGGCTTG TCAGAGCTCA TTCGACAGTT AAAGCCATTG	600
	TTTAAAGAAA CGGTGCTTTG CTCTGTGTTT GTGCTCCTGA TTTCCCTGGA GGTCTGGAT	660
40	GAAGGCTGAA CACAGGCTTG TTAATGTCAG TCTGTGCTGA GGACCTCAGG GACTTGAGGT	720
	TGCATTTTTG AGCATGGGGT GCAGGAGCCT TTCTGGATTT GGATGTGGCT ATGGAAAGAA	780
45	CACAGAAGCC AAGGTCATGT GCATGAAATG AGGAGTTTGA GTTAGTCACC TCGGGGATTT	840
	TTTCCATTTT GCAGTAAAAT GTTAAATPAA TGTAGCCTGC CTCTATTGTT TGGGCAGGTA	900
	ATTTCAAAGG GTTATTTGCC TCATCTCCTA TCTTTAGTGA AATCTTATGT GTAATTGTGT	960
50	GTATTTATTC CACCGTGGGA ACAGAGAATA CCTGTTTAGT GTTGCACTTT AGACTGGTGT	1020
	CTGTTTTGTT AATGCAGCTG TGCCACAAAT TCTCCTTTAT CTTTTAAAAA TGTATAGCT	1080
55	TTAAATTTTG ATTTATTTTG ACTGTGGAAT AAATACATGA ATGAAAAATT TTAAGTTTGA	1140
	AGTTCTTTGA ATGACCTTTC AGAGTAATTT CAGAACACCA GCAGCATCTT AAACCTGAGT	1200
	CTAATTTCTT TCTTGTTAAT TAGGCACCAG ATAATCTTTA TAAATGGTC TTAAGGCTA	1260
60	GTAATAGGAG CTTAATGGCA ATKGATGATT ACCACAKGGT TTTTATAAAA AACCTGCCTG	1320

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CCCCTWAGTG AAAGGTACCT GTAACYCACA GTYCATTTAG AACTAATTTT CCTYTGCYGT 1380
CATGATTGGK AGACTTCACT TACCCTATAT TAATTTTGAA AAAAGGTGGA ATTTTATTAT 1440
ATATGAAGGA ATAGTTTGTA TCTTACCATA GCACAGAACA GTGACCTCTT GCTCAGGATA 1500
AGATGTGGTG ATTTGAAAAT ACTCATAGTA GCCTGTCAGT GATACCTCTC TCNCTCTCTC 1560

(2) INFORMATION FOR SEQ ID NO: 56:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1507 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

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GGAACGCAGA GCGGAGCGTG GAGAGCGGAG CGAAGCTGGA TAACAGGGGA CCGATGATGT 60
GGCGACCATC AGTTCTGCTG CTTCTGTTGC TACTGAGGCA CGGGGCCAG GGAAGCCAT 120
CCCCAGACGC AGGCCCTCAT GGCCAGGGGA GGTGACCA GCGGCCCCC CTGAGCGACG 180
CTCCCCATGA TGACGCCAC GGAACCTTC AGTACGACCA TGAGGCTTTC CTGGGACGGG 240
AAGTGGCCAA GGAATTCGAC CAACTCACCC CAGAGGAAAG CCAGGCCCGT CTGGGGCGGA 300
TCGTGGACCG CATGGACCGC GCGGGGACG GCGACGGCTG GGTGTCGCTG GCCGAGCTTC 360
GCGCGTGGAT CGCGCACACG CAGCAGCGGC ACATACGGGA CTCGGTGAGC GCGGCCTGGG 420
ACACGTACGA CACGGACCGC GACGGGCGTG TGGTTGGGA GGAGCTGCGC AACGCCACCT 480
ATGGCCACTA CGCGCCCGGT GAAGAATTTT ATGACGTGGA GGATGCAGAG ACCTACAAAA 540
AGATGCTGGC TCGGGACGAG CGGCGTTTCC GGTGGCCGA CCAGGATGGG GACTCGATGG 600
CCACTCGAGA GGAGCTGACA GCCTTCCTGC ACCCGAGGA GTTCCCTCAC ATGCGGGACA 660
TCGTGATGTC TGAAACCTG GAGGACCTGG ACAGAAACAA AGATGGCTAT GTCCAGGTGG 720
AGGAGTACAT CGCGGATCTG TACTCAGCCG AGCCTGGGA GGAGGAGCCG GCGTGGGTGC 780
AGACGGAGAG GCAGCAGTTC CGGGACTTCC GGGATCTGAA CAAGGATGGG CACCTGGATG 840
GGAGTGAGGT GGGCCACTGG GTGCTGCCCC CTGCCCAGGA CCAGCCCCTG GTGAAGCCA 900
ACCACCTGCT GCACGARAGC GACACGGACA AGGAYGGCG GCTGAGCAA GCGSAAATCC 960
TGGGTAATTG GAACATGTTT GTGGCAGTC AGGCCACCAA CTATGGYGAG GACCTGACCC 1020
GGCACCACGA TGAGCTGTGA GCMCCGNGCA CCTGCCACAG CCTCAGAGGC CCGCACAATG 1080
ACCGGAGGAG GGGCCGCTGT GGTCTGGCCC CCTCCCTGTC CAGGCCCCGC AGGAGGCAGA 1140

TGCAGTCCCA GGCATCCTCC TKCCCCTGGG CTCTCAGGGA CCCCCTGGGT CGGCTTCTGT 1200
CCCTGTCACA CCCCCAACCC CAGGGAGGGG CTGTCATAGT CCCAGAGGAT AAGCAATACC 1260
5 TATTTCTGAC TGAGTCTCCC AGCCCAGACC CAGGGACCCT NGGCCCCAAG CTCAGCTCTA 1320
AGAACC GCCC CAACCCCTCC AGCTCCAAAT CTGAGCCTCC ACCACATAGA CTGAAACTCC 1380
CCTGGCCCCA GCCCTCTCCT GCCTGGCCTG GCCTGGGACA CCTCCTCTCT GCCAGGAGGC 1440
10 AATAAAAGCC AGCGCCGGGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1500
AAAAAAN 1507

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(2) INFORMATION FOR SEQ ID NO: 57:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

GAATTCGGCA CGAGCAGTGT CCAACACTGT AGCTGGTGCC TGCCAGGTTC CCAGTGGCTG 60
30 GGGTCACCAG GTCTGAAGAG AGATGTGCTG GCTGCGGGCA TGGGSCCAGA TCYTCTTGCC 120
AGTTTTCYTC TCCYTCTTTC TCATCCAATT GCTTATCAGC TTCTCAGAGA ATGGTTTAT 180
CCACAGCCCC AGGAACAATC AGAAACCAAG AGATGGGAAT RAAGAGGAAT GTGCTGTAAA 240
35 GAAGAGTTGT CAATTGTGCA CAGAAGATAA GAAATATATG ATGAATAGAT AATTGAAAAG 300
AGATCCTCCA GAAAGAGCAG AAGGAAGTTT CTTCAATGGC TTCCTTCAGG ATTTTAATCA 360
40 TCCTTACAGC CTCTTTGAGA ATGATTGAAC TTCCAAATTC CCTGAAGTTA AAATTTTAAA 420
TTCTATTAAA CATTTTTCG AGTAAAAAAA 450

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(2) INFORMATION FOR SEQ ID NO: 58:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GGCACGAGAC CCATTGAGCA GAAGGAGGCC AGGTGGGAAA GCTCCTGGGA AGAGCAGCCA 60
GACTGGACAC TGGGCTGCTT GAGTCCTGAG TCACAATTCA GAAATCCTGG GCTCCCTGGG 120
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	TGCATCTCTAT CATTCAGTT GAAAGTTTGC TTCCTTCCAG TCATGTGGCT CTTCACTCTA	180
	CTCTCCTTGG CTCTCATTTT AGATGCCATG GTCATGGATG AAAAGGTCAA GAGAAGCTTT	240
5	GTGCTGGACA CGGCTTCTGC CATCTGCAAC TACAATGCCC ACTACAAGAA TCACCCCAA	300
	TACTGGTGCC GAGGCTATTT CCGTGACTAC TGCAACATCA TCGCCTTCTC CCCTAACAGC	360
	ACCAATCATG TGGCCCTGAA GGACACAGGG AACCAGCTCA TTGTCACTAT GTCTGCCTG	420
10	AACAAAGAAG ACACGGGCTG GTACTGGTGT GGCATCCAGC GGGACTTTGC CAGGGATGAC	480
	ATGGATTTTA CAGAGCTGAT TGTAAGTAC GACAAAGGAA CCTGGCCAAT GACTTTGGTC	540
15	TGGGAAAGAC TATCAGGCAC AAAACCAGAA GCTGCAAGGC TCCCAAAGTT GTCCGCAAGG	600
	CTGACCGCTC CAGGACGTCC ATTCTCATCA TTTGCATACT GATCACGGGT TTGGGAATCA	660
	TCTCTGTAAT CAGTCATTTG ACCAAAAGGA GGAGAAGTCA AAGGAATAGA AGGGTAGGCA	720
20	ACACTTTGAA GCCCTTCTCG CGTGTCTGA CTCCAAAGGA AATGGCTCCT ACTGAACAGA	780
	TGTGACTGAA GATTTTTTTA ATTTAGTTCA TAAAGTGATG CTACAACAGA ATAATCACCA	840
25	TGACAACTGG CCCCACACCT CAGAGACTGA TTCTGATCTC CCAGGAATTC TGAAGGTCCC	900
	TCTATCCTTG ACAACAATCA TTTGCAGCCA GGTAGCAACG GCAGTAGTCA GAGGAGCTAT	960
	GATAGACCAC ACCCAAGCAA GGCTGCCCTC AAATAACATC TCAAGATCTT AGTTCTTATG	1020
30	CATTCCATCA GTCAGAAGTG AAGAAGAGGT GGAGAATCTG GATTGGGGAC CAGGAAATCA	1080
	CTTGTATTTT GTTAGCCAAT AAATTCCTAG CCAGTGTGA ATGAAAAAA AAAAAAAA	1140
35	AAAAAA	1147

40 (2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 777 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

50	GGCAGAGGCT CCTCAGAAGG GCGTGGGCTC TCCAGTCTTC CACAGTCCCC ACCATGCCCT	60
	GTGCGCTTAC CGCTGACGTA GCTCACCCAT CTTTACTTG CCTGGCTAAG ATGCATGGCA	120
	TYWCATTTCC TCCTTGTTGC ACTGCAGTCA GTCCCTCACT GCCCCATCT CCTGGAAGAG	180
55	GAGCATAAGC TTTGCAAGGT CAGCCACTTC TCTGGGTCA CACTAGTTAC ATCAAGACAG	240
	GACTCCAGCT CATATGTGCC AGTGCAGACA CTCTCATCC ACCTGGGGCC CTGGGCTTGG	300
60	GACCTGGYTC CTTGCACAGC AGARGACCCG GAGGCTGAGA GGAGCTTGCG GTTGTGTCAT	360

5 AGTCACCTGG CCAGARGGAA CGTGAGCCCC TCCCAAGCTG CAGARGGARG GARCARGCGT 420
 GGCTGTCAGC ACCGAGGTAG CAGAGAATTA ACATTCTTGT CAGCAGAGAA TGAAGCAGGA 480
 ATATAATTAA AACTTTGCCC TTGGAATAGC TGATTCAATT GAATTTTATT CCACACGTTT 540
 GAAAGAGGAA AGAAAATGTG AAGACTTGCA GCCTGGTTCT CGCCTGGCCT GGGCTGGCCC 600
 10 AGCTGTCAGG CCCGGTTCCT TTCTGAGCAT TCAGTCCACT GATGTTGACT GAGGGCCAGG 660
 AGAGACCCTC AGCAGGGTAT TACCATATCA GCCTCCTATC GCTGCTGGGA GAAATTACCA 720
 15 TGAATTCAGT GGCTTAAAC AACACACGAG CCTCTCTGAG CCTACCCTGG CTCAGGA 777

20 (2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1191 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

30 AAGANTGATT TTCCTTACTC TCCAAAGCGT CAGCATTTTG AAGTTCTTT TATGAAAGTG 60
 GGGGCAAGAA TCAGGGTGAA AATGAGTGTA AACAAAGCCC ATCCTGTGGT CAGCACCAC 120
 TGGAGGTGGC CAGCAGAGTG GCCTCAGATG TTCCTGCACC TGGCCCAGGA GCCCAGGACA 180
 35 GAGGTCAAAT CTAGGCCCCCT TGGTCTGGCT GGATTCATCA GGCAAGATTC GAAAACAAGA 240
 AAACCTCTAG AACAAGAAAC AATCATGTCT GCAGCAGATA CGGCACTGTG GCCCTATGGC 300
 CATGGCAATC GTGAGCACCA AGAGAATGAG TTACAGAAAT ATCTCCAATA CAAAGACATG 360
 40 CATCTCCTGG ACAGTGGACA GTCGCTGGGA CACACACACA CACTTCAAGG CTCACACAAC 420
 CTAACAGCCT TAAATATCTG AAGAAACAGA ATCAGCAGAT TAAGTCAGCA GAGGGAGAGG 480
 45 TAGGCTGAAG CAGCAGGAGG CCAATTTTAT ATCCCACAGA TTTTMTTAAA AATGACTCCC 540
 CAGCAAGGGG TGGGGAGAAA GCCACTGATT TAGGAGAGTT CTTGGCTCAG CCAACCACTG 600
 50 CGGTTATCTA CACGTTTAC AAAGGCACRG AAGTAGAGAG GGGCTGCACT CACGACCCTC 660
 CCCAGGGCCC GCACAGCCAG ACACGGTGGG TTCTTCCTTT TTCCCTTCTG GCCTTGGTGG 720
 AATTCTACC ACGGTGGCCT CTGCCTTTGG GACAATGCCT TCATGCTCAT CCCCAGGTCA 780
 55 AGGATGGAGT CTGTTACCAT TTTCCAGGGG AAATTCCAAG GACCAGCCCC GCCTCATTAC 840
 GTTACCCCA CAGGAAGGTG ATCTGGAAAG CCTGTAAACA CGTACTCTGG GTGGCTGAGT 900
 60 GGTGTCACCA AGCTGCTTTT GTGCAGGGCT GAAGCACAGA CAAGAGGGCA GGCAGCTGCC 960

GGAGGCCTGA AGTGGGGAGA GATCCCCGCA GGCCTGCAGG AGCCAGGGAG AACCTCCAAC 1020
 TGGATCTAAA CTGTGGGACA GCCCAGGCGT GCCCCTCTTC ACATGGCTCC CAGGCTCCCT 1080
 5 CAAAGCCCTT CCCAGGCCCT GCAGGAAGAG AGGGAGGGTG AGGAGAGGCA GGGAGGGCAG 1140
 AGGTCGCCTG AAAGCCTGGG CTCCGAACCT CCTCAGCAGA GCTTTAAAGT G 1191

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(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 1580 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CCCCGCCCC CGCCACGAA GGAAGTGGCT GCTGCTCCGG CGCGACCCA GAGCCGGTTC 60
 GGCGCGTCGA CTGCCAGAG TCCGCGGCCG GGCGCGGGAG GAGCCAAGCC GCCATGGCCT 120
 25 ACCACAGCTT CCTGGTGGAG CCCATCAGCT GCCACGCCTG GAACAAGGAC CGCACCAGA 180
 TTGCCATCTG CCCCAACAAC CATGAGGTGC ATATCTATGA AAAGAGCGGT GCCAAATGGA 240
 30 CCAAGGTGCA CGAGCTCAAG GAGCACAACG GGCAGGTGAC AGGCATCGAC TGGGCCCCCG 300
 AGAGTAACCG TATGTGTACC TGCGGCACAG ACCGCAACGC CTACGTGTGG ACGCTGAAGG 360
 GCCGCACATG GAAGCCACG CTGGTCATCC TGCGGATCAA CCGGGCTGCC CGCTGCGTGC 420
 35 GCTGGGCCCC CAACGAGAAC AAGTTTGCTG TGGGCAGCGG CTCTCGTGTG ATCTCCATCT 480
 GTTATTTCTGA GCAGGAGAAT GACTGGTGGG TTTGCAAGCA CATCAAGAAG CCCATCCGCT 540
 40 CCACCGTCCT CAGCCTGGAC TGGCACCCCA ACAATGTGCT GCTGGCTGCC GGCTCCTGTG 600
 ACTTCAAGTG TCGATCTTT TCAGCTACA TCAAGGAGGT GGAGGAACGG CCGGCACCCA 660
 CCCCCTGGGG CTCCAAGATG CCCTTTGGGG AACTGATGTT CGAATCCAGC AGTAGCTGCG 720
 45 GCTGGGTACA TGGCGTCTGT TTCTCAGCCA GCGGGAGCCG CGTGGCCTGG GTAAGCCACG 780
 ACAGCACCGT CTGCCTGGCT GATGCCGACA AGAAGATGGC CGTCGCGACT CTGGCCTCTG 840
 50 AAACACTACC ACTGCTGGCG CTGACCTTCA TCACAGACAA CAGCCTGGTG GCAGCGGGCC 900
 ACGACTGCTT CCCGGTGTG TTCACCTATG ACGCCGCCG GGGGATGCTG AGCTTCGGCG 960
 GGCGGCTGGA CGTTCCTAAG CAGAGCTCGC AGCGTGGCTT GACGGCCCCG GAGCGCTTCC 1020
 55 AGAACCTGGA CAAGAAGGCG AGCTCCGAGG GTGGCACGGC TGCGGGCGCG GGCCTAGACT 1080
 CGCTGCACAA GAACAGCGTC AGCCAGATCT CGGTGCTCAG CGGCGCAAG GCCAAGTGCT 1140
 60 CGCAGTTCTG CACCACTGGC ATGGATGGCG GCATGAGTAT CTGGGATGTG AAGAGCTTGG 1200

5 AGTCAGCCTT GAAGGACCTC AAGATCAAAT GACCTGTGAG GAATATGTTG CCTTCATCCT 1260
 AGCTGCTGGG GAACCGGGGA GAGGGGTCAG GGAGGCTAAT GGTTCGCTTTG CTGAATGTTT 1320
 CTGGGGTACC AATACGAGTT CCCATAGGGG CTGCTCCCTC AAAAAGGGAG GGGACAGATG 1380
 GGGAGCTTTT CTTACCTATT CAAGGAATAC GTGCCTTTTT CTTAAATGCT TTCATTTATT 1440
 10 GAAAAA AAAAATGCCC CCAAAGCACT ATGCTGGTCA TGAAGTCTT CAAAATGTGG 1500
 AGGTAATAAA ATGCAACTGT GTAAAAA AAAAATAA AAATGACCCT CGCGATCTAG 1560
 15 AACTAGNCGG ACGCNTGGGT 1580

20 (2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

30 GGCACGAGGC GCGATGCAGC ACAGGCTAGA GGCTGCGCAA SGCGGGGGCC CGCCCCTGGG 60
 ACCCTCCGGG CCGGGCGGTT TGGCCCTTA GCGCCCGGC GTCGGGGCGG TAAAAGGCCG 120
 GCAGAAGGGA GGCACCTGAG AAATGTCTTT CCTCCAGGAC CCAAGTTTCT TCACCATGGG 180
 35 GATGTGGTCC ATTGGTGCAG GAGCCCTGGG GGCTGCTGCC TTGGCATGTC TGCTTGCCAA 240
 CACAGACGTG TTTCTGTCCA AGCCCCAGAA AGCGGCCCTG GAGTACCTGG AGGATATAGA 300
 40 CCTGAAAACA CTGGAGAAGG AACCAAGGAC TTTCAAAGCA AAGGAGCTAT GGGAAAAA 360
 TGGAGCTGTG ATTATGGCCG TCGGAGGCC AGGCTGTTTC CTCTGTCGAG AGGAAGCTGC 420
 GGATCTGTCC TCCCTGAAAA GCATGTGGGA CCAGCTGGGC GTCCCCCTCT ATGCAGTGGT 480
 45 AAAGGAGCAC ATCAGGACTG AAGTGAAGGA TTTCCAGCCT TATTTCAAAG GAGAAATCTT 540
 CCTGGATGAA AAGAAAAAGT TCTATGGTCC ACAAAGGCGG AAGATGATGT TTATGGGATT 600
 TATCCGTCTG GGAGTGTGGT ACAACTTCTT CCGAGCCTGG AACGGAGGCT TCTCTGGAAA 660
 50 CCTGGAAGGA GAAGGCTTCA TCCTTGGGGG AGTTTTCGTG GTGGGATCAG GAAAGCAGGG 720
 CATCTTCTT GAGCACCGAG AAAAGAATT TGGAGACAAA GTAAACCTAC TTTCTGTCT 780
 55 GGAAGCTGCT AAGATGATCA AACCACAGAC TTTGGCCTCA GAGAAAAAAT GATTGTGTGA 840
 AACTGCCCAG CTCAGGGATA ACCAGGGACA TTCACCTGTG TTCATGGGAT GTATTGTTTC 900
 60 CACTCGTGTC CCTAAGGAGT GAGAAACCCA TTTATACTCT ACTCTCAGTA TGGATTATTA 960

ATGTATTTTA ATATTCTGTT TAGGCCCACT AAGGCAAAAT AGCCCCAAA CAAGACTGAC 1020
 AAAAATCTGA AAAACTAATG AGGATTATTA AGCTAAAACC TGGGAAATAG GAGGCTTWAA 1080
 5 ATGACTGCCM GCTGGTGCR T GCTCACACTT GGCCAC 1117

10 (2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

20 CCCACGCGTG CKGGCGCCTG GCAGCCACCG CCTGGGAGGT TACTGTAAGG CCCGCAGCTC 60
 CCGCCAGCTC CCGCGGACTS CTGCCGCCTC CTTACCATGA AGCCAGTAAG TCGTCGCACG 120
 CTGGACTGGA TTTATTCACT GTTGCTGCTT GCCATCGTTT TAATCTCCTG GGGCTGCATC 180
 25 ATCTATGCTT CGATGGTGTG TGCAAGACGA CAGCTAAGGA AGAAATACCC AGACAAAATC 240
 TTTGGGACGA ATGAAAATTT GTAACCTCTC TGGATTTAAT TATCTGAAAA TACAGTTCTT 300
 30 TCCCTCATGC TTATGTAGAT ATAAAAATAA AATTCATAAT GCAAAAAAAA AAAAAAAAAA 360
 G 361

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(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1668 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GGCACGAGGT CTGCCAAGCT ATAGACCATG GCTGTGAACA CATTTGTGTG AACAGTGACG 60
 ACTCATACAC GTGCGAGTGC TTGGAGGGAT TCCGGCTCGC TGAGGATGGG AAACGCTGCC 120
 50 GAAGAAGGAT GTCTGCAAAT CAACCCACCA TGGCTGCGAA CACATTTGTG TTAATAATGG 180
 GAATTCCTAC ATCTGCAAAT GCTCAKAGGG ATTTGTCTTA GCTGAGGACG GAAGACGGTG 240
 55 CAAGAAATGC ACTGAAGGCC CAATTGACCT GGTCTTTGTG ATCGATGGAT CCAAGAGTCT 300
 TGGAGAAGAG AATTTTGAGG TCGTGAAGCA GTTTGTCACT GGAATTATAG ATTCCTTGAC 360
 AATTTCCCCC AAAGCCGCTC GAGTGGGGCT GCTCCAGTAT TCCACACAGG TCCACACAGA 420
 60

	GTTCACTCTG AGAAACTTCA ACTCAGCCAA AGACATGAAA AAAGCCGTGG CCCACATGAA	480
	ATACATGGGA AAGGGCTCTA TGACTGGGCT GGCCCTGAAA CACATGTTTG AGAGAAGTTT	540
5	TACCCAAGGA GAAGGGGCCA GGCCCTTTCC ACAAGGGTGC CCAGAGCAGC CATTGTGTTT	600
	ACCGACGGAC GGGCTCAGGA TGACGTCTCC GAGTGGGCCA GTAAAGCCAA GGCCAATGGT	660
10	ATCACTATGT ATGCTGTTGG GGTAGGAAAA GCCATTGAGG AGGAACTACA AGAGATTGCC	720
	TCTGAGCCCA CAAACAAGCA TCTCTTCTAT GCCGAAGACT TCAGCACAAT GGATGAGATA	780
	AGTGAAAAAC TCAAGAAAGG CATCTGTGAA GCTCTAGAAG ACTCCGATGG AAGACAGGAC	840
15	TCTCCAGCAG GGGAACTGCC AAAAACGGTC CAACAGCCAA CAGTGCAACA CAGATATCTG	900
	TTTGAAGAAG ACAATCTTTT ACGGTCTACA CAAAAGCTTT CCCATTCAAC AAAACCTTCA	960
20	GGAAGCCCTT TGGGAAGAAA ACACGATCAA TGCAAATGTG AAAACCTTAT AATGTTCCAG	1020
	AACCTTGCAA ACGAAGAAGT AAGAAAATTA ACACAGCGCT TAGAAGAAAT GACACAGAGA	1080
	ATGGAAGCCC TGGAAAATCG CCTGAGATAC AGATGAAGAT TAGAAATCGC GACACATTTG	1140
25	TAGTCATTGT ATCACGGATT ACAATGAACG CAGTGCAGAG CCCCAAAGCT CAGGCTATTG	1200
	TTAAATCAAT AATGTTGTGA AGTAAACAA TCAGTACTGA GAAACCTGGT TTGCCACAGA	1260
30	ACAAAGACAA GAAGTATACA CTAACCTGTA TAAATTTATC TAGGAAAAAA ATCCTTCAGA	1320
	ATTCTAAGAT GAATTTACCA GGTGAGAATG AATAAGCTAT GCAAGGTATT TTGTAATATA	1380
	CTGTGGACAC AACTTGCTTC TGCCTCATCC TGCCTTAGTG TGCAATCTCA TTTGACTATA	1440
35	CGATAAAGTT TGCACAGTCT TACTTCTGTA GAACACTGGC CATAGGAAAT GCTGTTTTTT	1500
	TGTAYTGAC TTTACCTTGA TATATGTATA TGGATGTATG CATAAAATCA TAGGACATAT	1560
40	GTACTTGTGG AACAAGTTGG ATTTTTTATA CAATATTAAA ATTCACCACT TCAGAGRAAA	1620
	AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAANAAAA	1668

45

(2) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

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GGGTCGACCC ACGCGTCCGC CCACGCGTCC GGATGGCTGC GCTGTTGCTG AGACACGTTG 60

GTCGTCATTG CCTCCGAGCC CACTTTAGCC CTCAGCTCTG TATCAGAAAT GCTGTTTCCTT 120

60

TGGGAACCAC GGCCAAAGAA GAGATGGAGC GGTTCCTGGAA TAAGAATATA GGTTCAAACC 180

5 GTCTCTGTC TCCCCACATT ACTATCTACA GTTGGTCTCT TCCCATGGCG ATGTCCATCT 240
 GCCACCGTGG CACTGGTATT GCTTTGAGTG CAGGGGTCTC TCTTTTGGC ATGTCGGCCC 300
 TGTACTCCC TGGGAACTTT GAGTCTTATT TGGAACTTGT GAAGTCCCTG TGTCTGGGGC 360
 CAGCACTGAT CCACACAGCT AAGTTGCAC TTGTCTTCCC TCTCATGTAT CATACTGGA 420
 10 ATGGGATCCG ACACTTGATG TGGGACCTAG GAAAAGGCCT GAAGATTCCC CAGCTATACC 480
 AGTCTGGAGT GGTGTCTCTG GTTCTTACTG TGTGTCTCTC TATGGGGCTG GCAGCCATGT 540
 GAAGAAAGGA GGCTCCAGC ATCATCTTCC TACACATTAT TACATTCACC CATCTTTCTG 600
 15 TTTGTCAATC TTATCTCCAG CCTGGGAAAA GTTCTCCTTA TTTGTTTGA TCCTTTTGTA 660
 TTTTCAGATC TCCTTGGAGC AGTAGAGTAC CTGGTAGACC ATAATAGTGG AAAAGGTCT 720
 20 AGTTTCCCC TTGTTTCTAA AGATGAGGTG GCTGCAAAAA CTCCCCTTTT TTGCCCACAG 780
 CTGCTTACT CTCGGCTAG AAGCAGTTAT TCTCTCTCCA TATTGGGCTT TGATTTGTGC 840
 TGAGGGTCAG CTTTGGCTC CTCTTCTCTG AGACAGTGA AACAATGCCA GCTCTGTGGC 900
 25 TTCTGCCCTG GGGATGGGCC GGGTTGGGG GTGGTTGGT GAGGCTTTGG GTGCCACTGC 960
 CTGTGGGTTG CTGGCTTAAA GGACAATTCT CTTCATTGGT GAGAGCCCAG GCCATTAACA 1020
 30 CCTACACAGT GTTATTGAAA GAAGAGAGGT GGGGTGGAG GGAATTAGT CTGTCCCAGC 1080
 TAGAGGGAGA TAAAGAGGC TAGTTAGTTC TTGGAGCAGC TGCTTTTGAG GAGAAAATAT 1140
 ATAGCTTTGG ACACGAGGAA GATCTAGAAA ATTATCATG AACATAATTAA TGGTTATTTC 1200
 35 TTTTCTTGG ATTTCCAGAA AAGCCTCTTA ATTTATGCT TTCTCATCGA AGTAATGTAC 1260
 CCTTTTTC TGAACTGAA TTAAATACTC ATTTTATCTT TGAAAAAAA AAAAAAACC 1320
 40 TNGGGGGGG CCCCAGACC NAATTGGCCC TAT 1353

45 (2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1011 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

55 CGGAAGAAAG CAGCCATCCA GACATTCAG AACACGTACC AGGTGTTAGC TGTGACCTTC 60
 AATGACACAA GTGATCAGAT TATTTCTGGT GGAATAGACA ATGATATCAA GGTCTGGGAC 120
 60 TCGCCAGAA CAAGCTAACC TACACCATGA GAGGCCATGC AGATTCAGTG ACTGGCCTGA 180

GTTTAAGTTC TGAAGGCTCT TATCTTTTGT CCAATGCAAT GGACAATACA GTTCGTGTCT 240
 GGGATGTCCG GCCATTTGCC CCCAAAGAGA GATGTGTAAA GATATTTCAA GGAAATGTGC 300
 5 ACAACTTTGA AAAGAACCTT CTGAGATGTT CTTGGTCACC TGATGGAAGC AAAATAGCAG 360
 CTGGCTCAGC CGACAGGTTT GTTTATGTGT GGGATACCAC AAGCAGGAGA ATATTGTATA 420
 10 AGCTGCCCCG CCATGCTGGC TCCATCAATG AAGTGGCTTT CCACCCTGAT GAGCCCATCA 480
 TTATCTCAGC ATCGAGTGAC AAGAGACTGT ATATGGGAGA GATTCAGTGA AGATATGGAC 540
 TGGAAGACTC CAAGGCCGCT TGTCTTTGAG ACCTCAGACT GCATAAGTGA TGCCAAATGT 600
 15 TGGATGTCCA GGYTAGCACC CTCCCTTCAG ATGACCATTG CTAGCAAGAA ACAGGAGGCG 660
 GTGGCCATAT TCCAAAACC ACTTCTGTCC CATTTACCA GGATGACTAA GGCAAGCTCC 720
 20 CTGTGGCCTC TAAAAACCAC CTGCCAGATT TCAGGGACTG TTTTTTTTTT TCTTTTCTT 780
 TTTTCTGTT TTCTAATGCA GGCCCAATGT GACAAATTG TTGGTTGGGA TTTTTTTTTT 840
 TTTTGTAAAC TGGCTTGTAT GATATTTTCT TTCTGTATTT CTCTATATCA TTTTGTATTA 900
 25 AAAGCCAAAT AGATGCCTTT TTACAAGARM AAAAAAAAAA AAAAAAAAAA NNAAAAAAAA 960
 CTGGGAGGGG GGGCCCGTA CCCAAATCGC CGGATATGAT CGTAAACAAT C 1011

30

(2) INFORMATION FOR SEQ ID NO: 67:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1193 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

GGCCGGGCGG TGCCTACTGC GGGCGCATCC CTGCCCCGGC GCCGTCCGTG CCCGCGGGAC 60
 CTGACAGCCG GGTGAGAGG CGAACTGTGC TCAGGCCCGG GCTGGACGCA GAGCCAGAGC 120
 45 TGTCCCCAGA GGAGCAGAGG GTCCTGGAAG GGAAGCTGAA AAAGGAACGG AAGAAAGAGG 180
 AGAGGCAGCG TCTGCGGGAG GCAGGCCTTG TGGCCCAGCA CCCGCTGCC AGGCGCTCGG 240
 50 GGGCCGAAC TGCCTGGGAC TACCTCTGCA GATGGGCCCA AAAGCACAAG AACTGGAGGT 300
 TTCAGAAGAC GAGGCAGACG TGGCTCCTGC TGCACATGTA TGACAGTGAC AAGGTTCCCG 360
 55 ATGAGCACTT CTCCACCCTG CTGGCCTACC TGGAGGGGCT GCAGGGCCGG GCGGAGAGC 420
 TGACGGTGCA GAAGGCGGAA GCCTGATGCG GGAGCTGGAT GAGGAGGGCT CTGATCCCCC 480
 CCTGCCGGGG AGGGCCGAGC GCATCCGACA GNTGCTGCAG CTGCTCTCCT AGTGGGTTCA 540
 60 GCGCGGGGCG GGGCCGCTGC CCAAGTGCAGG GCTGCCTCAG ACCACACAGG GTGCAGCTCC 600

TCCGGCGGTG GGGGCCGGGT TCACCAGCAG GGCAGCGGCT GAGCAAGGGC TTTCAGCTCC 660
 TCCGGTGGTG GGGGCCGGGA TCACCAGCAC CAGAGCCTCG CAAGGGCCCC TTCCCTCCTC 720
 5 CAGACCCTCC TTGGCCGGTG ACGCTGTGAC AGTGATGGCA GGTTCAGTGC CTTCAGCGCA 780
 GAGCGTGGAT GCTCTGGAAT CACCCGGACC CCTGGCCTTG GAGGGACCCT CCAGCCCCAG 840
 10 GAATCTGCTT TGGAGGGAAA TGTCTATTTT TCTACCGGGA ATATTTTAGA GATTGGGGCA 900
 TGCTGGCTCC TCCCCCAGC TGCAAACCTG CACCTTCCGC CTGATTCCCG ATCCCCCTGC 960
 GTGGGCCGCA TTCCTGGTCC CCTGCCTGCG TCCATCGAGG GGCCTGGCTG TGGCCTGTTT 1020
 15 TCCTTTGACC CCACACAGCG TCATTGCGGG TCATGGGGAG CCCCTGGTGG GAGCTTGTGG 1080
 AGTCGGATCA CGTACCTGTG CAGAAACCGC CTCTGTGGCT GCAITTTGAAA TAAAACCCGA 1140
 20 CCCAGCAGCA AAAAAAAAAA AAAAAANCNC NAGGGGGGGC CCGGNACCCA ATT 1193

25 (2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 560 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

35 GAATTCGGCA CGAGTTGGCA CATGATGCAA AATGCAITTC TCAGAGTAGA TTGCAGTCAA 60
 AAATGTTGGA AACTACTAAG CATGTGCARA TAGCATGCAT GCTGCTGCTG ACCTGCCAGA 120
 TATTTCTCCC TTCCTCCCTT TCTCCCTCAT TTATTCATTC ATTAAGTGAT TCATTCATCC 180
 40 CATTAAGAAA ATTATATGTA TGTTTTGTGC AAAGCACCTT ACTCAAGGCT GCGGGGTACA 240
 AAAGTATATC AGAAGCCTTG GGCTTTGACM WACTTCTCTG TAGTAGTGCT AGATTTGTGT 300
 45 GGATCTGCCA CACTTACTCC AGGCCTCTTG TGACCTGTGC TTTGCATTAA TCTCTTAGGC 360
 TAAGCCACAT ACCTTTTCAT TATACAATCT TTGCTGATGC TAAGGACAGA TTCCAAAGTG 420
 CCCTCCTTAT AATTTTGTGA TTTAATGCAA AGTGTAATCA AGAATAGGCC ATTGTTAGGT 480
 50 CAATTGCTTT TCTGTATTTA TCTTTTCAA CAATAAATAA TCAGTGGGAT GAAAAAGGGC 540
 CGGAAAAAAA AAAAAAAAAA 560

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(2) INFORMATION FOR SEQ ID NO: 69:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1657 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

	CGGACNGAGC CGCCGCCGGG CACTTCCTGT GGAGGCCGCA GCGGGTGCGG GCGCCGACGG	60
10	GCGAGAGCCA GCGAGCGAGC GAGCGAGCCG AGCCGAGCCT CCCGCCGTCG CCATGGGCCA	120
	GAACGACCTG ATGGGCACGG CCGAGGACTT CGCCGACCAG TTCCTCCGTG TCACAAAGCA	180
15	GTACCTGCCC CACGTGGCGC GCCTCTGTCT GATCAGCACC TTCCTGGAGG ACGGCATCCG	240
	TATGTGGTTC CAGTGGAGCG AGCAGCGCGA CTACATCGAC ACCACCTGGA ACTGCGGCTA	300
	CCTGCTGGCC TCGTCCTTCG TCTTCCTCAA CTTGCTGGGA CANTGACTGG CTGCGTCCTG	360
20	GTGTTGAGCA GGAACCTTCGT GCAGTACGCC TGCTTCGGGC TCTTTGGAAT CATAGCTCTG	420
	CAGACGATTG CCTACAGCAT TTTATGGGAC TTGAAGTTT TGATGAGGAA CCTGGCCCTG	480
25	GGAGGAGGCC TGTTCCTGCT CTTAGCAGAA TCCCCTTCG AAGGGAAGAG CATGTTTGCG	540
	GGCGTCCCCA CCATGCGTGA GAGCTCCCCC AAACAGTACA TGCAGCTCGG AGGCAGGGTC	600
	TTGCTGGTTC TGATGTTTAT GACCTCCTT CACTTTGACG CCAGCTTCTT TTCTATTGTC	660
30	CAGAACATCG TGGGGCACAG CTCTGATGAT TTTAGTGGCC ATTGGTTTAA AAACCAAGCT	720
	GGCTGCTTIG ACTCTGTGTG TGTGGCTCTT TGCCATCAAC GTATATTTCA ACGCCTTCTG	780
35	GACCATTTCA GTCTACAAGC CCATGCATGA CTTCTGAAA TACGACTTCT TCCAGACCAT	840
	GTCGGTGATT GGGGGCTTGC TCCTGGTGGT GGCCCTGGGC CCTGGGGGTG TCTCCATGGA	900
	TGAGAAGAAG AAGGAGTGGT AACAGTCACA GATCCCTACC TGCCTGGCTA AGACCCGTGG	960
40	CCGTCAAGGA CTGGTTCGGG GTGGATTCAA CAAAACAGCC AGCTTTTATG TATCCTCTTC	1020
	CCTTCCCCCTC CTTTGGTAAA GGCACAGATG TTTTGAGAAC TTTATTTGCA GAGACACCTG	1080
45	AGAATCAATG GCTTCAGGAC ATGGGTCTCT TTCTCCTGTG ATCATTCAAG TGCTCACTGC	1140
	ATGAAGACTG GCTTGTCTCA GTGTTTCAAC CTCACCAGG CTGTCTCTTG GTCCACACCT	1200
	CGCTCCCTGT TAGTGCCGTA TGACAGCCCC CATCAAATGA CCTTGGCCAA GTCACGGTTT	1260
50	CTCTGTGGTC AAGGTTGGTT GGCTGATTGG TGGAAAGTAG GGTGGACCAA AGGAGGCCAC	1320
	GTGAGCAGTC AGCACCAGTT CTGCACCAGC AGCGCCTCCG TCCTAGTGGG TGTTCTGTGT	1380
55	TCTCCTGGCC CTGGGTGGGC TAGGGCCTGA TTCGGGAAGA TGCCTTTGCA GGGAGGGGAG	1440
	GATAAGTGGG ATCTACCAAT TGATTCTGGC AAAACAATTT CTAAGATTTT TTTGCTTTAT	1500
	GTGGGAAACA GATCTAAATC TCATTTTATG CTGTATTTTA TATCTTAGTT GTGTTTGAAA	1560
60	ACGTTTIGAT TTTTGAAAC ACATCAAAT AAATAATGGC GTTGTGTGTA AAAAAAAAAA	1620

AAAAAACTC GRGGGGGGC CCGGTACCCA AATCGCC

1657

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(2) INFORMATION FOR SEQ ID NO: 70:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 711 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

GGCACGAGCG AAGACCCTGT TCGGACCCTG CCCCATTCC AGACTCAGGT AGATCGTCGG 60
CATACCCTCT ACCGTGGACA CCAGGCAGCC CTGGGGCTGA TGGAGAGAGA TCAGGTATCC 120
20 CCCAGGGAGT AGGGGCTACC TTGAGGGGAT GATAGACCTC CCCCCTCCC AGTGKCACTC 180
TGGAAATATG AAGGAACTAG GGAGTGAAG AGATTTCAGA GCTGGGGAGA GGAGTCCTC 240
25 CCTTCAAAGC CAGCAACTGC CTTTGGGGAA TGTCGGGGGG TCTCTCCTTT CTCCTGCTTG 300
TTTRAGGTGG TACACAGTCC CCCCTTCAMC TGGSGGGAAG CTGTNCCGA CARACTCATC 360
TCAGCTTTCC CTMTGGGGCAG GATCGGGGGC AGCAGCTCCA GCAGAAACAG CAGGATCTGG 420
30 AGCAGGAAGG CCTCGAGGCC ACACAGGGGC TGCTGGCCGG CGAGTGGGCC CCACCCCTCT 480
GGRAGCTGGG CAGCCTCTTC CAGGCCTTCG TGAAGAGGA GAGCCAGGCT TATGCGTAAG 540
35 CTTTCATAGCT TCTGCTGGCC TGGGGTGGAC CCAGGACCCC TGGGGCCTGG GTGCCCTGAG 600
TGGTGGTAAA GTGGAGCAAT CCCTTCACGC TCCTTGGCCA TGTTCTGAGC GGCCAGCTTG 660
GCCTTTCCT TAATAAATGT GCTTTATTTT CAAAAAAAAA AAAAAAAAC T 711
40

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(2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 935 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

GGCACAGGT GAAAGCCAGC TAAACCCCAA GTGGAGAAGT GAAAGACATG GTTGTTCCTA 60
55 TAAGTTTATT GCTCACAATA TGAAAGAAGC CATAGTCATG AGTGAACCAC TCCCTAGGTT 120
GATAAGGAAA CCAACACGGA AGATCTCTTT CTGGAAGAAG CAGCCAGCCT CGTGAAGGAG 180
60 CGGCCAGCC GCCGGGCCC AGGGTCGCCT TTTGTTCGGA GTGGCACGAT TGTCCGTTCC 240

	CAGACATTCT CGCCTGGAGC ACGAAGCCAG TATGTTTGCA GACTTTATCG TAGTGACAGC	300
5	GACAGTTCAA CGCTGCCCCG GAAGTCCCCC TTTGTCCGAA ATACTTTGGA AAGACGAACC	360
	CTTCGCTATA AGCAGTCATG CAGGTCTTCC CTGGCTGAGC TCATGGCCCCG CACCTCCCTG	420
	GACTTGGAGC TGGATCTCCA GGCCTCGAGA ACACGGCAGA GGCAGCTGAA TGAGGAGCTC	480
10	TGCGCCCTCC GTGAGCTGCG GCAGCGGTTN GGAGGACGCC CAGCTCCGTG GCCAGACTGA	540
	CCTCCACCCC TGGGTGCTTC GGGACGAGCG GCTCCGTGGC CTGCTGCGGG AGCCGAGCGG	600
15	CAGACAAGAC AGACCAAAC TGA CTACCGT CATGAGCAGG CGGCTGAGAA GATGCTGAAG	660
	AAGGCCTCCA AGGAGATCTA CCAGCTGCGT GGCAGAGCCA CAAAGAGCCC ATCCAAGTGC	720
	AGACCTTTAG GGAGAAGATA GCATTCTTCA CAAGGCCAAG GATCAACATA CCTCCTCTCC	780
20	CAGCCGACGA CGTCTGATGG AGTGCATTGT GCACATGAAG TATTTATCCA CCTGTTTTAT	840
	TTTCATGAAG TTCTTAGACT AGCTGAATTT GTCTTTAAAA TATTTGTGCA AAGCTATTAA	900
25	TATACACATT TTGTAAAAA AAAAAAAAAA AACT	935

- (2) INFORMATION FOR SEQ ID NO: 72:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

40	GCAGGGGCGA GGGGYTGGGG ACCGCGGGGC GGACGGGAGC GAGTATGTCC GCTCTGACTC	60
	GGCTGGCGTC TTTCGCTCGC GTTGAGGCC GCCTTTTCAG AAGCGGCTGC GCACGGACTG	120
	CTGGAGATGG TGGAGTCCGT CATGCCGGTG GTGGTGTGCA CATGAGCCC CGGTATAGAC	180
45	AGTTCCCCCA GCTGACCAGA TCCAGGTGT TCCAGAGCGA GTTCTTCAGC GGACTCATGT	240
	GGTTCTGGAT TCTCTGGCGC TTTTGGCATG ACTCAGAAGA GGTGCTGGGT CACTTTCCGT	300
50	ATCCTGATCC TTCCCAGTGG ACAGATGAAG AATTAGGTAT CCTCCTGAT GATGAAGACT	360
	GAAGGTGTAG ACTCAGCCTC ACTCTGTACA AGAGCCAGGT GAGAATTTCA AGGATTATCG	420
	ACTTCATATT GCACATTAAA GTTACAAATT AAAGTGCTT GGTCAAGAAT GARAAAAAA	480
55	AAAAAAATT GGGGGGGGC CCCN	504

- 60 (2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 620 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

10 GAATTCGGCA CGAGGAGGAG GGGAGGCGGG GTAAGTTTGG TGGGAACTC TGTAATTTCC 60
WTTTTACTTT TCACAGCAAT AGTGCAGAAT CCAGAATGGA TGTCTCTTT GTAGCCATCT 120
TTGCTGTGCC ACTTATCCTG GGACAAGAAT ATGAGGATGA AGAAAGACTG GGAGAGGATG 180
15 AATATTATCA GGTGGTCTAT TATTATACAG TCACCCCCAG TTATGATGAC TTTAGTGCAG 240
ATTTCAACCAT TGATTACTCC ATATTTGAGT CAGAGGACAG GCTGAACAGG TTGGATAAGG 300
20 ACATAACAGA AGCAATAGAG ACTACCATTA GTCTTGAAAC AGCACGTGCA GACCATCCGA 360
AGCCTGTAAC TGTGAAACCA GTAACAACGG AACCTCAGAG TCCAGATCTG AACGATGCCG 420
TGTCCAGTTT GCGAAGTCCT ATTCCCCTCC TCCTGTCGTG TGCCTTTGTT CAGGTGGGGA 480
25 TGTATTTTCAT GTAGAAGGTG GAAGAAGGCT GCTATGACTC TTTGGATGGG AGTCTGGCAA 540
GAGGAAATTG GAAGATAAAA TAAATAATAA GTGAAATAAA AAAAAAAAAA AAAAAGCTCGA 600
30 GGGGGGGCCC GGTACCCAAT 620

35 (2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 581 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

45 ACAAGGTGTG TGTAAGTTT ATGTTTGTA ACTGAATTCT ATCTTAAATC CAAAAGAAC 60
TCGGGAGTAA TTCATTTTTG TAGCATAAAG ATCCCTAAGT TTTATTTTGA AATATCTGAT 120
TTTTACACGT TAAAAAATAA CAGGGCATCG AGAGGATTCC TAGGTGACAT CCAGACTCCT 180
50 TTAGCTTTGT GTGTGTGGCA CCGGTTAGTC TGCTTCTCTC TCCTTTCTTG CACTGCTTCA 240
CACAGCCATG CCCTGCCAGC CCGGGCAGGT GCCTTCCTGT CAATGTACAT TTGGGCTTCT 300
55 GCTCATGCTG CCCTCCCTCC CCTCCCCTGC CTCCCAACCC CGCCCCTTT GTTCCTCCAT 360
GGAGTACTTC CATGGGTGTG CCTCCCCCAG CCAAGCCATA ATAGGTGGTT TCCCCTTCGC 420
TTCTGTAGCC CTTGCAGACA TCCTCTGTTT ACAGTAGGTG TTGACTTACT TCCCCTCTCC 480
60

CCGSTAAAGC CATAAACTCC TTAAGGACAG GTAGCATTTCT TAGTATCTTC GTTCTTCTCA 540
 ATGACCAGTA GACCATTTAAA CATGTAGCAA ACAAATGTGA A 581

5

(2) INFORMATION FOR SEQ ID NO: 75:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

AAACCCAAACN CCCTCCGGTC CCCNAAAGAA AGCCCAGCCC AAATCCCAAG CCGGCAGTGA 60
 20 GCCCGCGAAC AAGGCCCTCA AGACGCCCAG NCGAACAAGC AGCCCCCAGG AGGCCCCGCA 120
 AGAGAACTCC CTGGCGGCCC AAGCGGGCAG CTTCTGTGCG GCAGAACTCA GCCACCGAGA 180
 GCGCAGACAG CATCGAGATT TATGTCCCGG AGNCCCAGAC CAGGCTCTGA GACCATGCAG 240
 25 GAGGAAAGAA ACGATTTTAA ATCATTTAAA ACACAAAAC TAAGTGCGAA CGGAACAGAG 300
 TTTTCTCAAC CTTTGCTATG GTTATTCTGT CTAGAGACCC TGAGCCAACT TTCAAATTGA 360
 30 CGCATAAAG GGCTCACAAT TTGGCTTTTT TGGGTCCCTC CCAGCTTTAG GTTATGAAGA 420
 TTTTACTCAC AAAAAAATC AACAAAATC ACGAACTAG AAAACTTTTT TTTTCCTCTT 480
 GCTGGCCGTG GTGGACTAGA TAGATGGACG TCGGCAACTC CCGGCCCAGC CTCCATACTG 540
 35 CGGTCTTTTT ACTCGTTCTA TCTGATGAGA ACTCACACTA GCTTGTTTAC AAGATGACGA 600
 CAGTCCAAGG GCAGCCTTGG GCACCTGCCA TGTCCTCCTT TTCCCCAGCT ATCCCCGCTC 660
 40 TGACCTTGAT TTTCATCTTT ATGTTTTTCT CTTTTCCTTT CAGAGCTCAC ACAGTGGTCA 720
 CCATGTGAGC AAGCGGCTTT CTGGGTCTCA GCCCTCTCTG CGGTTGAGGG CCCAGAGGAC 780
 AGAGAGATGG ACATGCGTCC CCTCCCTCCC CCCGCCAAGT GCTCACACAC AACCTCACGC 840
 45 GCACACACAC ACACGCAGAT GGAGGCGCCT CACTGGGAGG TGCCCCGCCA GCCCTGGGCA 900
 GTGTCAGGCA GGAATCACTC ACCGCTGAGC AGATGAGAGA AGTTTTAGTC TTGGCGGGTG 960
 50 GAAATGAGAC GAAGCCACAG TTATCACACT CCAGACTCCT GCCCTTTTAT TTTCTCCAGC 1020
 CCTTCTTTCC TTCAGCAAAA TCTAGGACTC CCGAGTGGCT TCCAGGGGGC CGTCAGTCTT 1080
 CAGCCGCGCC TGTGTCCGGT GCCCAGGGGG CGGGCGGCGG TGTCTGTATG TATGTGTACA 1140
 55 TATGCACATA GACCTTAGAG TGTATAGTTA ACAAACGCCC ATCTGCTCAC CCATGCCAC 1200
 CCAGCGCCGC CGCCGTGGC TCTCGGGGCA CCTGGCAGGA GGCGGGTGTG TGAATAGCAT 1260
 60 ATATTTTTAC ATGTACTATA TCTAGGTGTG TGTACAAGTG TGTGTAAAAA TATATACCTT 1320

GTGTGTAAGC AGCCCTTTTT TTTTTTGGTC TCCACCCCCC TCCCCCGCC CCGCACTCCT 1380
 AAGGGCCCAT CTGCCCAGCC TCTGAGTTTT CTGTTCATTT TTTTTTTTAA CCCCATTAT 1440
 5 CCTTCTCTCT CTCTGCCCC CGCATCCCAC TCCCAGGGTG TCACGAGCCC TGAGCTGCAA 1500
 TGGCCCGGGC CTGCAGGGCG GGGTAGGGGA GGGCARGGCT SAGCCCCGAA GCCAGCTCAG 1560
 10 TACCTGAGGG GCTGCTCTAT GCTGTGTATG CGCCTCTCTG GCATCCGAGA CATCCTCTTG 1620
 GTGGCGCTTG CTNGCAGGGG ACCCCCCCCC CGTCCCCAGG TGAACCAAGG GTCTGCTCCG 1680
 GGGCCCATTT CCAGCTTGGC CGCCGTCTGT GACCTTGGGC AAGTCACTTG ACCTCTGTGT 1740
 15 GCCTCAACTT CCTCCTCTGT AAAACGGGGA CAGTCCCTGC CCCTCCCTAC CTCACAGGCA 1800
 TGTGTGAGA ATAAATGAGG TAACGTGTAA AAAAAAAAAA AAT 1843
 20

(2) INFORMATION FOR SEQ ID NO: 76:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1441 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

TCGACCCACG CGTCCGGCTC CCCGAGCCCT GCCAACCATG GTGAACTTGG GTCTGTCCCG 60
 35 GGTGGACGAC GCCGTGGCTG CCAAGCACCC GGGACTCGGG GAGTATGCCG CATGCCAGTC 120
 ACACGCCTTC ATGAAGGGCG TTTTCACCTT CGTCACAGGC ACCGGCATGG CCTTTGGCTT 180
 GCAGATGTC ATTCAAGAGGA AGTTTCCATA CCCTTTGCAG TGGAGCCTCC TAGTGGCCGT 240
 40 GGTTCAGGC TCTGTGGTCA GCTACGGGGT GACGAGAGTG GAGTCGGAGA AATGCAACAA 300
 CCTCTGGCTC TTCCTGGAGA CCGGGCAGCT CCCCAAAGAC AGGAGCACAG ATCAGAGAAG 360
 45 CTAGGAGAGC TCCAGCAGGG GCACAGAGGA TTGGGGGCAG GAGGAGTCTG GAACACAGCC 420
 TTCATGCCCC CTGACCCAG GCCGACCTC CCCACACCT AGGGTACCCC AGTCGTATCC 480
 TCTGTCCGCA TGTKTGGCCA GGCCTGACAA ACACCTGCAG ATGGCTGCTG CCCCACCTG 540
 50 GGACCTGCCC AGRAGGTGG AGCAGAAAGG GCTCTCCCTG GGGTGGTGTT TCTCCTCTAG 600
 GGTATTGGGA TGCATGTTCT GCACTGCCAG CAGAGAGGGT GTGTCTGGGG GCCACCACCT 660
 55 ATGGGACACG GGGTCGAAGG GGCCTGTACA CTCTGTCAAT TCCTTTCTAG CCCCTGCATC 720
 TCCAACAAGT CCAAGGTGAC AGCTGGTGCT AGGGGCGTGG GGTAAATAAA TGGCTTATCC 780
 TTCTCTCCAC CCAAGTTTCC ACCTGACCAG GTGAAAAACA AATCAGAAGG GTAAGATGAT 840
 60

	GACAGGTCAC ATGAAACCTT TATTACCCCTA CAGTTGATAT ATGAGGATCA CATGCAAGTT	900
	ACATACTGAG GATGTACAGG GAAGTTCCCA GCGCTGAACC CCAGAATTAG ACGTTCGCAT	960
5	CAGCCCCGTA GGCACGTGG ACACCACCAC AGCCTCTCTG TATGGGGGTC TGCCTCTGTA	1020
	GCACCTTGGCA TGTAGGGGCA GAGCAAAAGG GGCCANGCTG GCCAGAGCCT GGCTGCTGGG	1080
10	NAGARGAGGG ACTTGTGGGS CACGCCACNT GCCTATCATT CCCAYTCAT CTATTAGCCA	1140
	AAGTCACTCC CCAGAGGCAG AGCTAGCCCG TTGTAGCCGT GTCTGTGTGG AGGGAAGCT	1200
	TCTGAGTGGG CAAGCCTACA CACAGCCCCG AGCCCCAAGA GGAGGAAGAG GTGGAGACCA	1260
15	GACGGAACCT CCACAAGTCC ATCATGGTTA CAGCTGGCTT CCCCAGCAGCA CCGAAGACCC	1320
	ACAGCATNGG CCCTGCTGCC CCCGACCCAG CTCAGCTGCC ANGCTCACC TTGCCAGGAA	1380
20	TTGAAAGAAA GTTATTGAGT ACTAATTGGC CTCAGAGTNA CAGGAAGCTC AAGTTAAAGT	1440
	G	1441

25

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 910 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

35	GGCAGAGCTG GCTTCGACT CGCTATGTCC ACTAACAATA TGTCGGACCC ACGGAGGCCG	60
	AACAAAGTGC TGAGGTGAGG ACCCCAGCGT CGTGGGCACG GGTTCGGGTT GTGGGTGTGG	120
40	ATCGGGGCCC TGGGAAGCGC CTGTCTATCC CGGGGGCAGG ACCTGAGCGC CCCTGACCCT	180
	CGAGCCTGTC GCAGGTACAA GCCCCGCCG AGCGAATGTA ACCCGGCCTT GGACGACCCG	240
45	ACGCCGGA CTACATGAACCT GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAG	300
	CTGAAGTGGT GTGCTTGGGT CGCTGTCTAC TGCTCCTTCA TCAGCTTTGC CAACTCTCGG	360
	AGCTCGGAGG ACACGAAGCA AATGATGAGT AGCTTCATGT GAGACTTGCC CTACAGAACA	420
50	ACTGACTCTT GAGTAAGGGG TGGGGGGACC CCAGCCTGGC CATCCTAGAC TGACACCTCT	480
	CTCCTGTCTT CATGCTGTCC ATCTCTGCCG TGGTGATGTC CTATCTGCAG AATCCTCAGC	540
55	CCATGACGCC CCCATGGTGA TACCAGCCTA GAAGGGTCAC ATTTTGGACC CTGTCTATCC	600
	ACTAGGCCTG GGCTTTGGCT GCTAAACCTG CTGCCTTCAG CTGCCATCCT GGACTTCCTT	660
	GAATGAGGCC GTCTCGGTGC CCCAGCTGG ATAGAGGGAA CCTGGCCCTT TCCTAGGGAA	720
60	CACCCTAGGC TTACCCCTCC TGCCTCCCTT CCCCTGCCTG CTGCTGGGGG AGATGCTGTC	780

5 CATGTTTCTA GGGGTATCA TTTGCTTTCT CGTTGAAACC TGTGTTAAT AAAGTTTTTC 840
ACTCTGAAAA AAAAAAAAAA AAAAAAAAAAC TYGRGGGGGG GCCCGGAACC CAATTCSCCG 900
GATAGTGAGT 910

10

(2) INFORMATION FOR SEQ ID NO: 78:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2776 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

TCGACCCACG CGTCCGGGCG GGCAGTGATG GCGGCTGGTG ATGGGGACGT GAAGCTAGGC 60
ACCCTGGGGA GTGGCAGCGA GAGCAGCAAC GACGGCGGCA GCGAGAGTCC AGCGACGCG 120
25 GGAGCGGCAG CGRAAGGGGG AGGCTGGGCG GCGGCGGCGT TGGCGCTTCT GACGGGGGGC 180
GGGAAATGC TGCTGAACGT GCGGCTGGTG GCTCTGGTGC TGCTGGGGGC CTACCGGCTG 240
TGGETGCGCT GGGGGCGGCG GGGTCTGGGG GCCGGGGCCG GGGCGGGCGA GGAGAGCCCC 300
30 GCCACCTCTC TGCCTCGCAT GAAGAAGCGG GACTTCAGCT TGGAGCAGCT GCGCCAGTAC 360
GACGGCTCCC GCAACCCGCG CATCCTGCTC GCGGTCAATG GGAAAGTCTT CGACGTGACC 420
35 AAAGGCAGCA AGTTCTACGG CCCGGCGGGT CCATATGGAA TATTTGCTGG TAGGGATGCC 480
TCCAGAGGAC TGGCCACATT TTGCCTAGAT AAAGATGCAC TTAGAGATGA ATATGATGAT 540
CTCTCAGATT TGAATGCAGT ACAAATGGAG AGTGTTCGAG AATGGGAAAT GCAGTTTAAA 600
40 GAAAAATATG ATTATGTAGG CAGACTCCTA AAACCAGGAG AAGAACCATC AGAATATACA 660
GATGAAGAAG ATACCAAGGA TCACAATAAA CAGGATTGAA CTTTGTAAC AACCAAAGTC 720
45 AGGGGCCTTC AGAACTGCAA TTCTTACTCC CTTTCACAGA CTGTCCGGAG TCTTTGGGTT 780
TGATTACCT GCTGCGAAAA ACATTCAACA AATTGTGTAC AAGATAAATT AATCTCACTA 840
TGAAGATTTG AATAACTAGA CATTTATTTAT GCTGCCAAAC TCATTTGTTG CAGTTGTTTG 900
50 TAATGTCTAG TGGGGCTTCA TCATCCTGAA AAGAAGGAGA CAGGGATTTT TTTAAAGAGC 960
AAGAAAGTCA CAATATTACT TCTTTCCTTC CTTTTTCCTT TCTTTCCTTT CTTCTTCTC 1020
55 TTTCTTTCTT TTTAAATAT ATTGAAGACA ACCAGATATG TATTTGCTAC TCAAGTGTAC 1080
AGATCTCCTC AAGAAACATC AAGGGACTCC TGTGTCACAT ACTGTGTTTT TATTTTAACA 1140
TGGGTGAGGG AGGCGACCTG ATCAGGGGAG GTGGGGGTAC ACATCAATTT GAGTTGTTCA 1200
60

	GGCTACTGAA ACATTAAAAAT GTGAATTCCC AAACCTTTTCT TTTTGGCTTT GTCAGGGAAA	1260
	AGAAAAATAT CTTTATAAAG AAATCTTTGG AAATTAGGAG AAGGAATTC AGGTGGGTTT	1320
5	AAGTCAGAGC TAGTTCCCCA ACAGAAAGAT CATTTGAAAC CAGTTTTTAT CCCTTCTCTT	1380
	TCCTTCCCTT TCCCTAAATC AAATCAATAT TAATTGTGCC TTATTTCACT TAACATAGAC	1440
10	TTGAATTATT TTTAGGGAAA GCCCCTATAA TGAATTCAGA AATCACTACA AGCAGCATTA	1500
	AGACTGAAGT TGAATATTC TGTGACCAT AAAACCTTGA TATCATCTG TGTATATAGA	1560
	ATGTAAAAGG AATATTACAG TGTAACTGC CATATATGTA ATATACACAA ACTCAATTAG	1620
15	CATTGTAATG GCCAAATGCA TTCCCCATG CTTTCTGTT TTCAAAAAA TTGAAAAACA	1680
	AATCAACTCT TATCCCCAAC AGCTGCCTAA TTTTAGGAGT CTGACCCTCC ACATCTCACT	1740
20	GGTGTGGGTG CATGGGGCTG TGGAGTGGT GTCAGTATGG ATGTGTCTGA ATGTGTGAGG	1800
	CCTTGAAGG GACTCTTTCT GCAGATACTG TAAATACAAG TACCATTTTA ATAAAGCATG	1860
	TACAATAAAC CAAAATAAGC TTGAGTTGGA CTTTATATAC AGAACTGTAA GCCAGTGCAT	1920
25	TATGATACAG TTGTAAGATT GTGCATTTGA TTCAAGATAA GGAAAAATCT TGGAAATGAA	1980
	AAGCAGGCAC KGGTTAACCA AGTTGTACAC ATTGTACCAC ATTCAGCATA ACTTTAGGAA	2040
30	GAAATTCAC TTTGTGAACA TTCTCCAGAA ATCCAAGATT ATTCAGGTAA GAATTGGTAT	2100
	ATTAAATGTA CATCTTTTTA CTTTCTATTT TGATGCCAAC TGATTATACT AGACAATTAG	2160
	CACTCCAGGT GGTATTGAA CACAAAACAG TAAAAGAATA TTGCACTGAT AGATACTAAA	2220
35	TTATTATTTT ATTAGGTTGA AAAAGCCCTT ACTAAAAGCC CCTCATATAT CAATTACTTT	2280
	ATTTCAATTAT GACTACTTAG GTTCCGGGCT GGGGACAAGT TCACTTAAAA AGGCAATGTT	2340
40	ATTTAACAGG TCACCAGTTA AGACTTCTGC TTTGTAGATA CATGCAGAAG CCATCAAACA	2400
	AGGGGGRGCT TTAACTGCA ACAATAAGCT AAAGTATGTA AAATACTACA TTCTATTCAG	2460
	TCCTGGAGTG TTTGTAGAA AGTTATCTTC AGCCAAATCT TTGCTGAAGA CTGGTTGTGG	2520
45	AGTGTGGTA AATGCTTGT GTTTTATGT AAAATATTTT CTAAACAAA AATGTTAAAA	2580
	GTACATGTCC TCTGTAGTAA ACTGATATCT ATATATATGA ATCATTCAG CCTAAAGTCT	2640
50	AGTAATAAAC TGTACTTGTG AATAGAGAAA CCCTAAATAT TCATGCAGWA AAAATTATGC	2700
	GGTCTGTAA GAAAAATGAG TAATTTGTGT TTTGGACTTG AAATAAACAG TGTCTGTAG	2760
55	ATAATTCCTC AACTTC	2776

(2) INFORMATION FOR SEQ ID NO: 79:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1525 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

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CCGCTGCTGA TAACTATGGC ATCCCCCGGG CCTGCAGGAA TTCGGCACGG AGCTACGGCG      60
10 CCGCCTGGCT CCTGCTGNCA CCTGCAGGCT CGTCGCGGGT GGAGCCCACC CAAGACATCA      120
    GCATCAGCGA CCAGCTGGGG GGCCAGGACG TGCCCGTGTT CCGGAACCTG TCCCTGCTGG      180
    TGGTGGGTGT CGGCGCCGTG TTCTCACTGC TATTCCACCT GGGCACCCCG GAGAGGCGCC      240
15 GGCCGCATGC GGASGAGCCA GGCGAGCACA CCCCCCTGTT GGCCCTGCC ACGGCCAGC      300
    CCCTGCTGCT CTGGAAGCAC TGGCTCCGGG AGCSGGCTTT CTACCAGGTG GGCATACTGT      360
20 ACATGACCAC CAGGCTCATC GTGAACCTGT CCCAGACCTA CATGGCCATG TACCTCACCT      420
    ACTCGCTCCA CTGCCCCAAG AAGTTCATCG CGACCATMCC CTGGTGATG TACCTCAGCG      480
    GCTTCTTGTC CTCCTTCCTC ATGAAGCCCA TCAACAAGTG CATTTGGAGG AACATGACCT      540
25 ACTTCTCAGG CTCCTGGTG ATCCTGGCCT TTGCCGCCTG GGTGGCGCTG GCGGAGGGAC      600
    TGGGTGTGGC CGTGACGCA GCGGCTGTGC TGCTGGGTGC TGGCTGTGCC ACCATCCTCG      660
30 TCACCTCGCT GGCCATGACG GCCGACCTCA TCGGTCCCCA CACGAACAGC GGACTIONCT      720
    GTACGGCTCC ATGAGCTTCT TGGATAAGGT GGCCAATGGG CTGGCAGTCA TGGCCATCCA      780
    GAGCCTGCAC CCTTGCCCCCT CAGAGCTCTG CTGCAGGGCC TGCGTGAGCT TTTACCACTG      840
35 GGCGATGGTG GCTGTGACGG GCGGCGTGGG CGTGGCCGCT GCCCTGTGTC TCTGTAGCCT      900
    CCTGCTGTGG CCGACCCGCC TGCAGCGCTG GGACCGTGAT GCGCGGCCCT GACTCCTGAC      960
40 AGCCTCCTGC ACCTGTGCAA GGAACCTGTG GGGACGCACG AGGATGCCCC CCARGGCCTT      1020
    GGGGAAAAGC CCCCCTGCC CTCACCTCTT CTCTGGACCC CCACCCTCCA TCCTCACCCA      1080
    GCTCCCGGGG GTGGGGTCGG GTGAGGGCAG CAGGGATGCC CGCCAGGGAC TTGCAAGGAC      1140
45 CCCCTGGGTT TTGAGGTGT CCCATTCTCA ACTCTAATCC ATCCCAGCCC TCTGGAGGAT      1200
    TTGGGTGCC CCTCTCGCA GGAACAGGA AGTAGGAATC CCAGAAGGGT CTGGGGGAAC      1260
50 CCTAACCTTG AGCTCAGTCC AGTTCACCCC TCACCTCCAG CCTGGGGGTC TCCAGACACT      1320
    GCCAGGGCCC CCTCAGGACG GCTGGAGCCT GGAGGAGACA GCCACGGGGT GGTGGGCTGG      1380
    GCCTGGACCC CACCGTGGTG GGCAGCAGGG CTGCCCGCA GGCTTGGTGG ACTCTGCTGG      1440
55 CAGCAAATAA AGAGATGACG GCAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA      1500
    AAAAAAAAAA AAACCCACCG TCCGC      1525

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60

(2) INFORMATION FOR SEQ ID NO: 80:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

	AATTCGGCAC GAGNCAGAAA CCTGCGGAAA ATGGTAGCGA TGGCGGCTGG GCCGAGTGGG	60
15	TGTCTGGTGC CGGCGTTTGG GCTACGGTTG TTGTTGGCGA CTGTGCTTCA AGCGGTGTCT	120
	GCTTPTGGGG CAGAGTTTTC ATCGGAGGCA TGCAGAGAGT TAGGCTTTTC TAGCAACTTG	180
20	CTTTGCAGCT CTTGTGATCT TCTCGGACAG TTCAACCTGC TTCAGCTGGA TCCTGATTGC	240
	AGAGGATGCT GTCAGGAGGA AGCACAATTT GAAACCAAAA AGCTGTATGC AGGAGCTATT	300
	CTTGAAGTTT GTGGATGAAA ATTGGGAAGG TTCCCTCAAG TCCAAGCTTT TGTTAGGAGT	360
25	GATAAACCCA AACTGTTTCAG AGGACTGCAA ATCAAGTATG TCCGTGGTTC AGACCCTGTA	420
	TTAAAGCTTT TGGACGACAA TGGGAACATT GCTGAAGAAC TGAGCATTCT CAAATGGAAC	480
30	ACAGACAGTG TAGAAGAATT CCTGAGTGAA AAGTTGGAAC GCATATAAAT CTGTCTTAAA	540
	TTTTGTCTTA TCCTTTTGT T ACCTTATCAA ATGAAATATT ACAGCACCTA GAAAATAATT	600
	TAGTTTTGCT TGCTTCCATT GATCAGTCTT TTAAGTGGAG CATTAATAT CTAATTAAAT	660
35	CGTGAAATGG CAGTATAGTC CATGATATCT AAGGAGTTGG CAAGCTTAAC AAAACCCATT	720
	TTTTATAAAT GTCCATCCTC CTGCATTTGT TGATACCACT AACAAAATGC TTTGTAACAG	780
40	ACTTGCGGTT AATTATGCAA ATGATAGTTT GTGATAATG GTCCAGTTTT ACGAACAACA	840
	GATTTCTAAA TTAGAGAGGT TAACAAGACA GATGATTACT ATGCCTCATG TGCTGTGTGC	900
	TCTTTGAAAG GAATGACAGC AGACTACAAA GCAAATAAGA TATACTGAGC CTCAACAGAT	960
45	TGCCTGCTCC TCAGAGTCTC TCCTATTTTT GTATTACCCA GCTTCTTTTT TAATACAAAT	1020
	GTTATTTATA GTTTACAATG AATGCACTGC ATAAAACTT TGTAGCTTCA TTATTGTAAA	1080
50	ACATATTCAA GATCCTACAG TAAGAGTGAA ACATTACAAA AGATTTGCGT TAATGAAGAC	1140
	TACACAGAAA ACCTTTCTAG GGATTTGTGT GGATCAGATA CATACTTGGC AAATTTTGA	1200
	GTTTTACATT CTTACAGAAA AGTCCATTTA AAAGTGATCA TTTGTAAGAC CAAAATATAA	1260
55	ATAAAAAGTT TCAAAAATCT ATCTGAATTT GGAATTCCTC TGGTTTGTTC TTTTATGTTT	1320
	AAAAATGATG TTTTCAATG CATTTTPTTC ATGTAAGCCC TTTTPTTAGC CAAAATGTAA	1380
60	AAATGGCTGT AATATTTAAA ACTTATAACA TCTTATTGTT GGTAATAGTG CTTTATATTT	1440

231

GTCTGATTTT ATTTTCAAA GTTTTTCAT TTATGAACAC ATTTTCATTG GTATATTATT 1500
TAAGGAATAT CTCTTGATAT AGAATTTTTA TATTAAAAAT GATTTTCTT TGCTTAAAAA 1560
5 AAA 1563

10 (2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1020 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

20 TGCACGCTGG CCATGTGGGN GTTGGGCCAC TGCGACCCCC GCGCTGCAC GGGCCGCAAG 60
CTGGCCCGCC TGGGCTGGT GCGCTGCCTG CGCCTGGGCC ACAGATTCGG CGGTCTGGTG 120
CTGAGCCCCG TGGCAAGCA GTACGCGTCC CCCGACAGCA GACAGCTGGT GCGCAGTCT 180
25 GGGGTCGCCG TCATCGACTG CTCCTGGGCC AGGCTGGACG AGACACCGTT TGGGAAGATG 240
CGAGGGAGCC ACTTGCGCCT GTTGCCCTAC CTGGTGGCCG CCAACCCCGT GAACTATGGC 300
30 CGGCCCTACA GACTTTCCTG CGTGGAAGCG TTTGCTGCCA CCTTCTGCAT CGTAGGCTTT 360
CCAGACCTTG CTGTCAATTT GCTGCGGAAG TTTAAATGGG GCAAGGGCTT CTTGACCTG 420
AACCGCCAGC TCCTGGACAA GTACGCGGCC TGCGGCAGCC CGGAGGAGGT GCTGCAGGCC 480
35 GAGCAGGAGT TCTTGCCAA TGCCAAGGAG AGCCCCCAGG AGGAGGAGAT CGATCCCTTC 540
GATGTGGATT CAGGGAGAGA GTTTGGAAC CCCAACAGGC CTGTGGCCAG CACCCGGCTG 600
40 CCCTCGGACA CTGATGACAG TGATGCGTCT GAGGACCCAG GGCCTKGC GCAGCGCGGA 660
GGAGCCAGCA GCAGCTGCTG TGAAGAGGAG CAGACCGAGG GACGGGGGGC TGAGGCCAGG 720
GCCCCGGCTG AGGTTTGGAA AGGAATCAAG AAACGCAGA GAGACTGAGG GTTGCAGACA 780
45 CATATATTTT TGAGGCTGGG TGACGAGAAA ATCTAGAGAC ATGAGGGACA TAAATGGGCC 840
TGGCAGCCTC GGCTCTTTC GGCTGCTGGC AGGACTGAGC TGTCCGGGT CTCCCCACAC 900
50 TTCCAGCACA GCTGTGCTCT GTGTCCTGCC TCGGCGCTCT CGCAAATGAA GCTGCAGGCC 960
AAGAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAG GGGGGGGGC 1020

55

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 770 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

	TCGACCCACG CGTCCGGGCC GCCGTAGCGC GTCTTGGGTC TCCCGGCTGC CGCTGCTGCC	60
10	GCCGCCGCCT CGGGTCGTGG AGCCAGGAGC GACGTCACCG CCATGGCAGG CATCAAAGCT	120
	TTGATTAGTT TGTCTTTTGG AGGAGCAATC GGACTGATGT TTTTTRATGCT TGGATGTGCC	180
	CTTCCAATAT ACAACAAATA CTGGCCCCCTC TTTGTCTCTAT TTTTITACAT CCTTTCACCT	240
15	ATTCCATACT GCATAGCAAG AAGATTAGTG GATGATACAG ATGCTATGAG TAACGCTTGT	300
	AAGGAACCTG CCATCTTTCT TACAACGGGC ATGTGTCGTGT CAGCTTTTGG ACTCCCTATT	360
20	GTATTTGCCA GAGCACATCT GATTGAGTGG GGAGCTTGTG CACTTGTCTCT CACAGGAAAC	420
	ACAGTCATCT TTGCAACTAT ACTAGGCTTT TTCTTGGTCT TTGGAAGCAA TGACGACTTC	480
	AGCTGGCAGC AGTGGTGAAG AGAAATTACT GAACTATTGT CAAATGGACT TCCTGTCAAT	540
25	TGTTGGCCAT TCACGCACAC AGGAGATGGG GCAGTTAATG CTGAATGGTA TAGCAAGCCT	600
	CTTGGGGGTA TTTTAGGTGC TCCCTTCTCA CTTTATTGT AAGCATACTA TTTTCACAGA	660
30	GACTTGCTGA AGGATTAAAA GGATTTTCTC TTTTGGAAAA AAAAAAAAAA AAAAAACYGA	720
	GGGGGGGCCC GTWCCCATTC SCCCATATG AATTCCNTTT TTACAATCCC	770

35

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 481 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

45	GAATTCGGCA CGAGCATAGT GTTAACCACT AGAATTCACCT GCCCTTCCTA TCCAAAAATG	60
	ACACTACTGA TCATTTTCTCT TCCTTTTCTCT TTTACAACAT TMACAAATTC AGGTGGCTCT	120
50	TTCCCAGTAC GGTAGGCTGA TTCGTATGGA TGCACCACGG TTGGTGACTC CCCCCACCCC	180
	ACAGAGTTTC TGGCGTTTCAT TCGGTTGAAC CCAAGGCCAG CAAGGGCTGA CTGGGAACAA	240
55	ACCGAACACT AGGCCGTGAA CCAATCGTCT CTCCGTGCCC GGGAGCGAMC CCGGGGGCCT	300
	TTCACTCTCC CAAGGACTCC ANGGGGGGGC CGGGTACCCA ATTCCGCCCC TATAGTGAAT	360
	CCGTNATTAC AATTCCACNT GGGCCGTCCN TTTTACAAA CGTTCCGTTG AACTGGGAAA	420
60	AACCCCTTGG CGGTTTACCC CAACTTTAAT CCGCCTTTGC AAGCACATCC CCCCCCTTTT	480

C

481

5

(2) INFORMATION FOR SEQ ID NO: 84:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

GCTGGGATAG AGCATGAAAG GAGAACTGCT CCCTTTTCTG TTTCTCACAG TTTGGTTATG	60
GCTTTATAAA CTTKTATTTG GTGAAAGCCC CAGATACCCA AATGTCATTG GCAAAACTTA	120
TTTTTTTTTC TGGACAGATC AGATTTCTAG AGAGAGCAGA TTTCTAGAGA GATTAGCATT	180
CATAGTAAGT GAAAATTGTC TAATTTTTTTT AATCCATGCT ATTACTGGGC AGTAGGTCTA	240
ATTTTTTTTG ACAAAAAATA GATCTATTTT CCTTATATAT TGATTTAGAA TCTTAAGTTA	300
GAATTTTATA GAAGAAATGT CTGAGCAGTT CTATGTATGG AGGAGCAATT CAGCTTTTCA	360
GCAGCAACTT TATCTTTTGC CACTAGAGGG AGATCTGTGG TTGCTTTCTC CTTGGAGAA	420
TAGCTGCTTT GCTTTTATTT TTAATTTCTA AGGTTGGAAT AGAACTTATT CTCAAAATTC	480
CTTTAGTGTT ATTAAATATT TTCATTTATT AGTCAAAGGT AAGTTAATTA AGCTTGTTTA	540
ATGATGCCAA TCTTATGCTT TTCTGTAATC TTCAATTTTT AATAAATGTG AGTTAGATAC	600
TAAGTGAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAA	644

40

(2) INFORMATION FOR SEQ ID NO: 85:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GGCACGAGTG CGCAGCGGTG GGGCTCTCTC CTTGTCTAGT GCGGCCGCGT GCGGGCTGGT	60
GGCTCTGTGG CAGCGGCGGC GGCAGGACTC CGGCACTATG AGCGGCTTCA GCACCGAGGA	120
GCGCGCCGCG CCNTTCTCCC TGGAGTACCG AGTCTTCCTC AAAAATGAGA AAGGACAATA	180
TATATCTCCA TTTCATGATA TTCCAATTTA TGCAGATAAG GATGTGTTTC ACATGGTAGT	240
TGAAGTACCA CGCTGGTCTA ATGCAAAAAT GGAGATTGCT ACAAAGGACC CTTTAAACCC	300

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5 TATTAAACAA GATGTGAAAA AAGGAAAACT TCGCTATGTT GCGAATTGTG TCCCGTATAA 360
 AGGATATATC TGGAACATATG GTGCCATCCC TCAGACTTGG GAAGACCCAG GGCACAATGA 420
 TAAACATACT GGCTGTTGTG GTGACAATGA CCCAATTGAT GTGTGTGAAA TTGGAAGCAA 480
 GGTATGTGCA AGAGGTGAAA TAATTGGCGT GAAAGTTCTA GGCATATTGG CTATGATTGA 540
 10 CGAAGGGGAA ACCGACTGGA AAGTCATTGC CATTAATGTG GATGATCCTG ATGCAGCCAA 600
 TTATAATGAT ATCAATGATG TCAAACGGCT GAAACCTGGC TACTTAGAAG CTACTGTGGA 660
 CTGGTTTAGA AGGTATAAGG TTCCTGATGG AAAACCAGAA AATGAGTTTG CGTTTAATGC 720
 15 AGAATTTAAA GATAAGGACT TTGCCATTGA TATTATTAAA AGCACTCATG ACCATTGGAA 780
 AGCATTAGTG ACTAAGAAAA CGAATGGAAA AGGAATCAGT TGCATGAATA CAACTTTGTC 840
 20 TGAGAGCCCC TTCAAGTGTG ATCCTGATGC TGCCAGAGCC ATTGTGGATG CTTTACCACC 900
 ACCCTGTGAA TCTGCCTGCA CAGTACCAAC AGACGTGGAT AAGTGGTTCC ATCACCAGAA 960
 AAATAATGA GATTTCTCTG GAATACAAGC TGATATTGCT ACATCGTGTG CATCTGGATG 1020
 25 TATTAGAAGT AAAAGTAGTA GCTTTTCAAA GCTTTAAATT TGTAGAACTC ATCTAACTAA 1080
 AGTAAATTC TCTGTGACTA ATCCAATATA CTCAGAATGT TATCCATCTA AAGCATTTTT 1140
 30 CATATCTCAA CTAAGATAAC TTTTAGCACA TGCTTAAATA TCAAAGCAGT TGTCATTTGG 1200
 AAGTCACTTG TGAATAGATG TGCAAGGGGA GCACATATTG GATGTATATG TTACCATATG 1260
 TTAGGAAATA AAATTATTTT GCTGAAAAAA AAAAAAAAAA AACCNCGGGG GGGGCCCCGG 1320
 35 TCCCCATTG GCCCTTTGGG GGGNGGTTTT A 1351

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(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 2527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

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CTCTTGCTAC CTTCCCGGCG CAGAGAACCC CGGCTGCTCA GCGCGCTCCG GGGTCATGGA 60
 GATCCCCGGG AGCCTGTGCA AGAAAGTCAA GCTGAGCAAT AACGCGCAGA ACTGGGGAAT 120
 GCAGAGAGCA ACCAATGTCA CCTACCAAGC CCATCATGTC AGCAGGAACA AGAGAGGTCA 180
 GGTGGTGGGG ACCAGAGGTG GCTTTCGTGG TTGCACAGTT TGGCTAACAG GCTTGTCTGG 240
 AGCGGGAAAG ACTACTGTGA GCATGGCCTT GGAGGAGTAC CTGGTTTGTC ATGGTATTCC 300

	ATGCTACACT CTGGATGGTG ACAATATTCG TCAAGGTCTC AATAAAAATC TTGGCTTTAG	360
	TCCTGAAGAC AGAGAAGAGA ATGTTTCGACG CATCGCAGAA GTTGCTAAAC TGTTTGCAGA	420
5	TGCTGGCTTA GTGTGCATCA CAAGTTTCAT ATCACCTTAC ACTCAGGATC GCAACAATGC	480
	AAGGCAAATT CATGAAGGTG CAAGTTTACC GTTTTGTGAA GTATTTGTTG ATGCTCCTCT	540
10	GCATGTTTGT GAACAGAGGG ATGTCAAAGG ACTCTACAAA AAAGCCCGGG CAGGAGAAAT	600
	TAAAGGTTTC ACTGGGATCG ATTCTGAATA TGAAAAGCCA GAGGCCCTG AGTTGGTGCT	660
	GAAAACAGAC TCCTGTGATG TAAATGACTG TGTCCAGCAA GTTGTGGAAC TTCTACAGGA	720
15	ACGGGATATT GTACCTGTGG ATGCATCTTA TGAAGTAAAA GAACTATATG TGCCAGAAAA	780
	TAAACTTCAT TTGGCAAAAA CAGATGCGGA AACATTACCA GCACTGAAAA TTAATAAAGT	840
	GGATATGCAG TGGGTGCAGG TTTTGGCAGA AGGTTGGGCA ACCCCATTGA ATGGCTTTAT	900
20	GAGAGAGAGG GAGTACTTGC AGTGCCCTCA TTTTGATTGT CTTCTGGATG GAGGTGTCAT	960
	TAACTTGTC A GTACCTATAG TTCTGACTGC GACTCATGAA GATAAAGAGA GGCTGGACGG	1020
25	CTGTACAGCA TTTGCTCTGA TGTATGAGGG CCGCCGTGTG GCCATTCTTC GCAATCCAGA	1080
	GTTTTTTAG CACAGGAAAG AGGAGCGCTG TGCCAGACAG TGGGGAACGA CATGCAAGAA	1140
	CCACCCCTAT ATTAAGATGG TGATGGAACA AGGAGATTGG CTGATTGGAG GAGATCTTCA	1200
30	AGTCTTGGAT CGAGTTTATT GGAATGATGG TCTTGATCAG TATCGTCTTA CTCCTACTGA	1260
	GCTAAAGCAG AAATTTAAAG ATATGAATGC TGATGCTGTC TTTGCATTTC AACTACGCAA	1320
35	CCCAGTGCAC AATGGACATG CCCTGTTAAT GCAGGATACC CATAAGCAAC TTCTAGAGAG	1380
	GGGCTACCGG CGCCCTGTCC TCCTCCTCCA CCCTCTGGGT GGCTGGACAA AGGATGACGA	1440
40	TGTTCCTTTG ATGTGGCGTA TGAAGCAGCA TGCTGCAGTG TTGGAGGAAG GAGTTCTGAA	1500
	TCCTGAGACG ACAGTGGTGG CCATCTTCCC ATCTCCCATG ATGTATGCTG GACCAACTGA	1560
	GGTCCAGTGG CATTGCAGAG CACGGATGGT TGCAGGAGCC AACTTTTACA TTGTTGGACG	1620
45	AGACCCTGCT GGCATGCCTC ATCCAGAAAC AGGGAAGGAT CTTTATGAGC CAAGTCATGG	1680
	TGCCAAAGTG CTGACGATGG CCCCTGGTTT AATCACTTTG GAAATAGTTC CCTTTGAGT	1740
	TGCAGCTTAC AACAAGAAAA AGAAGCGTAT GGACTACTAT GACTCTGAAC ACCATGAAGA	1800
50	CTTTGAATTT ATTTCAAGAA CACGAATGCG CAAACTTGCT CGAGAAGGCC AGAAACCACC	1860
	TGAAGGTTTC ATGGCTCCCA AGGCTTGGAC CGTGCTGACA GAATACTACA AATCCTTGGA	1920
55	GAAAGCTTAG GCTGTTAACC CAGTCACTCC ACCTTTGACA CATTTACTAGT AACAAGAGGG	1980
	GACCACATAG TCTCTGTTGG CATTTCTTTG TGGTGTCTGT CTGGACATGC TTCCTAAAAA	2040
60	CAGACCATTT TCCTTAACCT GCATCAGTTT TGGTCTGCCT TATGAGTTCT GTTTTGAACA	2100

AGTGTAACAC ACTGATGGTT TTAATGTATC TTTTCCACTT ATTATAGTTA TATTCCCTACA 2160
 ATACAATTTT AAAATGTGCT TTTTATATTA TATTTATGCT TCTGTGTCAT GATTTTTCAT 2220
 5 AGCTGTTATA TTAGTTGTAA CCAGTAGTAT TCACATTAAA TCTTGCTTTT TTTCCCTTCA 2280
 AAAAAAGAAA AAAATTACCA AACAATAAAC TTGGCTAGAC CTGTGTTTGA GGATTTTACA 2340
 10 AGACCTTTGT AGCGATTAGA TTTTTTTCT ACATTGAAAA TAGAACTGC TTCCTTTCTT 2400
 CTTTCCAGTC AGCTATTGGT CTTTCCAGCT GTTATAATCT AAAGTATTCT TATGATCTGT 2460
 GTAAGCTCTG AATGAACTTC TTTACTCAAT AAAATTAATT TTTGGCTTC TTAACAAAAA 2520
 15 AAAAAA 2527

20 (2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2566 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

30 CCCAAGAATT CGGCACGAGC GNGGCAWAAK TGGGATTCTT GAAACCTGTA GGCCCCAAGC 60
 CCATCAACTT GCCCAAAGAA GATTCCAAAC CTACATTTC CTGGCCTSCT GGAAACAAGC 120
 35 CATCTCTTCA CAGTGTAAC CAAGACCATG ACTTAAAGCC ACTAGGCCGA AATCTGGGCC 180
 TACTCTCCA ACCTCAGAAA ATGAACAGAA GCAAGCKTTT CCCAAATTGA CTGGGGTTAA 240
 AGGGAAATTT ATGTCAGCAT CACAAGATCT TGAACCAAG CCCCTCTTCC CCAAACCCGC 300
 40 CTTTGGCCAG AAGCCGCCCC TAAGTACCGA GAACTCCCAT GAAGACGAAA GCCCATGAA 360
 GAATGTGTCT TCATCAAAAG GGTCCCCAGC TCCCCTGGGA GTCAGGTCCA AAAGCGCCCC 420
 45 TTAAAACCA GCAAGGAAG ACTCAGAAAA TAAAGACCAT GCAGGGGAGA TTTCAAGTTT 480
 GCCCTTTCTT GGAGTGTTT TGAAACCTGC TGCGAGCAGG GGAGGCCAG GTCTCTCCAA 540
 AAATGGTGAA GAAAAAAGG AAGATAGGAA GATAGATGCT GCTAAGAACA CCTTCCAGAG 600
 50 CAAAATAAAT CAGGAAGAGT TGGCTCAGG GACTCCTCCT GCCAGGTTCC CTAAGGCCCC 660
 TTCTAAGCTG ACAGTGGGGG GGCCATGGGG CCAAAGTCAG GAAAAGGAAA AGGGAGACAA 720
 55 GAATTCAGCC ACCCCGAAAC AGAAGCCATT GCCTCCCTTG TTTACCTTGG GTCCACCTCC 780
 ACCAAAACCC AACAGACCAC CAAATGTTGA CCTGACGAAA TTCCACAAAA CCTCTTCTGG 840
 AAACAGTACT AGCAAAGGCC AGACGTCTTA CTCAACAAC TCCCTGCCAC CACCTCCACC 900
 60 ATCCCATCCG GCCAGCCAAC CACCATTGCC AGCATCTCAC CCATCACAAC CACCAGTCCC 960

	AAGCCTACCT CCCAGAAACA TTAAACCTCC GTTTGACCTA AAAAGCCCTG TCAATGAAGA	1020
5	CAATCAAGAT GGTGTCACGC ACTCTGATGG TGCTGGAAAT CTAGATGAGG AACAAGACAG	1080
	TGAAGGAGAA ACATATGAAG ACATAGAAGC ATCCAAAGAA AGAGAGAAGA AAAGGGAAAA	1140
	GGAAGAAAAG AAGAGGTTAG AGCTGGAGAA AAAGGAACAG AAAGAGAAAG AAAAGAAAGA	1200
10	ACAAGAAATA AAGAAGAAAT TTAAACTAAC AGGCCCTATT CAAGTCATCC ATCTTGCAAA	1260
	AGCTTGTTGT GATGTCAAAG GAGGAAAGAA TGAAGTGAAG TTCAAGCAAG GAGAGCAAAT	1320
15	TGAAATCATC CGCATCACAG ACAACCCAGA AGGAAAATGG TTGGGCAGAA CAGCAAGGGG	1380
	TTTCATATGGC TATATTAAAA CAACTGCTGT AGAGATTGAC TATGATTCTT TGAAACTGAA	1440
	AAAAGACTCT CTTGGTGCCC CTTCAAGACC TATTGAAGAT GACCAAGAAG TATATGATGA	1500
20	TGTTGCAGAG CAGGATGATA TTAGCAGCCA CAGTCAGAGT GGAAGTGGAG GGATATTCCC	1560
	TCCACCACCA GATGATGACA TTTATGATGG GATTGAAGAG GAAGATGCTG ATGATGGCTC	1620
25	CACACTACAG GTTCAAGAGA AGAGTAATAC GTGGTCCTGG GGGATTTTGA AGATGTTAAA	1680
	GGGAAAAGAT GACAGAAAGA AAAGTATACG AGAGAAACCT AAAGTCTCTG ACTCAGACAA	1740
	TAATGAAGGT TCATCTTTCC CTGCTCCTCC TAAACAATTG GACATGGGAG ATGAAGTTTA	1800
30	CGATGATGTG GATACCTCTG ATTTCCCTGT TTCATCAGCA GAGATGAGTC AAGGAACTAA	1860
	TGTTGGAAAA GCTAAGACAG AAGAAAAGGA CCTTAAGAAG CTAAAAAGC AGRAAAAARA	1920
35	ARAAAAAGAC TTCAGGAAAA AATTTTAAATA TGATGGTGAA ATTAGAGTCC TATATTCAAC	1980
	TAAAGTTACA ACTTCCATAA CTTCTAAAAA GTGGGGAACC AGAGATCTAC AGGTAAACC	2040
	TGGTGAATCT CTAGAAGTTA TACAAACCAC AGATGACACA AAAGTTCTCT GCAGAAATGA	2100
40	AGAAGGGAAA TATGGTTATG TCCTTCGGAG TTACCTAGCG GACAATGATG GAGAGATCTA	2160
	TGATGATATT GCTGATGGCT GCATCTATGA CAATGACTAG CACTCAACTT TGGTCATTCT	2220
45	GCTGTGTTCA TTAGGTGCCA ATGTGAAGTC TGGATTTTAA TTGGCATGTT ATTGGGTATC	2280
	AAGAAAATTA ATGCACAAAA CCACTTATTA TCATTTGTTA TGAAATCCCA ATTATCTTTA	2340
	CAAAGTGT'TT AAAGTTTGAA CATAGAAAAT AATCTCTCTG CTTAATMGTT ATCTCAGAAG	2400
50	ACTACATTAG TGAGATGTAA GAATTATTAA ATATTCCATT TCCGCTTTGG CTACAATTAT	2460
	GAAGAAGTTG AAGTACTTC TTTTAGACCA CCAGTAAATA ATCCTCCTTC AAAAAATAAA	2520
55	AATAAAAAAA AAAAAAAA ACTCGAGGGG GGGCCCGGTA CCCAAT	2566

(2) INFORMATION FOR SEQ ID NO: 88:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

10 GAATTCGGCA CGAGGCTTTC TGTGTCCTCT GTGGCTGCTT TAGTGTGCCA CCAGGGGCAG 60
 ACTTGGGTGG GTTGCAGCAG AGATGGCATG GCCCTCAAGG TCCAAGATGT TTACTCTCTT 120
 GCCGGTCCTC TGTTATCTCT GGTCTTTGTG GTTGCCACAG TTTTCTTGGA TCCAGGAGTT 180
 15 AAAGGCAGTC CTGAGGGATG ATGGCCTCAT CTCCGCAGTT GCYTGAATG CTGAATTTCA 240
 GACGTGCTAA AGGAGGGTTG CAGACATTGT GTGGWATGCA TTCAGACCCC AGATGTGGGT 300
 GCAGGAAGGC AGGCATGGCA CAGCCAGGTA GAGACTGGTT TCCAGGCCCA AGCAGCCTTC 360
 20 AGCAGCTGTG CGCCTTGTTT CTGATGTTGT TTGGGAGTAA GAATAATGTA GACATGGGGG 420
 GTCATGARGC TCAATAAAAA CTTCAAGGAA ACCTCCCATG GCATGGTTGG GCGCAGTGAC 480
 25 TCATGCCTGT AACCCCAGCA CTGTGGAATG CCAAGGTGGA AGGATCGCTT GAGGCCAAGA 540

30 (2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1863 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

40 TCGACCCACG CGTCCGGCGA GATCCCTACC GCAGTAGCCG CCTCTGCCGC CGCGGAGCTT 60
 CCCGAACCTC TTCAGCCGCC CGGAGCCGCT CCCGGAGCCC GGCCGTAGAG GCTGCAATCG 120
 CAGCCGGGAG CCCGCAGCCC GCGCCCCGAG CCCGCCCGG CCCTTCGAGG GCGCCCCAGG 180
 45 CCGCGCCATG GTGAAGGTGA CGTTCAATC CGCTCTGGCC CAGAAGGAGG CCAAGAAGGA 240
 CGAGCCCAAG AGCGGCGAGG AGGCGCTCAT CATCCCCCCC GACGCCGTCG CGGTGGACTG 300
 50 CAAGGACCCA GATGATGTGG TACCAGTTGG CCAAAGAAGA GCCTGGTGTT GGTGCATGTG 360
 CTTTGGACTA GCATTTATGC TTGCAGGTGT TATTCTAGGA GGAGCATACT TGTACAAATA 420
 TTTTGCACCT CAACCAGATG ACGTGTACTA CTGTGGAATA AAGTACATCA AAGATGATGT 480
 55 CATCTTAAAT GAGCCCTCTG CAGATGCCCC AGCTGTCTCT TACCAGACAA TTGAAGAAAA 540
 TATTAAATC TTTGAAGAAG AAGAAGTTGA ATTTATCAGT GTGCCTGTCC CAGAGTTTGC 600
 60 AGATAGTGAT CCTGCCAACA TTGTTTCATGA CTTTAACAAG AAACCTTACAG CCTATTTAGA 660

TCTTAACCTG GATAAGTGCT ATGIGATCCC TCTGAACACT TCCATTGTTA TGCCACCCAG 720
 AAACCTACTG GAGTTACTTA TTAACATCAA GGCTGGAACC TATTTGCCTC AGTCCTATCT 780
 5 GATTCATGAG CACATGGTTA TTAATGATCG CATTGAAAAC ATTGATCACC TGGGTTTCTT 840
 TATTTATCGA CTGTGTCATG ACAAGGAAAC TTACAACTG CAACGCAGAG AAACATTTAA 900
 10 AGGTATTCAG AAACGTGAAG CCAGCAATTG TTTCGCAATT CGGCATTTTG AAAACAAATT 960
 TGCCGTGGAA ACTTTAATTT GTTCTTGAAC AGTCAAGAAA AACATTATTG AGGAAAATTA 1020
 ATATCACAGC ATAACCCAC CTTTACATT TTGTGCAGTG ATTATTTTTT AAAGTCTTCT 1080
 15 TTCATGTAAG TAGCAAACAG GGCTTTACTA TCTTTTCATC TCATTAATTC AATTAAAACC 1140
 ATTACCTTAA AATTTTTTTC TTTCGAAGTG TGGTGTCTTT TATATTTGAA TTAGTAACTG 1200
 20 TATGAAGTCA TAGATAATAG TACATGTCAC CTTAGGTAGT AGGAAGAATT ACAATTTCTT 1260
 TAAATCATTT ATCTGGATTT TTATGTTTTA TTAGCATTTT CAAGAAGACG GATTATCTAG 1320
 AGAATAATCA TATATATGCA TACGTAAAAA TGGACCACAG TGACTTATTT GTAGTTGTTA 1380
 25 GTTGCCCTGC TACCTAGTTT GTTAGTGCAT TTGAGCACAC ATTTTAATTT TCCTCTAATT 1440
 AAAATGTGCA GTATTTTCAG TGTCAAATAT ATTTAACTAT TTAGAGAATG ATTTCCACCT 1500
 30 TTATGTTTTA ATATCCTAGG CATCTGCTGT AATAATATTT TAGAAAATGT TTGGAATTTA 1560
 AGAAATAACT TGTGTTACTA ATTGTATATA CCCATATCTG TGCAATGGAA TATAAATATC 1620
 ACAAAGTTGT TTAAC TAGAC TCGTGTGTGT TTTTCCCGTA TAATAAAACC AAAGAATAGT 1680
 35 TTGGTTCTTC AAATCTTAAG AGAATCCACA TAAAGAAGA AACTATTTTT TAAAAATTCA 1740
 CTTCTATATA TACAATGAGT AAAATCACAG ATTTTTCCTT TAAATAAAAA TAAGTCATTT 1800
 40 TAATAACTAA ACCAGATTCT TTGTGATACT ATTAANGTAA CATTTAGCCC CAAAAAATAA 1860
 AAA 1863

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(2) INFORMATION FOR SEQ ID NO: 90:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2478 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

GGCACAGCGG CACGAGGTGA GCTGAGCCGG TGGGTGAGCG GCGGCCACGG CATCCTGTGC 60
 TGTGGGGGCT ACGAGGAAAG ATCTAATTAT CATGGACCTG CGACAGTTTC TTATGTGCCT 120
 60

	GTCCCTGTGC ACAGCCTTTG CCTTGAGCAA ACCCACAGAA AAGAAGGACC GTGTACATCA	180
	TGAGCCTCAG CTCAGTGACA AGGTCACAA TGATGCTCAG AGTTTGTATT ATGACCATGA	240
5	TGCCTTCTTG GGTGCTGAAG AAGCAAAGAC CTTTGATCAG CTGACACCAG AAGAGAGCAA	300
	GGAAAGGCTT GGAAAGATTG TAAGTAAAAT AGATGGCGAC AAGGACGGGT TTGTCACGTG	360
10	GGATGAGCTC AAAGACTGGA TTAAATTTGC ACAAAGCGC TGGATTTACG AGGATGTAGA	420
	GCGACAGTGG AAGGGGCATG ACCTCAATGA GGACGGCCTC GTTTCCTGGG AGGAGTATAA	480
	AAATGCCACC TACGGCTACG TTTTAGATGA TCCAGATCCT GATGATGGAT TTAACATAA	540
15	ACAGATGATG GTTAGAGATG AGCGGAGGTT TAAATGCA GACAAGGATG GAGACCTCAT	600
	TGCCACCAAG GAGGAGTTCA CAGCTTTCCT GCACCCTGAG GAGTATGACT ACATGAAAGA	660
20	TATAGTAGTA CAGGAAACAA TGGAAGATAT AGATAAGAAT GCTGATGGTT TCATTGATCT	720
	AGAAGAGTAT ATTGGTGACA TGTACAGCCA TGATGGGAAT ACTGATGAGC CAGAATGGGT	780
	AAAGACAGAG CGAGAGCAGT TTGTTGAGTT TCGGGATAAG AACCGTGATG GGAAGATGGA	840
25	CAAGGAAGAG ACCAAAGACT GGATCCTTCC CTCAGACTAT GATCATGCAG AGGCAGAAGC	900
	CAGGCACCTG GTCTATGAAT CAGACCAAAA CAAGGATGGC AAGCTTACCA AGGAGGAGAT	960
30	CGTTGACAAG TATGACTTAT TTGTTGGCAG CCAGGCCACA GATTTTGGGG AGGCCTTAGT	1020
	ACGGCATGAT GAGTTCTGAG CTRCGGAGGA ACCCTCATTT CCTCAAAAGT AATTTATTTT	1080
	TACAGCTTCT GGTTCACAT GAAATTGTTT GCGCTACTGA TACTGTTACT ACAAACTTT	1140
35	TAAGACATGA AAAGGCGTAA TGAAAACCAT CCCGTCCCCC TCTCCTCC TCTCTGAGGG	1200
	ACTGGAGGGA AGCCGTGCTT CTGAGGAACA ACTCTAATTA CTACACTTGT GTTTGTAGAT	1260
40	TTACACTTTG TATTATGTAT TAACATGGCG TGTATTATTT TGTATTTTTC TCTGGTTGGG	1320
	AGTATGATAT GAAGGATCAA GATCCTCAAC TCACACATGT AGACAAACAT TAGCTCTTTA	1380
	CTCTTTCTCA ACCCTTTTTA TGATTTTAAT AATTCTCACT TAACTAATTT TGTAAGCCTG	1440
45	AGATCAATAA GAAATGTTCA GGAGAGAGGA AAGAAAAAA ATATATGCTC CACAATTTAT	1500
	ATTTAGAGAG AGAACACTTA GTCTTGCCTG TCAAAAAGTC CAACATTTCA TAGGTAGTAG	1560
50	GGGCCACATA TTACATTTCAG TTGCTATAGG TCCAGCAACT GAACCTGCCA TTACCTGGGC	1620
	AAGGAAAGAT CCCTTTGCTC TAGGAAAGCT TGGCCCAAAT TGATTTTCTT CTTTTTCCCC	1680
	CTGTAGGACT GACTGTTGGC TAATTTTGTC AAGCACAGCT GTGGTGGGAA GAGTTAGGGC	1740
55	CAGTGTCTTG AAAATCAATC AAGTAGTGAA TGTGATCTCT TTGCAGAGCT ATAGATAGAA	1800
	ACAGCTGGAA AACTAAAGGA AAAATACAAG TGTTTTCGGG GCATACATTT TTTTCTGGG	1860
60	TGTGCATCTG TTGAAATGCT CAAGACTTAA TTATTTGCCT TTTGAAATCA CTGTAAATGC	1920

CCCCATCCGG TTCCTCTTCT TCCCAGGTGT GCCAAGGAAT TAATCTTGGT TTCACTACAA 1980
 TTAAAATTCA CTCCTTTCCA ATCATGTCAT TGAAAGTGCC TTAAACGAAA GAAATGGTCA 2040
 5 CTGAATGGGA ATTCTCTTAA GAAACCCTGA GATTAAAAAA AGACTATTTG GATAACTTAT 2100
 AGGAAAGCCT AGAACCTCCC AGTAGAGTGG GGATTTTTTTT CTCTCTCCCT TTCTCTTTTG 2160
 GACAATAGTT AAATTAGCAG TATTAGTTAT GAGTTTGGTT GCAGTGTCTT TATCTTGTGG 2220
 10 GCTGATTTCC AAAAACCACA TGCTGCTGAA TTTACCAGGG ATCCTCATACT CTCACAATGC 2280
 AAACCACTTA CTACCAGGCC TTTTCTGTG TCCACTGGAG AGCTTGAGCT CACACTCAAA 2340
 15 GATCAGAGGA CCTACAGAGA GGGCTCTTTG GTTTGAGGAC CATGGCTTAC CTTTCTGCCC 2400
 TTTGACCCAT CACACCCCAT TTCCTCTCTT TTCCCTCTCC CCGCTGCCAA TTCCTGCAGC 2460
 CCGGGGGAAC CACTAGTT 2478
 20

(2) INFORMATION FOR SEQ ID NO: 91:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2058 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

TCGGCCTTGC TTTGTGGYC TTCCTCTGTG GCCAGAGCGT TTTCATCACC AAGCCTCCTG 60
 35 ATGGCAGTNC CTTCAACGAT ATGTTCAAGA TACTGACGTA TTCCTGCTGT TCCCAGAAGC 120
 GAAGTGGAGA GCGCCAGAGT AATGGTGAAG GCATTGGAGT NTTCAGCAA TCTTCTAAAC 180
 40 AAAGTCTGTT TGATTCATGT AAGATGTCTC ATGGTGGGCC ATTTACAGAA GAGAAAGTGG 240
 AAGATGTGAA AGCTCTGGTC AAGATTGTCC CTGTTTCTT GGCTTTGATA CCTTACTGGA 300
 CAGTGTATTT CCAAATGCAG ACAACATATG TTTTACAGAG TCTTCATTG AGGATTCAG 360
 45 AAATTTCAAA TATTACAACC ACTCCTCACA CGCTCCCTGC AGCCTGGCTG ACCATGTTTG 420
 ATGCTGTGCT CATCCTCCTG CTCATCCCTC TGAAGGACAA ACTGGTCGAT CCCATTTTGA 480
 50 GAAGACATGG CCGCTCCCA TCCTCCCTGA AGAGGATCGC CGTGGGCATG TTCTTTGTCA 540
 TGTGCTCRGC CTTTGCTGCA GGAATTTTGG AGAGTAAAAG GCTGAACCTT GTTAAAGAGA 600
 AAACCATTA TCAGACCATC GGCAACGTCG TCTACCATGC TGCCGATCTG TCGCTGTGGT 660
 55 GGCAGGTGCC GCAGTACTTG CTGATTGGGA TCAGCGAGAT CTTTGCAAGT ATCGCAGGCC 720
 TGGAATTTGC ATACTCAGCT GCCCCAAGT CCATGCAGAG TGCCATAATG GGCTTGTCTT 780
 60 TTTCTTCTC TGGCGTCGGG TCGTTCGTGG GTTCTGGACT GCTGGCACTG GTGTCTATCA 840

AAGCCATCGG ATGGATGAGC AGTCACACAG ACTTTGGTAA TATTAACGGC TGCTATTTGA 900
 ACTATTACTT TTTCTCTCTG GCTGCTATTC AAGGAGCTAC CCTCCTGCTT TTCCTCATTA 960
 5 TTTCTGTGAA ATATGACCAT CATCGAGACC ATCAGCGATC AAGAGCCAAT GGCGTGCCCA 1020
 CCAGCAGGAG GGCCTGACCT TCCTGAGGCC ATGTGCGGTT TCTGAGGCTG ACATGTCAGT 1080
 10 AACTGACTGG GGTGCACTGA GAACAGGCAA GACTTTAAAT TCCCATAAAA TGTCTGACTT 1140
 CACTGAAACT TGCATGTTGC CTGGATTGAT TTCTTCTTTC CCTCTATCCA AAGGAGCTTG 1200
 GTAAGTGCCT TACTGCAGCG TGTCTCCTGG CACGCTGGGC CCTCCGGGAG GAGAGCTGCA 1260
 15 GATTTTCGAGT ATGTCGCTTG TCATTCAAGG TCTCTGTGAA TCCTCTAGCT GGGTTCCCTT 1320
 TTTTACAGAA ACTCACAAAT GGAGATTGCA AAGTCTTGGG GAACTCCACG TGTTAGTTGG 1380
 20 CATCCCAGTT TCTTAAACAA ATAGTATCAC CTGCTTCCCA TAGCCATATC TCACTGTAAA 1440
 AAAAAAATT AATAAACTGT TACTTATATT TAAGAAAGTG AGGATTTTTT TTTTTTAAAG 1500
 ATAAAGCAT GGTGAGATGC TGCAAGGATT TTACATAAAT GCCATATTTA TGGTTTCCTT 1560
 25 CCTGAGAACA ATCTTGCTCT TGCCATGTTT TTTGATTAG GCTGGTAGTA AACACATTTT 1620
 ATCTGCTGCT TCAAAAAGTA CTTACTTTTT AAACCATCAA CATTACTTTT CTTTCTTAAG 1680
 30 GCAAGGCATG CATAAGAGTC ATTTGAGACC ATGTGTCCCA TCTCAAGCCA CAGAGCAACT 1740
 CACGGGGTAC TTCACACCTT ACCTAGTCAG AGTGCTTATA TATAGCTTTA TTTTGGTACG 1800
 ATTGAGACTA AAGACTGATC ATGGTTGTAT GTAAGGAAAA CATTCCTTTG AACAGAAATA 1860
 35 GTGTAATTAA AAATAATTGA AAGTGTTAAA TGTGAACTTG AGCTGTTTGA CCAGTCACAT 1920
 TTTTGTATTG TFACTGTACG TGTATCTGGG GCTTCTCCGT TTGTTAATAC TTTTCTGTGA 1980
 40 TTTGTTGCTG TATTTTTGGC ATAACCTTAT TATAAAAAGC ATCTCAAATG CGAAAWAAAA 2040
 AAAAAAAAAA AAAAAAAC 2058

45

(2) INFORMATION FOR SEQ ID NO: 92:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1411 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

60 GGCACAGGAG CGACCCGGGA GAAGGAGGGC CAMGAKGCGG AAGCGGAGGA GTCTCCAGGA 60
 GACCCGGGGA CAGCATCGCC CAGGCCCTG TTTGAGGCC TTTCAGATAT ATCCATCTCA 120

243

CAAGACATCC CCGTAGAAGG AGAAATCACC ATTCCCTATGA GATCTCGCAT CCGGGAGTTT 180
 GACAGCTCCA CATTAAATGA ATCTGTTTCGC AATACCATCA TCGTGATCT AAAAGCTGTT 240
 5 GGGAAAAAAT TCATGCATGT TTTGTACCCA AGGAAAAGTA ATACTCTTTT GAGAGATTGG 300
 GATTGTGGG GCCCTTTGAT CCTTTGTGTG AACTCGCAT TAATGCTGCA AAGAGACTCT 360
 GCAGATAGTG AAAAAGATGG AGGGCCCCAA TTTGCAGAGG TGTTCGTCAT TGTCTGGTTT 420
 10 GGTGCAGTTA CCATCACCTT CAACTCAAAA CTTCTTGGAG GGAACATATC TTTTTTTCAG 480
 AGCCTCTGTG TGCTGGGTTA CTGTATACTT CCCTTGACAG TAGCAATGCT GATTTGCCGG 540
 15 CTGGTACTTT TGGCTGATCC AGGACCTGTA AACTTCATGG TTCGGCTTTT TGTGGTGATT 600
 GTGATGTTTG CCTGGTCTAT AGTTGCCTCC ACAGCTTTCC TTGCTGATAG CCAGCCTCCA 660
 AACC GCAGAG CCTAGCTGT TTATCCTGTT TTCCTGTTTT ACTTTGTCAT CAGTTGGATG 720
 20 ATTCTCACCT TTA CTCTCA GTAAATCAGG AATGGGAAAT TAAAAACCAG TGAATTGAAA 780
 GCACATCTGA AAGATGCAAT TCACCATGGA GCTTTGTCTC TGGCCCTTAT TTGTCTAATT 840
 25 TTGGAGGTAT TTGATAACTG AGTAGGTGAG GAGATTAAAA GGGAGCCATA TAGCACTGTC 900
 ACCCCTTATT TGAGGAAGT ATGTTTGAAA GGCTGTTCTT TTCTCTCTTA ATGTCATTTT 960
 TTTAAAAATA CATGTGCATA CTACACACAG TATATAATGC CTCCTTAAGG CATGATGGAG 1020
 30 TCACCGTGGT CCATTTGGGT GACAACCACT GACTTGGGAA GCACATAGAT ACATCTTACA 1080
 AGTTGAATAG AGTTGATAAC TATTTTCAGT TTTGAGAATA CCAGTTCAGG TGCAGCTCTT 1140
 35 AAACACATTG CCTTATGACT ATTAGAATAT GCCTCTCTTT TCATAAATAA AAATACATGG 1200
 TCTATATCCA TTTCTTTT TTTCTCTCTC TTAAGCTTAA AAAGGCAATG AGAGAGGTTA 1260
 GGAGTGGGTT CATAACGGA GAATGAGAAA ACATGCATTA ACCAATATTC AGATTTTGAT 1320
 40 CAGGGGAAAT TCTAYACTTG TTGCAAAAAA AAAAAAAAAA AACTCGAGG GGGGCCCGGT 1380
 ACCCAATCGC NGTATATGAT CGNAAACAAT C 1411

45

(2) INFORMATION FOR SEQ ID NO: 93:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

GCTTTGGCTT TTTTGGCGG ACTGGGCGC CCTCCGAAG CGTTCCAAC TTTCCAGAAG 60
 60 TTTCTCGGA CGGCAGGAG GGGTGGGA CTGCCATATA TAGATCCCG GAGCAGGGGA 120

	GCGGGCTAAG AGTAGAATCG TGTCGCGCTC GAGAGCGAGA GTCACGTCCC GGCGCTAGCC	180
5	CAGCCCGACC CAGGCCACC GTGGTGCACG CAAACCACTT CCTGGCCATG CGCTCCCTCC	240
	TGCTTCTCAG CGCCTTCTGC CTCTGGAGG CGGCCCTGGC CGCCGAGGTG AAGAAACCTG	300
	CAGCCGCAGC AGCTCCTGGC ACTGCGGAGA AGTTGAGCCC CAAGGCGGCC ACGCTTGCCG	360
10	AGCGCAGCCG GCCTGGCCTT CAGCTTGATC CAGGCCATGG CCAAGGACCA GGCAGTGGAG	420
	AACATCCTGG TGTCACCCGT GGTGGTGGCC TCGTCGCTGG GGCTCGTGTC GCTGGGCGGC	480
15	AAGCGACCA CGGCGTCGCA GGCCAAGGCA GTGCTGAGCG CCGAGCAGCT GCGCGACGAG	540
	GAGGTGCACG CCGGCCTGGG CGAGCTGCTG CGCTCACTCA GCAACTCCAC GCGCGCAAC	600
	GTGACCTGGA AGCTGGGCAG CCGACTGTAC GGACCCAGCT CAGTGAGCTT CGCTGATGAC	660
20	TTCTGTCGCA GCAGCAAGCA GCACTACAAC TCGAGCAGCT CCAAGATCAA CTCCCGCAG	720
	AAGCGCAGCG CGCTGCAGTC CATCAACGAG TGGGCCGCGC AGACCACCGA CGGCAAGCTG	780
25	CCCCAGGTCA CCAAGGACGT GGAGCGCAGC GACGGCGCCC TGTTAGTCAA CGCCATGTTT	840
	TTCAAGCCAC ACTGGGATGA GAAATTCCAC CACAAGATGG TGGACAACCG TGGCTTCATG	900
	GTGACTCGGT CCTATACCGT GGGTGTCTATG ATGATGCACC GGACAGGCCT CTACAACTAC	960
30	TACGACGACG AGAAGGAAAA GCTGCAAATC GTGGAGATGC CCCTGGCCCA CAAGCTCTCC	1020
	AGCCTCATCA TCCTCATGCC CCATCACGTG GAGCCTCTCG AGCGCCTTGA AAAGCTGCTA	1080
35	ACCAAGAGC AGCTGAAGAT CTGGATGGGG AAGATGCAGA AGAAGGCTGT TGCCATCTCC	1140
	TTGCCCCAAGG GTGTGGTGA GGTGACCCAT GACCTGCAGA AACACCTGGC TGGGCTGGGC	1200
	CTGACTGAGG CCATTGACAA GAACAAGGCC GACTTGTGAC GCATGTCAGG CAAGAAGGAC	1260
40	CTGTACCTGG CCAGCGTGTT CCACGCCACC GCCTTTGAGT TGGACACAGA TGGCAACCCT	1320
	TTGACCAGAA TTACGGGCGG AGGAGTGCGC ACCCAAGTGT TCTACGCCGA CCACCCCTTC	1380
45	ATTTCCTAGT GCGGGACACC CAAAGCGGTC CCTGCTATTC ATTGGGCGCC TGGTCCGGCC	1440
	TAAGGGTGAC AAGATGCGAG ACGAGTTATA GGCCTCAGG TGCACACAGG ATGGCAGGAG	1500
	GCATCCAAAG GCTCCTGAGA CACATGGGTG CTATTGGGGT TGGGGGGGAG GTGAGGTACC	1560
50	AGCCTTGGAT ACTCCATGGG GTGGGGTGA AAAGCAGACC GGGGTTCCTG TGTGCCTGAG	1620
	CGGACTTCCC AGCTAGAATT CACTCCACTT GGACATGGGC CCCAGATACC ATGATGCTGA	1680
55	GCCCGGAAAC TCCACATCCT GTGGGACCTG GGCCATAGTC ATTCTGCCTG CCCTGAAAGT	1740
	CCCAGATCAA GCCTGCCTCA ATCAGTATTC ATATTTATAG CCAGGTACCT TCTCACCTGT	1800
	GAGACCAAAT TGAGCTAGGG GGTGAGCCA GCCCTCTTCT GACACTAAAA CACCTCAGCT	1860
60	GCCTCCCCAG CTCTATCCCA ACCTCTCCCA ACTATAAAAC TAGGTGCTGC AGCCCCCTGGG	1920

ACCAGGCACC CCCAGAATGA CCTGGCCGCA GTGAGGCGGA TTGAGAAGGA GCTCCCAGGA 1980
GGGGCTTCTG GGCAGACTCT GGTCAAGAAG CATCGTGTCT GCGTGTGTGG GGATGAACTT 2040
5 TTTGTTTTGT TTCTTCCTTT TTTAGTTCTT CAAAGATAGG GAGGGAAGGG GGAACATGAG 2100
CCTTTGTTGC TATCAATCCA AGAACTTATT TGTACATTTT TTTTTCAT AAACCTTTTC 2160
10 CAATGACAAA AAAAAAAAAA AAAAAAA 2187

15 (2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 757 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

25 GACAGTACGG TCGGATTCCC GGGTCGACCC ACGCGTCCGC GGACGGTGAA GAAGGTGAAG 60
ATGGCGGTGG CCAGGGCCCG GGTCTTGGGA GTCCAGTGGC TGCAAAGGGC ATCCCGGAAC 120
GTGATGCCGC TGGGCGCACG GACAGCCTCC CACATGACCA AGGACATGTT CCCGGGGCCC 180
30 TATCCTAGGA CCCAGAAGA ACGGGCCGCC GCCGCCAAGA AGTATAATAT GCGTGTGGAA 240
GACTACGAAC CTTACCCGGA TGATGGCATG GGGTATGGCG ACTACCCGAA GCTCCCTGAC 300
35 CGCTCACAGC ATGAGAGAGA TCCATGGTAT AGCTGGGACC AGCCGGGCCT GAGGTGAAC 360
TGGGGTGAAC CGATGCACTG GCACCTAGAC ATGTACAACA GGAACCGTGT GGATACATCC 420
CCCACACCTG TTTCTTGGCA TGTCATGTGT ATGCAGCTCT TCGGTTTCCT GGCTTTCATG 480
40 ATATTCATGT GCTGGGTGGG GGACGTGTAC CCTGTCTACC AGCCTGTGGG ACCAAAGCAG 540
TATCCTTACA ATAATCTGTA CCTGGAACGA GGCGGTGATC CCTCCAAAGA ACCAGAGCGG 600
45 GTGGTTCACT ATGAGATCTG AGGAGGCTTC GTGGGCTTTT GGGTCCTCTA ACTAGGACTC 660
CCTCATTCCT AGAAATTTAA CCTTAATGAA ATCCCTAATA AAACCTAGTG CTGTGTTAAA 720
AAAAAAAAA AAAAAAAAAA AAAAAGGGGG GCCCCNN 757
50

(2) INFORMATION FOR SEQ ID NO: 95:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2394 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

5	GGCACGAGCA CTCCTGCACT TCCCCACCCC CACGACCGAA CCTGGCTTCG CTAACGCCCT	60
	CCCAGCTCCC TCGGGCCTGA CTTCGGTTT CCTCGCGCGT CCCTGGCGCC GAGCCGCGGA	120
	CAGCAGCCCC TTTTCCGGCT GAGAGCTCAT CCACACTTCC AATCACTTTC CGGAGTGCTT	180
10	CCCCTCCCTC CGGCCCGTGC TGGTCCCGAC GGC GGCGCTG GGTCTCGCGC GCGTATTGCT	240
	GGGTAACGGG CCTTCTCYCG CGTCGGCCCG GCCCTCCTG CCTCGGCTCG TCCCTCCTTC	300
	CAGAACGTCC CGGGCTCCTG CCGAGTCAGA AGAAATGGGA CTCCCTCCGC GACGTGCCCCG	360
15	GAGCAGCTCC CTTCTGCTGTG GAAGCGGCGG TGTCTTCGAA GAAACCGAA GCCCGTGGTG	420
	ACCCCTGGCG ACCCGGTTTG TTTTCGGTCC GTTTCCAAAC ACTAAGGAAT CGAAACTCGG	480
20	CGGCCTTGGG GCGGCCCTA CGTAGCCTGG CTCTGGTTG TCATGGATGC ACTGGTAGAA	540
	GATGATATCT GTATTCTGAA TCATGAAAAA GCCCATAAGA GAGATACAGT GACTCCAGTT	600
	TCAATATATT CAGGAGATGA ATCTGTTGCT TCCCATTTTG CTCTTGTCAC TGCATATGAA	660
25	GACATCAAAA AACGACTTAA GGATTCAGAG AAAGAGAACT CTTTGTTAAA GAAGAGAATA	720
	AGATTTTGG AAGAAAAGCT AATAGCTCGA TTTGAAGAAG AAACAAGTTC CGTGGGACGA	780
30	GAACAAGTAA ATAAGGCCTA TCATGCATAT CGAGAGGTTT GCATTGATAG AGATAATTTG	840
	AAGAGCAAAC TGGACAAAAT GAATAAAGAC AACTCTGAAT CTTTGAAAGT ATTGAATGAG	900
	CAGCTACAAT CTAAAGAAGT AGAACTCCTC CAGCTGAGGA CAGAGGTGGA AACTCAGCAG	960
35	GTGATGAGGA ATTTAAATCC ACCTTCATCA AACTGGGAGG TGGAAAAGTT GAGCTGTGAC	1020
	CTGAAGATCC ATGGTTTGGA ACAAGAGCTG GAACTGATGA GGAAAGAATG TAGCGATCTC	1080
40	AAAATAGAAC TACAGAAAGC CAAACAAACG GATCCATATC AGGAAGACAA TCTGAAGAGC	1140
	AGAGATCTCC AAAAATAAG CATTTCAAGT GATAATATGC AGCATGCATA CTGGGAACTG	1200
	AAGAGAGAAA TGTCTAATTT ACATCTGGTG ACTCAAGTAC AAGCTGAACT ACTAAGAAAA	1260
45	CTGAAAACCT CAACTGCAAT CAAGAAAGCC TGTGCCCTG TAGGATGCAG TGAAGACCTT	1320
	GGAAGAGACA GCACAAAAC GCACTTGATG AATTTTACTG CAACATACAC AAGACATCCC	1380
50	CCTCTCTTAC CAAATGGCAA AGCTCTTTGT CATACCACAT CTTCCCTTT ACCAGGAGAT	1440
	GTAAAGGTTT TATCAGAGAA AGCAATCTC CAATCATGGA CAGACAATGA GAGATCCATT	1500
	CCTAATGATG GTACATGCTT TCAGGAACAC AGTCTTATG GCAGAAATTC TCTGGAAGAC	1560
55	AATTCCTGGG TATTTCCAAG TCCTCCTAAA TCAAGTGAGA CAGCATTTGG GGAAACTAAA	1620
	ACTAAAACCT TGCCTTTACC CAACCTTCCA CCACTGCATT ACTTGATCA ACATAATCAG	1680
60	AACTGCCTTT ATAAGAATTA ATTTGGAAGA GATTCACGAT TTCACCATGA GGACACTTAT	1740

CTCTTTCAGT GGTCTCCCA AGAATTATT TAACAACTG AANGGAGATT TTGATTAAAA 1800
 TTTTGCAGAG GTCTTCAGTA TCTATATTTG AACACACTGT ACAATAGTAC AAAAACCAAC 1860
 5 ATAGTTGGTT TTCTAGTATG AAAGAGCACC CTCTAGCTCC ATATTCTAAG AATCTGAAAT 1920
 ATGCTACTAT ACTAATTAAT AAGTAACTT AAGGTGTTTA AAAA ACTCTG CCTTCTATAT 1980
 10 TAATTGTAAA ATTTTGCCTC TCAGAAGAAT GGAATTGGAG ATTGTAGACG TGGTTT TACA 2040
 AAATGTGAAA TGTCTAAATA TCTGTTTATA AAAATAAAAG GAAAACATGT TTCTTCAAAT 2100
 TGCATAATGG AACAAATGGC AATGTGAGTA GGTACATTT CTGTTGTTAT AATGCGTAAA 2160
 15 GATATTGAAA ATATAATGAA ATAAAAGCAT CTTAGGTTAT ACCATCTTTA TATGCTATTG 2220
 CGTTTCAATA TTAAAGATTT AAAGTGATTT TTTGGTCACA GTGTTTGTGT GATAAAATTT 2280
 20 TTTTAGAATT GAAGTTTGAA TTCTAAGACT TGAAACAACC TGATCACTGA AGCCAAC TTT 2340
 GTCCCAGCAC ATTCCTTAAG TCCTAATTGG GGAAAAAAA AAAAAAAAC TCGA 2394

25

(2) INFORMATION FOR SEQ ID NO: 96:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 672 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

AGTGCTCTGT TGCCAGGCT GGAGTGC GTT AGTGTAATGT CAGTCCACTG CAACCTCCAC 60
 CCCAGGTTT AAGCAATTCT CATGCCTCAG CCTCCCAAGT AGCTGAAATT ACTGGCATGC 120
 40 ACCACCACAC CCAGCTGATG TTTATTTATT TATTTATATA TTTATTTATT TTAGGTGTTT 180
 TTTTTTTTTT TTTTGTGAGAC GGAGTCTTGC TCTGTTGCCC TGGGTGTGGT TACGTGGRAT 240
 45 TACCATYCTG GGTGACTCAC TGAAATGTAC TCMCAGTGAG TCATGCCTTC MAATGACATC 300
 TCAAGTTCTG CTGCTTGA GATACATCTG GGGATCTTAA GGGGTGAGGG ACTACTCAAC 360
 AAGAAGGAAT TTAGCTGTG TTTTAAATA AACGGCATTT CTTTTTCCTA KAAAAATGGG 420
 50 AAATCTTTCA ATTCTCTAAT ACAGGGACAC TGAGATAACA AAGAGGAAAG TGTCTGGTTG 480
 GAGGTGGGA RGCCACCCTG GGTCTCTCC TACAAAAATG GAAAAGAAAA GAACGGTGAR 540
 55 AAATCMAGCA AAGCACAARA AAKTTTCCCT TTGCTAAAAG GGAAAAGATG CCCCMAATG 600
 CCCATAAACA TGAAGTGGG ATAAGGAGGA RAATGTCTCT YCTTGGCACC CCCAAACAAA 660
 CGTTAATTAC CC 672
 60

(2) INFORMATION FOR SEQ ID NO: 97:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1419 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

15

TAAGAACAGA ACAGCAAGTA TGAACCACAT GGAACCTAAA ACATATGGGT GTGAAGTCCA 60

CTTATGTAGA CAAAACTTAT AATTTCCTAAA CTGTTGTCTA GTATACAGTG ATCAGTTGCT 120

CTCTGTTCAA GTCATTCCAC ACATTTCCCT ATTTTtaggCT ATTATAATAT AGAAAGAAAA 180

20

TGGGAAGCAT TAGTTGGAGC TAGAAAATGA ACTGTATATT ATTGCTATAT TTGCTAATAC 240

CAACTATTTT AATAAGTGTT GTACCATATG TAGCATTAAA TATAAAATAC ATAAAAGAAT 300

25

GTACAGAAAA TAGCTTTTAT TGAGTAATAT TACATTTCAT TTATACTGTA GCAATATATT 360

TGTAAGTATA CTCTGTAAGG GCTTTAAATA AAAGAGGTCC ATTAATACTT CCTTATAAAA 420

ATTCTAGTCT GTTTCATTAC TGCCAGATG TTTTAGAGAT AAATATTTAT GCAGAAGGTA 480

30

TTTTKGAAAG TCYCCYTTTG TCTGATAGAG TTTAACNAGA TATTTAAATT TAGTGCYCNA 540

GAAATCCCAC AAGTCACGGT CTAAACACAC TTAGAATACT ACAGCATAAA TCTGTTAGCA 600

35

TTANTTGCCA AATAAGACAG TTGGGATCCC AAACCCCAAG TCCTTGAGCA ATGTTTTTCC 660

TCAAAAAGCT GCTATNCCAA TGATATAGGA AAAWACATTG TGTTTTCCCTA AACACACTTT 720

TCTTTTAAA TGTGCTTCAT TGTTTGATTT GGTCTGCTT AAATTTTACA AGCTAGGCCA 780

40

ATGAAGGCTG AATCAAAGAC ATTTTCATCCA CCAATATCAT GTGTAGATAT TATGTATAGA 840

AAATAAAATA AATTATGGCT CTAACCTCTG TGTTGCTGTT TATCTTGTTA TTTTTCGGCG 900

45

TTATACTAAT GNGTTTATMG AGAGCATTTT ACCTTCCAGA CTTCTCATGG CTAACCTTTG 960

GTCTGWATTT TGSTCCTTAG ATGKGAATAT TTCTTATTAG TYTGCTYCCT GCWACGCAAT 1020

GACTGCATTT CTATCATTTT TCAGTTTGTT AGWATATGTG GATAGTATTC TACTGTATAA 1080

50

ATGATTGCAA AGTTTATCAA AAACAAATTA TTATATGTAG CTTTCTTACA GTGCTTTGCT 1140

AAACCATGTA GTACTAGTTA AGTSTTCCTT GAAAATAAAG ATACACTCTT ATAGGGGACA 1200

55

GTTCTGTTC ACTCCCAGGA AACTTTTTTTA AAAGATGACA CTGAATGTTT ATTGCACTTT 1260

AGTGCACTGA AGTGGCAATA AAACCTAACA TGAATCAAGG TTGTTTATGG CAGATGCATG 1320

TGTTGCTTTA CAGAGTTTAG CAAAAGCTCT TAATTTTATG TCATACTGTA TTCTACTGAA 1380

60

TAATAAAGCT AACATTATTC AATAATAAAA TGGAAAAAA 1419

5 (2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1487 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

15 GCGACCGCGC CCCTTTCAGC TAGCTCGCTC GCTCGCTCTG CTTCCCTGCT GCCGGCTGCG 60
CATGGCKWTG GCGTTGGCGG CGCTGGCGGC GGTGAGCCG GCCTGCGCAG CCGGTACCAG 120
CAGTTGCAGA ATGAAGAAGA GTCTGGAGAA CCTGAACAGG CTGCAGGTGA TGCTCCTCCA 180
20 CCTTACAGCA GCATTCTGC AGAGAGCGCA GTTTTCCACC TATTTCCCTG GATATTTTGA 240
TGGTCAGTAC TGGCTCTGGT GGGTGTTCCT TGTMTTAGGC TTTCTCCTGT TTCTCAGAGG 300
25 ATTTATCAAT TATGCAAAAG TTCGGAAGAT GCCAGAACT TTCTCAAATC TCCCCAGGAC 360
CAGAGTTCTC TTTATTTATT AAAGATGTTT TCTGGCAAAG GCCTTCCTGC ATTTATGAAT 420
TCTCTCTCAA GAAGCAAGAG AACACCTGCA GGAAGTGAAT CAAGATGCAG AACACAGAGG 480
30 AATAATCACC TGCTTTAAAA AAATAAAGTA CTGTTGAAAA GATCATTTCT CTCTATTGTG 540
TCCTAGGTGT AAAATTTTAA TAGTTAATGC AGAATTCTGT AATCATTGAA TCATTAGTGG 600
35 TTAATGTTTG AAAAAGCTCT TGCAATCAAG TCTGTGATGT ATTAATAATG CCTTATATAT 660
TGTTGTAGT CATTTTAAAGT AGCATGAGCC ATGTCCCTGT AGTCGGTAGG GGGCAGTCTT 720
GCTTTATTCA TCCTCCATCT CAAATGAAC TTGGAATTAA ATATTGTAAG ATATGTATAA 780
40 TGCTGGCCAT TTAAAGGGG TTTTCTCAAA AGTTAAACTT TTGTTATGAC TGTGTTTTTG 840
CACATAATCC ATATTGCTG TTCAAGTTAA TCTAGAAATT TATTCAATTC TGTATGAACA 900
45 CCTGGAAGCA AAATCATAGT GCAAAAATAC ATTTAAGGTG TGGTCAAAAA TAAGTCTTTA 960
ATTGGTAAAT AATAAGCATT AATTTTATAT AGCCTGTATT CACAATTCTG CCGTACCTTA 1020
TTGTACCTAA GGGATTCTAA AGGTGTGTCT ACTGTATAAA ACAGAAAGCA CTAGGATACA 1080
50 AATGAAGCTT AATTACTAAA ATGTAATTCT TGACACTCTT TCTATAATTA GCGTTCTTCA 1140
CCCCACCCC CACCCCACC CCCCTTATTT TCCTTTTGTC TCCTGGTGAT TAGGCCAAAG 1200
55 TCTGGGAGTA AGGAGAGGAT TAGGTACTTA GGAGCAAAGA AAGAAGTAGC TTGGAACCTT 1260
TGAGATGATC CCTAACATAC TGTAATACTT GCTTTTACAA TGTGTTAGCA GAAACCAGTG 1320
GGTTATAATG TAGAATGATG TGCTTTCTGC CCAAGTGGTA ATTCATCTTG GTTTGCTATG 1380
60

TTAAACTGT AAATACAACA GAACATTAAT AAATATCTCT TGTGTAGCAC CTTTAAAAAA 1440
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAAN CCCGGGGGGG GGCCCCN 1487

5

(2) INFORMATION FOR SEQ ID NO: 99:

10

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1653 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

GCGACCGCGC CCTTCAGCTA GCTCGCTCGC TCGCTCTGCT TCCCTGCTGC CGGCTGCGCA 60
 20 TGGCTTNGGC GTTGGCGGCG CTGGCGGCGG CTCGAGCCGC CTGCGSAGCC GGTACCAGCA 120
 GTTGCAGAAT GAAGAAGAGT CTGGAGAACC TGAACAGGCT GCAGGTGATG CTCCTCCACC 180
 25 TTACAGCAGC ATTTCTGCAG AGAGCGCACA TNATTTTGAC TACAAGGATG AGTCTGGGTT 240
 TCCAAAGCCC CCATCTTACA ATGTAGCTAC AACACTGCCC AGTTATGATG AAGCGGAGAG 300
 GACCAAGGCT GAAGCTACTA TCCCTTTGGT TCCTGGGAGA GATGAGGATT TTGTGGGTCG 360
 30 GGATGATTTT GATGATGCTG ACCAGCTGAG GATAGGAAAT GATGGGATTT TCATGTTAAC 420
 TTTTTTCATG GCATTCCTCT TTAAGTGGAT TGGGTTTTTC CTGTCTTTTT GCCTGACCAC 480
 TTCAGCTGCA GGAAGGTATG GGGCCATTTT AGGATTTGGT CTCTCTCTAA TTAAATGGAT 540
 35 CCTGATTGTC AGGTTTTCCA CCTATTTCCC TGCATTTATG AATTCTCTCT CAAGAAGCAA 600
 GAGAACACCT GCAGGAAGTG AATCAAGATG CAGAACACAG AGGAATAATC ACCTGCTTTA 660
 40 AAAAAATAAA GACTGTGTA AAAGATCATT TCTCTCTATT GTTCCTAGG TGTAATAATT 720
 TAATAGTTAA TGCAGAATTC TGTAATCATT GAATCATTAG TGGTTAATGT TTGAAAAAGC 780
 TCTTGCAATC AAGTCTGTGA TGTATTAATA ATGCCCTATA TATTGTTTGT AGTCATTTTA 840
 45 AGTAGCATGA GCCATGTCCC TGTAGTCGGT AGGGGGCAGT CTTGCTTTAT TCATCCTCCA 900
 TCTCAAAATG AACTTGGAAT TAAATATTGT AAGATATGTA TAATGCTGGC CATTTTAAAG 960
 50 GGGTTTTCTC AAAAGTTAAA CTTTGTATAT GACTGTGTTT TTGCACATAA TCCATATTTG 1020
 CTGTTCAAGT TAATCTAGAA ATTTATTCAA TTCTGTATGA ACACCTGGAA GCAAAATCAT 1080
 AGTGCAAAAA TACATTTAAG GTGTGGTCAA AAATAAGTCT TTAATTGGTA AATAATAAGC 1140
 55 ATTAATTTTT TATAGCCTGT ATTCACAATT CTGCGGTACC TTATTGTACC TAAGGGATTC 1200
 TAAAGGTGTT GTCAGTGTAT AAAACAGAAA GCACTAGGAT ACAAATGAAG CTTAATTACT 1260
 60 AAAATGTAAT TCTTGACACT CTTTCTATAA TTAGCGTTCT TCACCCCCAC CCCCACCCCC 1320

ACCCCCCTTA TTTTCCTTTT GTCTCCTGGT GATTAGGCCA AAGTCTGGGA GTAAGGAGAG 1380
 GATTAGGTAC TTAGGAGCAA AGAAAGAAGT AGCTTGGAAC TTTTGAGATG ATCCCTAACA 1440
 5 TACTGTACTA CTTGCTTTTA CAATGTGTTA GCAGAAACCA GTGGGTATA ATGTAGAATG 1500
 ATGTGCTTTC TGCCCAAGTG GTAATTCATC TTGGTTTGCT ATGTTAAAAC TGTAATACA 1560
 10 ACAGAACATT AATAAATATC TCTTGTGTAG CACCTTTTAW AAAAAAAAAA AAAAAAAAAA 1620
 AAAAAAAAAA AAAAAANCCCG GGGGGGGGCC CCN 1653

15

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 1145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

TTTTTTTTTT TTTTTTTTTT TTGACTGAAC TAAGTGCTT TTTTATTAGA GAAAGCCAGA 60
 ATTACAAAAG ACTTCCCTTT TCTTGGGGTA TGGCTGTCTC AGCACAATAC TCAACATAAC 120
 30 TGCAGAACTG ATGTGGCTCA GGCACCCTGG TTTTAATTCC TTGAGGATCT GGCAATTGGC 180
 TTACGCAAAA GGTCAACATT TGAGGTCCTG CCTTACTAAT TATGTGCTGC CCAACAATA 240
 35 AATTGTGAAT TTGTTTTTCT CTAGTTTGAG CAGGGTCTGA ATTTTTTCAT TTATTTCTTT 300
 TTTTGCCAGC AGACAGACTT GAGTCTGTAA AGACAAGCAA ATACACTGAC AGAAGTTTAC 360
 CATAGTTTCT AAAATGTAAA AAAGAAAACC CCCAAAAGAC TCAAGAAAAT TAGACCACAA 420
 40 ATTTTGCATT GTTCATTGTA GCACTATTGG TAATAAAATA ACAAATGTTT GTGCATTTTT 480
 ATGTGAAGAT CCTTCTCGTA TTTTATTGGA AAAGATGAGC AAGAGGTCTG CTTCTTTCAT 540
 45 TTTACTTCCC CTTCTGTTTT TGAAAGGCAG TTTCGCCAAG CTTAATGCAA GAATATCTGA 600
 CTGTTTAGAA GAAAGATATT GCCACAATCT CTGGATGGTT TTCCAGGGTT GTGTTATTAC 660
 TGAGCTTCAT CTTTCCAGAA TGAGCAAAAC ACTGTCCAGT CTTTGTACG ATTTTGTAAT 720
 50 AAATGTGTAC ATTTTTTTTA AATTTTTTGA CATCACATGA ATAAAGGTAT GTATGTACGA 780
 ATGTGTATAT ATTATATATA TGACATCTAT TTTGGAAAAT GTTTGCCCTG CTGTACCTCA 840
 55 TTTTAGGAG GTGTGCATGG ATGCAATATA TGAAATGGG ACATTCTGGA ACTGCTGGTC 900
 AGGGGACTTT GTCGCCCTGT GCACTAAAAG GGCCAGATTT TCAGCAGCCA AGGACATCCA 960
 TACCCAAGTG AATGTGATGG GACTTAAAAG AAGTGAAGTG AGACAATTCA CTCTGGCTGT 1020
 60

TTGAACAGCA GCGTTTCATA GGAAGAGAAA AAAAGATCAA TCTTGTATTT TCTGACCACA 1080
TAAAGGCTTC TTCTCTTTGT AATAAAGTAG AAAAGCTCTC CTCAAAAAAA AAAAAAAAAA 1140
5 AAAAA 1145

10 (2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 734 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

20 TACCCGGCGG ATTCCAGGAA GGTAATTTA GTCCTATAAT TTTCAGCTTA ATTATAAACA 60
AAGGAACAAA TAAGTGAAG GGCAGCTATT ACCATTCGCT TAGTCAAAAC ATTCGGTTAC 120
TGCCCTTTAA TACACTCCTA TCATCAGCAC TTCCACCATG TATTACAAGT CTGACCCAT 180
25 CCCTGTCGTA ACTCCAGTAA AAGTTACTGT TACTAGAAAA TTTTATCAA TTAAGTGACA 240
AATAGTTTCT TTTTAAAGTA GTTCTTCCA TCTTATTCT GACTAGCTTC CAAAATGTGT 300
30 TCCCTTTTGT AATCGAGGTT TTTTGTGTTT GTTTGTGTTT CTGAAAAAT CATACAACTT 360
TGTGCTTCTA TTGCTTTTTT GTGTTTGTGTT AAGCATGTCC CTTGGCCCAA ATGGAAGAGG 420
AAATGTTTAA TTAATGCTTT TTAGTTTAAA TAAATTGAAT CATTTATAAT AATCAGTGTT 480
35 AACAATTTAG TGACCCTTGG TAGGTTAAAG GTTGCAATTAT TTATACTTGA GATTTTTTTC 540
CCCTAACTAT TCTGTTTTTT GACTTTTAAA ACTATGGGGG AAATATCACT GGTCTGTCAA 600
40 GAAACAGCAG TAATTATTAC TGAGTTAAAT TGAAAAGTCC AGTGGACCAG GCATTTCTTA 660
TATAAATAAA ATTGGTGGTA CTAATGTGAA AAAAAAAAAA AAAAAAACT CGAGGGGGGC 720
45 CCGGTACCTT ATTA 734

50 (2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 713 base pairs
(B) TYPE: nucleic acid
55 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

60 CCGCGGGAAC GCTGTCCTGG CTGCCGNCAC CCGAACAGCC TGTCTGGTG CCGCGGCTCC 60

253

CTGCCCCGCG CCCAGTCATG ACCCTGCGCC CCTCACTCCT CCCGCTCCAT CTGCTGCTGC 120
 TGCTGCTGCT CAGTGCGGCG GTGTGCCGGG CTGAGGCTGG GCTCGAAACC GAAAGTCCCG 180
 5 TCCGGACCCT CCAAGTGGAG ACCCTGGTGG AGCCCCCAGA ACCATGTGCC GAGCCCGCTG 240
 CTTTGGAGA CACGCTTCAC ATACACTACA CGGGAAGCTT GGTAGATGGA CGTATTATTG 300
 ACACCTCCCT GACCAGAGAC CCTCTGGTTA TAGAACTTGG CCAAAGCAG GTGATTCCAG 360
 10 GTCTGGAGCA GAGTCTTCTC GACATGTGTG TGGGAGAGAA GCGAAGGGCA ATCATTCTTT 420
 CTCACTTGGC CTATGGAAAA CGGGGATTTC CACCATCTGT CCCAGCGGAT GCAGTGGTGC 480
 15 AGTATGACGT GGAGCTGATT GCACTAATCC GAGCCAACTA CTGGCTAAAG CTGGTGAAGG 540
 GCATTTTGCC TCTGGTAGGG ATGGCCATGG TGCCACCCTC CTGGGCCTCA TTGGGTATCA 600
 CCTATACAGA AAGGCCAATA GACCCAAAGT CTCCAAAAG AAGCTCAAGG AAGAGAAACG 660
 20 AAACAAGAGC AAAAAGAAAT AATAAATAAT AAATTTTAAA AACTTAAAA AAA 713

25

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1080 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

35

CCGATGTGGA CATCATCCTG TCTATCCCCA TGTTCCTGCG CCTGTACCTG ATCGCCCGAG 60
 TCATGCTGCT GCACAGAAGC TCTTCACCGA TGCTCGTCC CGCAGCATCG GGGCCCTCAA 120
 40 CAAGATCAAC TTCAACACCC GCTTTGTCAT GAAGACGCTC ATGACCATCT GCCCTGGCAC 180
 TGTGCTGCTC GTGTTAGCA TCTCTCTGTG GATCATGTCT GCCTGGACCG TCCGTGTCTG 240
 TGAAAGTCCT GAATCACCAG CCCAGCCTTC TGGCTCATCA CTTCTGCTT GGTACCATGA 300
 45 CCAGCAGGAC GTAAC TAGTA ACTTTCTGGG TGCCATGTGG CTCATCTCCA TCACATTCCT 360
 TTCCATTGGT TATGGGGACA TGGTGCCCCA CACATACTGT GGGAAAGGTG TCTGTCTCCT 420
 50 CACTGGCATC ATGGGTGCAG GCTGCACTGC CCTTGTGGTG GCCGTGGTGG CCCGAAAGCT 480
 GGAATCACC AAAGCGGAGA AGCACGTTCA TAANTTCATG ATGGACACTC AGCTCACCAA 540
 GCGGATCAAG AATGYTGCAG CCAATGTCCT TSGGGAAACA TGGTTAATCT ATAAACACAC 600
 55 AAAGYTGYTA AAGAAGATTG ACCATGCCAA AGTGAGGAAC ACCAGAGGAA GTTCYTCCAA 660
 GTATCCACCA GTTGAGGAGC GTCAAGATGG AACAGAGGAA GCTGAGTGAC CAAGCCAACA 720
 60 NICTGGTGGA CCTTTCCAAG ATGCAGAATG TCMTGTATGA CTTAATCACA GAACTCAATG 780

ACCGGAGCGA AGACCTGGAG AAGCAGATTG GCAGCCTGGA GTCGAAGCTG GAGCATCTCA 840
CCGCCAGCTT CAACTCCCTG CCGCTGCTCA TCGCCGACAC CCTGCGCCAG CAGCAGCAGC 900
5 AGCTCCTGTC TGCCATCATC GAGGCCCGGG GTGTACGCGT GGCAGTGGGC ACCACCCACA 960
CCCCAATCTC CGATAGCCCC ATTGGGGTCA GCTCCACCTC CTTCCCGACC CCGTACACAA 1020
10 GTTCAAGCAG TTGCTAAATA AATCTCCCA CTCCAGAAGC ATTAAAAAA AAAAAAAAAA 1080

15 (2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

25 GGCACGAGAG GCTTTGAAGC ATTTTGTCT GTGCTCCCTG ATCTTCAGGT CACCACCATG 60
AAGTTCTTAG CAGTCCTGGT ACTCTGGGA GTTTCATCT TTCTGGTCTC TGCCAGAAT 120
CCGACAACAG CTGCTCCAGC TGACACGTAT CCAGCTACTG GTCTGCTGA TGATGAAGCC 180
30 CCTGATGCTG AAACCACTGC TGCTGCAACC ACTGCGACCA CTGCTGCTCC TACCACTGCA 240
ACCACCGCTG CTTCTACCAC TGCTCGTAAA GACATTCCAG TTTTACCCAA ATGGGTTGGG 300
35 GATCTCCCGA ATGGTAGAGT GTGTCCCTGA GATGGAATCA GCTTGAGTCT TCTGCAATTG 360
GTCACAAC TAATGCTTCT CTGTGATTTC ATCCAAC TACCTTGCC TACGATATCC 420
CCTTTATCTC TAATCAGTTT ATTTTCTTTC AAATAAAAAA TAACTATGAG CAACAAAAAA 480
40 AAAAAAAA 489

45 (2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 640 base pairs
(B) TYPE: nucleic acid
50 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

55 GCGGTCGCCG CTGTTGTTGT GGTCCCCATG GAGCTGCCGT AGCGGACCCA GCACAGCCAG 60
GAGCGTCCGG GATGAGCTCA GCCGCGGCCG ACCACTGGGC GTGGTTGCTG GTGCTCAGCT 120
60 TCGTGTTTGG ATGCAATGTT CTTAGGATCC TCCTCCGTC CTTCTCATCC TTCATGTCCA 180

255

5 GGGTGCTGCA GAAGGACGCG GAGCAGGAGT CACAGATGAG AGCGGAGATC CAGGACATGA 240
 AGCAGGAGCT CTCCACAGTC AACATGATGG ACGAGTTTGC CAGATATGCC AGGCTGGAAA 300
 GAAAGATCAA CAAGATGACG GATAAGCTCA AAACCCATGT GAAAGCTCGG ACAGCTCAAT 360
 TAGCCAAGAT AAAATGGGTG ATAAGTGTCT CTTTCTACGT ATTGCAGGCT GCCCTGATGA 420
 10 TCTCACTCAT TTGGAAGTAT TATTCTGTCC CTGTGGCTGT CGTGCCGAGT AAATGGATAA 480
 CCCTYTAGAC CGCCTGGTAG CCTTTCCYAY TAGAGTAGCA GGTGGTGTG GAATTACTGT 540
 TGGATTIART CTGTACAAAT TGTCTATTG TGCTTCACCG TYCASTGAAC AGGAGGTGGT 600
 15 ACAGCCGGAG TTAAAAACGG TTCCNTTCC AGTTTAAAT 640

20

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1529 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

30 GGGCACNAGA TGAGCTGCC GTAGCGGACC CAGCACAGCC AGGAGCGTCC GGGATGAGCT 60
 CAGCCGCGGC CGACCACTGG GCGTGGTTGC TGGTGCTCAG CTTCTGTGTT GGATGCAATG 120
 35 TTCTTAGGAT CCTCCTCCCG TCCTTCTCAT CTTTCATGTC CAGGGTGCTG CAGAAGGACG 180
 CGGACAGGAG TCACAGATGA GAGCGGAGAT CCAGGACATG AAGCAGGAGC TCTCCACAGT 240
 CAACATGATG GACGAGTTTG CCAGATATGC CAGGCTGGAA AGAAAGATCA ACAAGATGAC 300
 40 GGATAAGCTC AAAACCCATG TGAAAGCTCG GACAGCTCAA TTAGCCAAGA TAAAATGGGT 360
 GATAAGTGTC GCTTCTACG TATTGCAGGC TGCCCTGATG ATCTCACTCA TTTGGAAGTA 420
 45 TTATTCTGTC CCTGTGGCTG TCGTGCCGAG TAAATGGATA ACCCCTCTAG ACCGCCTGGT 480
 AGCCTTTCCT ACTAGAGTAG CAGGTGGTGT TGAATTACC TGTGGATTT TAGTCTGTAA 540
 CAAAGTTGTC GCTATTGTGC TTCATCCGTT CAGCTGAACA GGAGGATGGA TACAGCCGCG 600
 50 AGTAAAAAAA CGGATTTCCT CTCCTAGCT TAAAATCTGA TTTACTGT TTTGTTTTTT 660
 AAGAAACAAA AGTGCATAGT TTAGATTTTT TTTTGTGA ATATGTTTGT TCTTGACTT 720
 55 TATGAGATAG TCTTATAAGA ATCAGATTT TCTACACCTG TCATTGAGCC AAGAAAGTCC 780
 AGTTTATGAC ACGTATGTAC TAGTGAACAC CGTCCTCGAT CTGTACGAAA TGTGAAATGT 840
 60 TTAGGGACAT CTCCATGCTG TCACTTGTGA TTTGCCCTCT TATGTATTTT GGTCATATTG 900

256

CCAACTGGAA AGTCAAAATT TTCTAACAAC TTTAAGTAAG TTCTTTGAAG ACTTAGTGCT 960
 GTTTTAAATC CAGTTTAGAA AGTAACITAA TTTTAATACC RCTACTAAAA ATTGCGAAAAT 1020
 5 TTCTTCTTTA ATCACATTCA ATATGGTTAA AAGAACAACA CTAATTGACA TTGCGTGGGC 1080
 TTTTCTCCC TTTGTTTAAA ATGTCATTG TTGAGCAAGA GTTGATAGT ATTATCTACT 1140
 10 TACTTGAGGC TGTAAATTTT TCATTACAGT GTTTGTAAA TGTATCCACG AGACCATGAT 1200
 GCATTGTTTT GTGCTCAACT TGTGTTTTGT ATTTAAAGCA TTTTGAATGA AGTGTATTTT 1260
 ATAAGCATTT AATATTTATG CTCTTTAGAA TGGAACACAG AAAACAAACC TTATAAGTCC 1320
 15 TGATTAATCT GAACCAATAA CCTGTGTGGC CTACAAAGTA TAATTCTATT AAATGTTTCT 1380
 TAAACACTT TTTTCTAATT AAAATCTTTG CAAATGCTTG TGTAACITCC TGCCTTACAG 1440
 20 CTACTTGTTT GCTGTGAGCC ACCCGCAACT GACAAGTGGC TGTAACTGA GTCACCATAT 1500
 CCCAGTAAAG CTGAATTTTC TCACTAAAA 1529

25

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2435 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

35

ATGAAGGGTC GTTGGTGGGA AAGATGGCGG CGACTCTGGG ACCCCTTGGT CGTGGCAGCA 60
 GTGGCGRCGA TGTMTGTCGG CTCGGGATGG GTCCAGGATG TTACTCCTTC TTCTTTTGTT 120
 40 GGGGTCTGGG CAGGGGCCAC AGCAAGTCGG GCGGGTCAA ACGTTCGAGT ACTTGAAACG 180
 GGAGCACTCG CTGTCAAGC CCTACCAGGG TGTGGGCACA GGCAGTTCCT CACTGTGGAA 240
 45 TCTGATGGGC AATGCCATGG TGATGACCCA GTATATCCGC CTTACCCAG ATATGCAAAG 300
 TAAACAGGGT GCCTTGTGGA ACCGGGTGCC ATGTTTCCTG AGAGACTGGG AGTTGCAGGT 360
 GCACTTCAAA ATCCATGGAC AAGGAAAGAA GAATCTGCAT GGGGATGGCT TGGCAATCTG 420
 50 GTACACAAAG GRWTCGGATG CAGCCAGGCC CTGTTNTTGG GAAACATGGA CAAATTGTG 480
 GGGCTGGGAG TATTGTAGA CACCTACCCC AATGAGGAGA AGCAGCAAGA GCGGGTATTC 540
 55 CCCTRCMTCT CAGCCATGGT GAACAACGGC TCCCTCAGCT ATGATCATGA GCGGGATGGG 600
 CGGCCTACAG AGCTGGGAGG CTGCASAGCC ATTGTCCGCA ATCTTCATTA CGACACCTTC 660
 CTGGTGATTG GCTACGTCAA GAGGCATTTT ACGATAATGA TGGATATTGA TGGCAAGCAT 720
 60 GAGTGGAGGG ACTGCATTGA AGTGCCCGGA GTCCGCCTGC CCCGCGGCTA CTACTTCGGC 780

	ACCTCCTCCA TCACTGGGGA TCTCTCAGAT AATCATGATG TCATTTCCCTT GAAGTTGTTT	840
5	GAAC TGACAG TGGAGAGAAC CCCAGAAGAG GAAAAGCTCC ATCGAGATGT GTTCTTGCCC	900
	TCAGTGGACA ATATGAAGCT GCCTGAGATG ACAGCTCCAC TGCCGCCCTT GAGTGGCCTG	960
	GGCCTCTTCC TCATCGTCTT TTTCTCCCTG GGTGTTTCTT GTATTTGCCA TAGTCATTTG	1020
10	TATCATACTC TACAACAAAT GGCAGGAACA GAGCCGAAAG CGCTTCTACT GAGCCCTCCT	1080
	GCTGCCACCA CTTTGTGAC TGTACCCAT GAGGTATGGA AGGAGCAGGC ACTGGCCTGA	1140
15	GCATGCAGCC TGGAGAGTGT TCTGTCTCTT AGCAGCTGGT TGGGGACTAT ATTCTGTCAC	1200
	TGGAGTTTGT AATGCAGGGA CCCC GCATTC CCATGGTTGT GCATGGGGAC ATCTAACTCT	1260
	GGTCTGGGAA GCCACCCACC CCAGGCAAT GCTGCTGTGA TGTGCCTTTC CCTGCAGTCC	1320
20	TTCCATGTGG GAGCAGAGGT GTGAAGAGAA TTTACGTGGT TGTGATGCCA AAATCACAGA	1380
	ACAGAAITTC ATAGCCCAGG CTGCCGTGTT GTTTGACTCA GAAGGCCCTT CTAATTCAGT	1440
25	TTTGAATCCA CAAAGAATTA AAAACTGGTA ACACCACAGG CTTTCTGACC ATCCATTCTG	1500
	TGGGTTTTGC ATTTGACCCA ACCCTCTGCC TACCTGAGGA GCTTCTTTTG GAAACCAGGA	1560
	TGGAAACTTC TTCCCTGCCT TACCTTCCTT TCACTCCATT CATGTCTCTC TCTGTGTGCA	1620
30	ACCTGAGCTG GGAAAGGCAT TTGGATGCCT CTCTGTGGG GCCTGGGGCT GCAGAACACA	1680
	CCTGCGTTTC ACTGGCCTTC ATTAGGTGGC CCTAGGGAGA TGGCTTTCTG CTTTGGATCA	1740
35	CTGTTCCCTA GCATGGGTCT TGGGTCTATT GGCATGTCCA TGGCCTTCCC AATCAAGTCT	1800
	CTTCAGGCCC TCAGTGAAGT TTGGCTAAAG GTTGGTGTAA AAATCAAGAG AAGCCTGGAA	1860
	GACATCATGG ATGCCATGGA TTAGCTGTGC AACTGACCAG CTCCAGGTTT GATCAAACCA	1920
40	AAAGCAACAT TTGTCATGTG GTCTGACCAT GTGGAGATGT TTCTGGACTT GCTAGAGCCT	1980
	GCTTAGCTGC ATGTTTGTGA GTTACGATTT TTGGAATCCC ACTTTGAGTG CTGAAAGTGT	2040
45	AAGGAAGCTT TCTTCTTACA CCTTGGGCTT GGATATTGCC CAGAGAAGAA ATTGGCTTTT	2100
	TTTTTTNCTT AATGGACAAG AGACAGTTGC TGTCTCATG TTCCAAGTCT GAGAGCAACA	2160
	GACCCTCATC ATCTGTGCCT GGAAGAGTTC ACTGTCATTG AGCAGCACAG CCTGAGTGCT	2220
50	GGCCTCTGTC AACCTTATT CCACTGCCTT ATTTGACAAG GGGTTACATG CTGCTCACCT	2280
	TACTGCCCTG GGATTAAATC AGTTACAGGC CAGAGTCTCC TTGGAGGGCC TGGAACCTCTG	2340
55	AGTCCTCCTA TGAACCTCTG TAGCCTAAAT GAAATTCTTA AAATCACC GA TGGAACCAAA	2400
	AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAN	2435

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 805 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

10 ATGAAACTTA AGAATTGAAT TGGAAAGACT TCTCAAAGAG AATTGTATGT AACGATGTTG 60
TATTGATTTT TAAGAAAGTA ATTTAATTTG TAAACTTCT GCTCGTTTAC ACTGCACATT 120
15 GAATACAGGT AACTAATTGG AAGGAGAGGG GAGGTCATC TTTTGATGGT GGCCCTGAAC 180
CTCATTCTGG TTCCCTGCTG CGCTGCTTGG TGTGACCCAC GGAGGATCCA CTCCCAGGAT 240
GACGTGCTCC GTAGCTCTGC TGCTGATACT GGGTCTGCGA TGCAGCGGCG TGAGGCCTGG 300
20 GCTGGTTGGA GAAGGTCACA ACCCTTCTCT GTTGGTCTGC CTTCTGCTGA AAGACTCGAG 360
AACCAACCAG GGAAGCTGTC CTGGAGGTCC CTGGTCGGAG AGGGACATAG AATCTGTGAC 420
25 CTCTGACAAC TGTGAAGCCA CCCTGGGCTA CAGAAACCAC AGTCTTCCCA GCAATTATTA 480
CAATCTTGA ATTCCTTGGG GATTTTTTAC TGCCCTTTCA AAGCACTTAA GTGTTAGATC 540
TAACGTGTTT CAGTGTCTGT CTGAGGTGAC TTAAAAATC AGAACAAAAC TTCTATTATC 600
30 CAGAGTCATG GGAGAGTACA CCCTTTCCAG GAATAATGTT TTGGGAAACA CTGAAATGAA 660
ATCTTCCCAG TATTATAAAT TGTGTATTTA AAAAAAGAA ACTTTTCTGA ATGCCTACTG 720
35 GCGGTGTATA CCAGGCAGTG TGCCAGTTTA AAAAGATGAA AAAGAATAAA AACTTTTGAG 780
GAACAAAAAA AAAAAAAAAA AAATT 805

40

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GGCACGAGAG GCGCCAGTCG CAGGTGTGCT GCTGAGGCGT GAGAATGGCG TCCCGCGGCC 60
GGCGTCCGGA GCATGGCGGA CCCCAGAGC TGTTTTATGA CGAGACAGAA GCCCGGAAAT 120
55 ACGTTCGCAA CTCACGATG ATTGATATCC AGACCAGGAT GGCTGGGCGA GCATTGGAGC 180
TTCTTTATCT GCCAGAGAAT AAGCCCTGTT ACCTGCTGGA TATTGGCTGT GGCCTGGGC 240
60 TGAGTGGAAG TTATCTGTCA GATGAAGGGC ACTATGGGT GGGCCTGGAT ATCAGCCCTG 300

5 CCATGCTGGA TGAGGCTGTG GACCGAGAGA TAGAGGGAGA CCTGCTGCTG GGGGATATGG 360
 GCCAGGGCAT CCCATTCAAG CCAGGCACAT TTGATGGTTG CATCAGCATT TCTGCTGTGC 420
 AGTGGCTCTG TAATGCTAAC AAGAAGTCTG AAAACCCTGC CAAGCGCCTG TACTGCTTTT 480
 TTGCTTCTCT TTTTCTGTG CTCGTCCGGG GATCCCGAGC TGTCTGCAG CTGTACCCTG 540
 10 AGAACTCAGA GCAGTTGGAG CTGATCACAA CCCAGGCCAC AAAGGCAGGC TTCTCCGGTG 600
 GCATGGTGGT AGACTACCCT AACAGTGCCA AAGCAAAGAA ATTCTACCTC TGCTTGTMTT 660
 CTGGGCCTTC GACCTTTATA CCAGAGGGGC TGAGTGAAAA TCAGGATGAA GTTGAACCCA 720
 15 GGGAGTCTGT GTTCACCAAT GAGAGGTTCC CATTAAGGAT GTCGAGGCGG GGAATGGTGA 780
 GGAAGAGTCG GGCATGGGTG CTGGAGAAGA AGGAGCGGCA CAGGCGCCAG GGCAGGGAAG 840
 20 TCAGACCTGA CCCCCAGTAC ACCGGCCGCA AGCGCAAGCC CCGCTTCTAA GTCACCACGC 900
 GGTTCCTGAA AGGCACTTGC CTCTGCACTT TTCTATATTG TTCAGCTGAC AAAGTAGTAT 960
 TTTAGAAAAG TTCTAAAGTT ATAAAAATGT TTTCTGCAGT AAAAAAAAAG TTCTCTGGGC 1020
 25 CGGGCGTGGT GGCTCACANC TGTAATCCCA GCACCTTGGG AGGCTGAGGT GGGAGGATCA 1080
 TTTGAGGCCA GGAGTTTGAG ACCTGCCTGG GCAACATAAT GAACTTCCT TTCCAGGGAG 1140
 30 AAAAAAAAAA AAAAAAAAAA ACTCGA 1166

35 (2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 586 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

45 AGAGCGGACG AAGCTGGATA ACAGGGGACC GATGATGTGG CGACCATCAG TTCTGCTGCT 60
 TCTGTTGCTA CTGAGGCACG GGGCCCAGGG GAAGCCATCC CCAGACGCAG GCCCTCATGG 120
 CCAGGGGAGG GTGCACCAGG CGGCCCCCCT GAGCGACGCT CCCCATGATG ACGCCCACGG 180
 50 GAACTTCAG TACGACCATG AGGCTTTCCT GGGACGGGAA GTGGCCAAGG AATTCGACCA 240
 ACTCACCCCA GAGGAAAGCC AGGCCCGTCT GGGGCGGATC GTGGACCGCA TGGACCGCGC 300
 55 GGGGGACGGC GACGGCTGGG TGTCGCTGGC CGAGCTTCGC GCGTGGATCG CGCACACGCA 360
 GCAGCGGCAC ATACGGGACT CGGTGAGCGC GGCCTGGGAC ACGTACGACA CGGACCGCGA 420
 CGGGCGTGTG GGTGAGGAGG AGCTGCGCAA CGYCACCTAT GGCCACTASG SGCCCGKTGA 480
 60

AGAATTTTCAT GACGTGGAGG ATGCAGAGAC YTACAAAAAG ATGCTGGYTC GGGACGAGCG 540

GCGTTTCCGG GTGGCCGACC AGGATGGGGA CTCGATGGCC ACTCGA 586

5

(2) INFORMATION FOR SEQ ID NO: 111:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1134 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

ACCCATTGAG CAGAAGGAGG CCAGGTGGGA AAGCTCCTGG GAAGAGCAGC CAGACTGGAC 60

20

ACTGGGCTGC TTGAGTCCTG AGTCACAATT CAGAATTCCT GGGCTCCCTG GGTGCAITCT 120

ATCATTCAG TTGAAAGTTT GCTTCCTTCC AGTCATGTGG CTCTTCATT CACTCTCCTT 180

25

GGCTCTCATT TCAGATGCCA TGGTCATGGA TGAAAAGGTC AAGAGAAGTT TGTGCTGGAC 240

ACGGCTTCTG CCATCTGCAA CTACAATGCC CAYTACAAGA ATCACCCCAA ATACTGGTGC 300

CGAGGYTATT TCCGTGAYTA CTGCAACATC ATCGCCTTCT CCCCTAACAG CACCAATCAT 360

30

GTGGCCCTGA AGGACACAGG GAACCAGCTC ATTGTCACTA TGTCTGCCT GAACAAANAA 420

GACACGGGCT GGTACTGGTG TGGCATCCAR CGGGACTTTG CMAGGGATGA CATGGATTTT 480

35

ACAGAGCTGA TTGTAAGTGA CGACAAAGGA ACCCTGGCCA ATGACTTTTG GTCTGGGAAA 540

GACCTATCAG GCAACAAAAC CAGAAGCTGC AAGGCTCCCA AAGTTGTCCG CAAGCTGACC 600

GCTCCAGGAC GTCCATTCTC ATCATTTGCA TACTGATCAC GGGTTTGGGA ATCATCTCTG 660

40

TAATCAGTCA TTTGACCAA AGGAGGAGAA GTCAAAGGAA TAGAAGGGTA GGCAACACTT 720

TGAAGCCCTT CTCGCGTGTG CTGACTCCAA AGGAAATGGC TCCTACTGAA CAGATGTGAC 780

45

TGAAGWTTTT TTTAATTTAG TTNCATAAAG TGATGNCTAC AACAGAWTAA TCACCCATGA 840

CAACTGGCCC CACACCTCAG AGACTGATTC TGATCTCCCA GGAATCTCTGA AGGACCCTCT 900

ATCCTTGACA ACAATCATTT GCAGCCAGGT AGCAACGGCR GTAGTCAGAG GAGCTATGAT 960

50

AGACCACACC CAAGCAAGGC TGCCCTCAAA TAACATCTCA AGATCTTAGT TCTTATGCAT 1020

TCCATCAGTC AGAAGTGAAG AAGAGGTGGA GAATCTKGAT TGGGGACCAG GAAATCACTT 1080

55

GTATTTTGTT AGCCAATAAA TTTTAGCCA GTGTTGAATG AAAAAAAAAA AAAA 1134

(2) INFORMATION FOR SEQ ID NO: 112:

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

CACTTTAAAG CTCTGCTGAG GGAGTTCGGA GCCCAGGCTT TCAGGCGACC TCTGCCCTCC 60
 10 CTGCCTCTCC TCACCCTCCC TCTCTTCCTG CAGGGCCTGG GAAGGGCTTT GAGGGAGCCT 120
 GGGAGCCATG TGAAGAGGGG CACGCCTGGG CTGTCCCACA GTTTAGATCC AGTTGGAGGT 180
 15 TCTCCCTGGC TCCTGCAGGC CTGCGGGGAT CTCTCCCCAC TTCAGGCCTC CGGCAGCTGC 240
 CTGCCCTCTT GTCTGTGCTT CAGCCCTGCA CAAAAGCAGC TTGGTGACAC CACTCAGCCA 300
 CCCAGAGTAC GTGTTTACAG GCTTTCCAGA TCACCTTCCT GTGGGGTGAA CGTAATGAGG 360
 20 CGGGGCTGGT CCTTGAATT TCCCTGGAA AATGGAACA GACTCCATCC TTGACCCGGG 420
 GATGAGCATG AAGGCATTGT CCCAAAGGCA GAGGCCACCG TGGTAGGAAT TCCACCAAGG 480
 25 CCAGAAGGGA AAAAGGAAGA ACCCACCCTG TCTGGCTGTG CGGGCCCTGG GGAGGGTCGT 540
 GAGTGCAGCC CCTCTCTACT TCYGTGCCTT TGTA AACGT GTAGATAACC GCAGTGGTTG 600
 GCTGAGCCAA GAACTCTCCT AAATCAGTGG CTTTCTCCCC ACCCTTGCT GGGGAGTCAT 660
 30 TTTTAAAAA ATCTGTGGGA TATAAAATTG GCCTCTGCT GCTTCAGCCT ACCTCTCCCT 720
 CTGCTGACTT AATGTCGTGA TTCTGTTTCT TCAGATATTT AAGGCTGTTA GGTGTGTGA 780
 35 GCCTTGAAGT GTGTGTGTGT GTCCAGCGA CTGTCCACTG TCCAGGAGAT GCATGTCTTT 840
 GTATTGGAGA TATTTCTGTA ACTCATTCTC TTGGTGCTCA CGATTGCCAT GGCCATAGGG 900
 CCACAGTGCC GTATCTGCTG CAGACATGAT TGTTTCTTGT TCTAGAGGTT TTCTTGTTTT 960
 40 CGAATCTTGC CTGATGAATC CAGCCAGACC AAGGGGCCTA GATTGACCT CTGTCCTGGG 1020
 CTCCTGGGCC AGGTGCAGGA ACATCTGAGG CCACTCTGCT GGCCACCTCC AGTGGGTGCT 1080
 45 GACCACAGGA TGGGCTTTGT TTACACTCAT TTACACCCTG ATTCTTGCCC CCACTTTCAT 1140
 AAAAGAACT TCAAAATGCT GACGCTTTGG AGAGTAAGAA AATCAATCTT GGCTGGGCAC 1200
 GGTGGCTCCT GCCTGTGATC CTAGCACTTT GGGAGGCTGA AGCTGAAGGA TCACTGAGC 1260
 50 TCAGGAGTTG GAGACCAACC CTGGCAACAT AACAAGACCC TGTCTCTACA AAAAAAAAAA 1320
 AAAAAAACT CGA 1333

55

(2) INFORMATION FOR SEQ ID NO: 113:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1015 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

	GGCACGAGCG GCACGAGCGG CACGAGGTGA CTTCAAGTGT CGGATCTTTT CAGCCTACAT	60
10	CAAGGAGGTG GAGGAACGGC CGGCACCCAC CCCGTGGGCT CCAAGATGCC CTTTGGGGAA	120
	CTGATGTTTC AATCCAGCAG TAGCTGCGGC TGGGTACATG GCGTCTGTTC CTCAGCCAGC	180
	GGGAGCCGCG TGGCCTGGGT AAGCCACGAC AGCACCGTCT GCCTGGCTGA TGCCGACAAG	240
15	AAGATGGCCG TCGCGACTCT GGCTCTGAA AACTACCAC TGCTGGCGCT GACCTTCATC	300
	ACAGACAACA GCCTGGTGGC AGCGGGCCAC GACTGCTTCC CGGTGCTGTT CACCTATGAC	360
20	GCCGCCGCGG GGATGCTGAG CTTCGGCGGG CGGCTGGACG TTCCTAAGCA GAGCTCGCAG	420
	CGTGGCTTGA CGGCCCCGGA GCGCTTCCAG AACCTGGACA AGAAGGCGAG CTCCGAGGGT	480
	GGCACGGCTG CGGGCGCGGG CCTAGACTCG CTGCACAAGA ACAGCGTCAG CCAGATCTCG	540
25	GTGCTCAGCG GCGGCAAGGC CAAGTGTCTG CAGTTCTGCA CCACTGGCAT GGATGGCGGC	600
	ATGAGTATCT GGGATGTGAA GAGCTTGGAG TCAGCCTTGA AGGACCTCAA GATCAAATGA	660
30	CCTGTGAGGA ATATGTTGCC TTCATCCTAG CTGCTGGGGA AGCGGGGAGA GGGGTCAGGG	720
	AGGCTAATGG TTGCTTTGCT GAATGTTTCT GGGGTACCAA TACGAGTTCC CATAGGGGCT	780
	GCTCCCTCAA AAAGGGAGGG GACAGATGGG GAGCTTTTCT TACCTATTCA AGGAATACGT	840
35	GCCTTTTCT TAAATGCTTT CATTTATTGA AAAAAAAAAA AAATGCCCCC AAAGCACTAT	900
	GCTGGTCATG AACTGCTTCA AAATGTGGAG GTAATAAAAT GCAACTGTGT AAAAAAAAAA	960
40	AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AACNC	1015

45

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1076 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

55	GGCACGAGGG GAAAGCCATG CTCCCAGGAC TCCTTCCTTG CAGCCTTAAA TCGGTCTGTA	60
	CGGAAAATTC CGCGCCTTAG AAACCCACGC TTGGGTGTAA CTTATTATTG TTCTTCCTGA	120
60	CCTACTTCCT GTTTATCACT TCCGGGTTC TCAATTTGGC ATTTGCGTGA TCGGGTTGGA	180

	ACTATTGAAG CCCGCTTTCA GGTCTTTTC CCCATTMTCC CTTTGAAAGG AAGACTTCTG	240
	GCTTCTCCTA AATCTCCGTT CTCTGGGTAA GGGGAGTCCA AGCCTCTGTC ATGAGGAACG	300
5	GAAATGCGAG GGCCTCGGGT GTTACTCTAA AATCCGCCCT CAGCTTGAC GCGGAAGCT	360
	GCGATTCTTG CAGCGGAAGA GGCCTGATCT GGCCTTCGAC TCGCTATGTC CACTAACAAT	420
10	ATGTGCGACC CACGGAGGCC GAACAAAGTG CTGAGGTACA AGCCCCGCC GAGCGAATGT	480
	AACCCGGCCT TGGACGACCC GACGCCGAC TACATGAACC TGCTGGGCAT GATCTTCAGC	540
	ATGTGCGGCC TCATGCTTAA GCTGAAGTGG TGTGCTTGGG TCGCTGTCTA CTGCTCCTTC	600
15	ATCAGCTTTG CCAACTCTCG GAGCTCGGAG GACACGAAGC AAATGATGAG TAGCTTCATG	660
	CTGTCCATCT CTGCCGTGGT GATGTCCTAT CTGCAGAATC CTCAGCCCAT GACGCCCCCA	720
20	TGGTGATACC AGCCTAGAAG GGTACATTT TGGACCCTGT CTATCCACTA GGCCTGGGCT	780
	TTGGCTGCTA AACCTGCTGC CTTGAGTGC CATCTGGAC TTCCCTGAAT GAGGCCGTCT	840
	CGGTGCCCCC AGCTGGATAG AGGGAACCTG GCCCTTTCCT AGGGAACACC CTAGGCTTAC	900
25	CCCTCCTGCC TCCCTTCCCC TGCCTGCTGC TGGGGGAGAT GCTGTCCATG TTTCTAGGGG	960
	TATTCAATTG CTTTCTCGTT GAAACCTGTT GTTAATAAAG TTTTCACTC TGAAAAAAA	1020
30	AAAAAAAANA RAAACNCGN GGGGGGGCCC GGAACCCAAT TCSCCGGATA GTGAGT	1076

35 (2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

45	CCGCTGCTGA TAACTATGGC ATCCCCCGG CCTGCAGGAA TTCGGCACGG AGCTACGGCG	60
	CCGCCTGGCT CCTGCTGNCA CCTGCAGGCT CGTCGCGGGT GGAGCCCACC CAAGACATCA	120
	GCATCAGCGA CCAGCTGGGG GGCCAGGACG TGCCCGTGT TCCGGAACCTG TCCCTGCTGG	180
50	TGGTGGGTGT CGGCGCCGTG TTCTCACTGC TATTCACCT GGCACCCGG GAGAGGCGCC	240
	GGCCGCATGC GGASGAGCCA GGCGAGCACA CCCCCCTGTT GGCCCCTGCC ACGGCCAGC	300
55	CCCTGCTGCT CTGGAAGCAC TGGCTCCGGG AGCSGGCTTT CTACCAGGTG GGCATACTGT	360
	ACATGACCAC CAGGCTCATC GTGAACCTGT CCCAGACCTA CATGGCCATG TACCTCACCT	420
	ACTCGCTCCA CCTGCCCAAG AAGTTCATCG CGACCATTC CCTGGTGATG TACCTCAGCG	480
60	GCTTCTTGTC CTCCTTCCTC ATGAAGCCCA TCAACAAGTG CATTGGGAGG AACATGACCT	540

264

ACTTCTCAGG CCTCCTGGTG ATCCTGGCCT TTGCCGCCTG GGTGGCGCTG GCGGAGGGAC 600
 TGGGTGTGGC CGTGTACGCA GCGGCTGTGC TGCTGGGTGC TGGCTGTGCC ACCATCCTCG 660
 5 TCACCTCGCT GGCCATGACG GCCGACCTCA TCGGTCCCCA CACGAACAGC GGAGCKTTTCG 720
 TGTACGGCTC CATGAGCTTC TTGGATAAGG TGGCCAATGG GCTGGCAGTC ATGGCCATCC 780
 10 AGAGCCTGCA CCCTTGCCCC TCAGAGCTCT GCTGCAGGGC CTGCGTGAGC TTTTACCACT 840
 GGGCGATGGT GGCTGTGACG GCGGCGGTGG GCGTGGCCGC TGCCCTGTGT CTCTGTAGCC 900
 TCCTGCTGTG GCCGACCCGC CTGCGACGCT GATGAGACCT GCACGCANTG GCTCACAGCA 960
 15 GCACGATTTC TGACAGCCCG AGGCGGAGAA CACCGAACAC CCAGTGAAGG TGAGGGGATC 1020
 AGCACGGCGC GGCCACCCAC GCACCCACGC GCTGGAATGA GACTCAGCCA CAAGGAGGTG 1080
 20 CGAAGCTCTG ACCCAGGCCA CAGTGC GGAT GCACCTTGAG GATGTCACGC TCAGTGAGAG 1140
 ACACCAGACA CAGAAGGGTA CGCTGTGATC CCACCTCTAT GAAATGTCCA GGACAGACCA 1200
 ATCCACAGAA TCAGGGAGAG GATTCGTGGG TGCCGGGACT GGGGAGGGGG ACCTGGGGGT 1260
 25 GACTAGGTGA CATAATGGGG ACAGGGCTGC CTTCTGGGTG ATGAGAATGT TCTGGAATCA 1320
 GATGGGATGG CTGCACGGCG TGGTGAAGGT ACTGAACGCC ACCTCACTGT AAGACGGTAG 1380
 30 ATTTTGTATT TTACCACAAT AAACAAAACA AAACAAAACC AAAAAAAAAA AAAAAAAAAA 1440
 AAAAAAAGG AATTCGATAT CAAGCTTATC GATACCGTCG ACCTCGA 1487

35

(2) INFORMATION FOR SEQ ID NO: 116:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

GGCACGAGTG CGCANGCGTG GGGCTCTCTC CTTGTCAGTC GGCGCCGCGT GCGGGCTGGT 60
 GGCTCTGTGG CAGCGGCGGC GGCAGGACTC CGGCACTATG AGCGGCTTCA GCACCGAGGA 120
 50 GCGCGCCGCG CTTCTCCCT GGAGTACCGA GTCTTCCTCA AAAATGAGAA AGGACAATAT 180
 ATATCTCCAT TTCATGATAT TCCAATTTAT GCAGATAAGG ATGTGTTTCA CATGGTAGTT 240
 55 GAAGTACCAC GCTGGTCTAA TGCAAAAATG GAGATTGCTA CAAAGGACCC TTAAACCCT 300
 ATTAAACAAG ATGTGAAAAA AGGAAACTT CGCTATGTTG CGAATTGTGTT CCCGTATAAA 360
 GGATATATCT GGAACATATG TGCCATCCCT CAGACTTGGG AAGACCCAGG GCACAATGAT 420
 60

	AAACATACTG GCTGTTGTGG TGACAATGAC CCAATTGATG TGTGTGAAAT TGGAAGCAAG	480
	GTATGTGCAA GAGGTGAAAT AATTGGCGTG AAAGTTCTAG GCATATTGGC TATGATTGAC	540
5	GAAGGGGAAA CCGACTGGAA AGTCATTGCC ATTAATGTGG ATGATCCTGA TGCAGCCAAT	600
	TATAATGATA TCAATGATGT CAAACGGCTG AAACCTGGCT ACTTAGAAGC TACTGTGGAC	660
10	TGGTTTAGAA GGTATAAGGT TCCTGATGGA AAACCAGAAA ATGAGTTTGC GTTTAATGCA	720
	GAATTTAAAG ATAAGGACTT TGCCATTGAT ATTATTAAAA GCACTCATGA CCATTGGAAA	780
	GCATTAGTGA CTAAGAAAAC GAATGGAAAA GGAATCAGTT GCATGAATAC AACTTTGTCT	840
15	GAGAGCCCCT TCAAGTGTGA TCCTGATGCT GCCAGAGCCA TTGTGGATGC TTTACCACCA	900
	CCCTGTGAAT CTGCCTGCAC AGTACCAACA GACGTGGATA AGTGGTTCCA TCACCAGAAA	960
20	AACTAATGAG ATTTCTCTGG AATACAAGCT GATATTGCTA CATCGTGTTT ATCTGGATGT	1020
	ATTAGAAGTA AAAGTAGTAG CTTTCAAAAG CTTTAAATTT GTAGAACTCA TCTAACTAAA	1080
	GTAAATTCTG CTGTGACTAA TCCAATATAC TCAGAAATGT ATCCATCTAA AGCATTTTTC	1140
25	ATATCTCAAC TAAGATAACT TTTAGCACAT GCTTAAATAT CAAAGCAGTT GTCATTTGGA	1200
	AGTCACTTGT GAATAGATGT GCAAGGGGAG CACATATTGG ATGTATATGT TACCATATGT	1260
30	TAGGAAATAA AATTATTTTG CTGAAAAAAA AAAAAAAAAA ACCTSGGGGG GGGSCCCGGT	1320
	CCCCATTGG CCCTTTGGGG GGNGGTTTTA	1350

35

(2) INFORMATION FOR SEQ ID NO: 117:

	(i) SEQUENCE CHARACTERISTICS:
40	(A) LENGTH: 2527 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:
----	--

	CTCTTGCTAC CTTCCCGGCG CAGAGAACCC CGGCTGCTCA GCGCGCTCCG GGGTCATGGA	60
	GATCCCCGGG AGCCTGTGCA AGAAAGTCAA GCTGAGCAAT AACGCGCAGA ACTGGGGAAT	120
50	GCAGAGAGCA ACCAATGTCA CCTACCAAGC CCATCATGTC AGCAGGAACA AGAGAGGTCA	180
	GGTGGTGGGG ACCAGAGGTG GCTTTCGTGG TTGCACAGTT TGGCTAACAG GCTTGTCTGG	240
55	AGCGGGAAAG ACTACTGTGA GCATGGCCTT GGAGGAGTAC CTGGTTTGTC ATGGTATTCC	300
	ATGCTACACT CTGGATGGTG ACAATATTCG TCAAGGTCTC AATAAAAAATC TTGGCTTTAG	360
	TCCTGAAGAC AGAGAAGAGA ATGTTTCGACG CATCGCAGAA GTTGCTAAAC TGTTCGAGA	420
60	TGCTGGCTTA GTGTGCATCA CAAGTTTCAT ATCACCTTAC ACTCAGGATC GCAACAATGC	480

	AAGGCAAATT CATGAAGGTG CAAGTTTACC GTTTTTTGAA GTATTTGTGTG ATGCTCCTCT	540
5	GCATGTTTGT GAACAGAGGG ATGTCAAAGG ACTCTACAAA AAAGCCCGGG CAGGAGAAAT	600
	TAAAGGTTTC ACTGGGATCG ATTCTGAATA TGAAAAGCCA GAGGCCCTTG AGTTGGTGCT	660
	GAAAACAGAC TCCTGTGATG TAAATGACTG TGTCCAGCAA GTTGTGGAAC TTCTACAGGA	720
10	ACGGGATATT GTACCTGTGG ATGCATCTTA TGAAGTAAAA GAACTATATG TGCCAGAAAA	780
	TAAACTTCAT TTGGCAAAAA CAGATGCGGA AACATTACCA GCACTGAAAA TTAATAAAGT	840
15	GGATATGCAG TGGGTGCAGG TTTTGGCAGA AGGTTGGGCA ACCCCATTGA ATGGCTTTAT	900
	GAGAGAGAGG GAGTACTTGC AGTGCCTTCA TTTTGATTGT CTTCTGGATG GAGGTGTCAT	960
	TAACCTGTCA GTACCTATAG TTCTGACTGC GACTCATGAA GATAAAGAGA GGCTGGACGG	1020
20	CTGTACAGCA TTTGCTCTGA TGTATGAGGG CCGCCGTGTG GCCATTCTTC GCAATCCAGA	1080
	GTTTTTTGAG CACAGGAAAG AGGAGCGCTG TGCCAGACAG TGGGGAACGA CATGCAAGAA	1140
25	CCACCCCTAT ATTAAGATGG TGATGGAACA AGGAGATTGG CTGATTGGAG GAGATCTTCA	1200
	AGTCTTGGAT CGAGTTTATT GGAATGATGG TCTTGATCAG TATCGTCTTA CTCCTACTGA	1260
	GCTAAAGCAG AAATTTAAAG ATATGAATGC TGATGCTGTC TTTGCATTTT AACTACGCAA	1320
30	CCCAGTGCAC AATGGACATG CCCTGTTAAT GCAGGATACC CATAAGCAAC TTCTAGAGAG	1380
	GGGCTACCGG CGCCCTGTCC TCCTCCTCCA CCCTCTGGGT GGCTGGACAA AGGATGACGA	1440
35	TGTTCCTTTG ATGTGGCGTA TGAAGCAGCA TGCTGCACTG TTGGAGGAAG GAGTTC TGAA	1500
	TCCTGAGACG ACACTGGTGG CCATCTTCCC ATCTCCCATG ATGTATGCTG GACCAACTGA	1560
	GGTCCAGTGG CATTCAGAG CACGGATGGT TGCAGGAGCC AACTTTTACA TTGTTGGACG	1620
40	AGACCCTGCT GGCATGCCTC ATCCAGAAAC AGGGAAGGAT CTTTATGAGC CAAGTCATGG	1680
	TGCCAAAGTG CTGACGATGG CCCCTGTTTT AATCACTTTG GAAATAGTTC CCTTTCGAGT	1740
45	TGCAGCTTAC AACAAGAAAA AGAAGCGTAT GGACTACTAT GACTCTGAAC ACCATGAAGA	1800
	CTTTGAATTT ATTTCAAGAA CACGAATGCG CAAACTTGCT CGAGAAGGCC AGAAACCACC	1860
	TGAAGGTTTC ATGGCTCCCA AGGCTTGGAC CGTGCTGACA GAATACTACA AATCCTTGGA	1920
50	GAAAGCTTAG GCTGTAAACC CAGTCACTCC ACCTTTGACA CATTACTAGT AACAAGAGGG	1980
	GACCACATAG TCTCTGTTGG CATTTCTTTG TGGTGTCTGT CTGGACATGC TTCCTAAAAA	2040
55	CAGACCATTT TCCTTAACTT GCATCACTTT TGGTCTGCCT TATGAGTTCT GTTTTGAACA	2100
	AGTGTAACAC ACTGATGGTT TTAATGTATC TTTTCCACTT ATTATAGTTA TATTCCTACA	2160
	ATACAATTTT AAAATTGTCT TTTTATATTA TATTTATGCT TCTGTGTCAT GATTTTTCAT	2220
60	AGCTGTTATA TTAGTTGTAA CCAGTAGTAT TCACATTAAA TCTTGCTTTT TTTCCCTTA	2280

AAAAAAGAAA AAAATTACCA AACAATAAAC TTGGCTAGAC CTTGTTTGA GGATTTTACA 2340
AGACCTTTGT AGCGATTAGA TTTTCTTCT ACATTGAAAA TAGAACTGC TTCCTTTCTT 2400
5 CTTTCCAGTC AGCTATGGT CTTTCCAGCT GTTATAATCT AAAGTATTCT TATGATCTGT 2460
GTAAGCTCTG AATGAACCTC TTTACTCAAT AAAATTAATT TTTTGGCTTC TTAAAAAAA 2520
10 AAAAAA 2527

15 (2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1098 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

25 CGCATCACAG ACAACCCAGA AGGAAAATGG TTGGGCAGAA CAGCAAGGGG TTCATATGGC 60
TATATTAAAA CAACTGCTGT AGAGATTNNC TATGATTCTT TGAACTGAA AAAAGACTCT 120
CTTGGTGCCC CTTCAAGACC TATTGAAGAT GACCAAGAAG TATATGATGA TGTGCAGAG 180
30 CAGGATGATA TTAGCAGCCA CAGTCAGAGT GGAAGTGGAG GGATATTCCC TCCACCACCA 240
GATGATGACA TTTATGATGG GATTGAAGAG GAAGATGCTG ATGATGGTTT CCCTGCTCCT 300
35 CCTAAACAAT TGGACATGGG AGATGAAGTT TACGATGATG TGGATACCTC TGATTTCCTT 360
GTTTCATCAG CAGAGATGAG TCAAGGAACT AATGTTGGAA AAGCTAAGAC AGAAGAAAAG 420
GACCTTAAGA AGCTAAAAAA GCAGRAAAAA GAARAAAAAG ACTTCAGGAA AAAATTAAAA 480
40 TATGATGGTG AAATTAGAGT CCTATATTCA ACTAAAGTTA CAACTTCCAT AACTTCTAAA 540
AAGTGGGGAA CCAGAGATCT ACAGGTAAAA CCTGGTGAAT CTCTAGAAGT TATACAAACC 600
45 ACAGATGACA CAAAAGTTCT CTGCAGAAAT GAAGAAGGGA AATATGGTTA TGTCTTCGG 660
AGTTACCTAG CGGACAATGA TGGAGAGATC TATGATGATA TTGCTGATGG CTGCATCTAT 720
GACAATGACT AGCACTCAAC TTGGTCAAT CTGCTGTGTT CATTAGGTGC CAATGTGAAG 780
50 TCTGGATTTT AATTGGCATG TTATTGGGTA TCMAGAAAAT TAATGCACAR AACCCTTAT 840
TATCATTTGT TATGAAATCC CAATTATCTT TACAAAGTGT TTAAAGTTG AACATAGAAA 900
55 ATAATCTCTC TGCTTAATTG TTATCTCAGA AGACTACATT AGTGAGATGT AAGAATTATT 960
AAATATTCCA TTTCCGCTTT GGCTACAATT ATGAAGAAGT TGAAGGTACT TCTTTTAGAC 1020
CACCAGTAAA TAATCCTCCT TCAAAAAATA AAAATAAAAA AAAAAAAAAA AACTCGAGG 1080
60

GGGGGCCCCG TACCCAAT

1098

5

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 1679 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

20

TCGACCCACG CGTCCGGCGA GATCCCTACC GCAGTAGCCG CCTCTGCCGC CGCGGAGCTT 60

CCCGAACCTC TTCAGCCGCC CGGAGCCGCT CCCGGAGCCC GGCCGTAGAG GCTGCAATCG 120

CAGCCGGGAG CCCGCAGCCC GCGCCCCGAG CCCGCCGCCG CCCTTCGAGG GCGCCCCAGG 180

CCGCGCCATG GTGAAGGTGA CGTTCAACTC CGCTCTGGCC CAGAAGGAGG CCAAGAAGGA 240

25

CGAGCCCAAG AGCGGCGAGG AGGCGCTCAT CATCCCCCCC GACGCCGTCG CGGTGGACTG 300

CAAGGACCCA GATGATGTGG TACCAGTTGG CCAAAGAAGA GCCTGGTGTG GGTGCATGTG 360

CTTTGGACTA GCATTTATGC TTGCAGGTGT TATTCTAGGA GGAGCATACT TGTACAAATA 420

30

TTTTGCACTT CAACCAGATG ACGTGTACTA CTGTGGAATA AAGTACATCA AAGATGATGT 480

CATCTTAAAT GAGCCCTCTG CAGATGCCCC AGCTGCTCTC TACCAGACAA TTGAAGAAAA 540

35

TATTAAAATC TTTGAAGAAG AAGAAGTTGA ATTTATCAGT GTGCCTGTCC CAGAGTTTGC 600

AGATAGTGAT CCTGCCAACA TTGTTTCATGA CTTTAAACAAG AAACCTTACAG CCTATTTAGA 660

TCTTAACCTG GATAAGTGCT ATGTGATCCC TCTGAACACT TCCATTGTTA TGCCACCCAG 720

40

AAACCTACTG GAGTTACTTA TTAACATCAA GGCTGGAACC TATTTGCCTC AGTCCTATCT 780

GATTCATGAG CACATGGTTA TTACTGATCG CATTGAAAAC ATTGATCACC TGGGTTTCTT 840

45

TATTTATCGA CTGTGTCATG ACAAGGAAAC TTACAAACTG CAACGCAGAG AACTATTAA 900

AGGTATTCAG AAACGTGAAG CCAGCAATTG TTTTCGAATT CGGCATTTTG AAAACAAATT 960

TGCCGTGGAA ACTTTAATTT GTTCTTGAAC AGTCAAGAAA AACATTATTG AGGAAAATTA 1020

50

ATATCACAGC ATAACCCAC CCTTTACATT TTGTGCAGTG ATTATTTTTT AAAGTCTTCT 1080

TTCATGTAAG TAGCAAACAG GGCTTTACTA TCTTTTCATC TCATTAATTC AATTAAACC 1140

55

ATTACCTTAA AATTTTTTTC TTTCGAAGTG TGGTGTCTTT TATATTTGAA TTAGTAACTG 1200

TATGAAGTCA TAGATAATAG TACATGTCAC CTTAGGTAGT AGGAAGAATT ACAATTTCTT 1260

TAAATCATTT ATCTGGATTT TTATGTTTTA TTAGCATTTT CAAGAAGACG GATTATCTAG 1320

60

AGAATAATCA TATATATGCA TACGTAAAAA TGGACCACAG TGACTTATTT GTAGTTGTTA 1380

GTTGCCCTGC TACCTAGTTT GTTAGTGCAT TTGAGCACAC ATTTTAATTT TCCTCTAATT 1440
 AAAATGTGCA GTATTTTCAG TGTCAAATAT ATTTAACTAT TTAGAGAATG ATTTCCACCT 1500
 5 TTATGTTTTA ATATCCTAGG CATCTGCTGT AATAATATTT TAGAAAATGT TTGGAATTTA 1560
 AGAAATAACT TGTGTTACTA ATTTGTATAA CCCATATCTG TGCAATGGAA TATAAATATC 1620
 10 ACAAAGTTGT TTAAMWAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAAN 1679

15 (2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS: '
 (A) LENGTH: 1308 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

25 TTGGCANCNG GGAGAGGGAA AGAGGAGGAA ATGGGGTTTG AGGACCATGG CTTACCTTTC 60
 CTGCCTTTGA CCCATCACAC CCCATTTCTT CCTCTTTCCC TCTCCCCGCT GCCAAAAAAA 120
 AAAAAAAGG AAACGTTTAT CATGAATCAA CAGGGTTTCA GTCCTTATCA AAGAGAGATG 180
 30 TGGAAAGAGC TAAAGAAACC ACCCTTTGTT CCCAACTCCA CTTTACCCAT ATTTTATGCA 240
 ACACAAACAC TGTCCCTTTG GGTCCCTTTC TTACAGATGG ACCTCTTGAG AAGAATTATC 300
 35 GTATTTCCACG TTTTATAGCCC TCAGGTTACC AAGATAAATA TATGTATATA TAACCTTTAT 360
 TATTGCTATA TCTTTGTGGA TAATACATTC AGGTGGTGCT GGGTGATTTA TTATAATCTG 420
 AACCTAGGTA TATCCTTTGG TCTTCCACAG TCATGTTGAG GTGGGCTCCC TGGTATGGTA 480
 40 AAAAGCCAGG TATAATGTAA CTTCAACCCA GCCTTTGTAC TAAGCTCTTG ATAGTGGATA 540
 TACTCTTTTA AGTTTATAGCCC CAATATAGGG TAATGGAAAT TTCCTGCCCT CTGGGTTCCC 600
 45 CATTTTACT ATTAAGAAGA CCAGTGATAA TTAAATAATG CCACCAACTC TGGCTTAGTT 660
 AAGTGAGAGT GTGAACTGTG TGGCAAGAGA GCCTCACACC TCACTAGGTG CAGAGAGCCC 720
 AGGCCTTATG TTAAATCAT GCACCTGAAA AGCAAACCTT AATCTGCAA GACAGCAGCA 780
 50 AGCATTATAC GGTCACTTG AATGATCCCT TTGAAATTTT TTTTGTGTTT GTTTGTTTAA 840
 ATCAAGCCTG AGGCTGGTGA ACAGTAGCTA CACACCCATA TTGTGTGTTT TGTGAATGCT 900
 55 AGCTCTCTTG AATTTGGATA TTGGTTATTT TTTATAGAGT GTAAACCAAG TTTTATATTC 960
 TGCAATGCGA ACAGGTACCT ATCTGTTTCT AAATAAACT GTTTACATTC ATTATGGGGT 1020
 ATGTATGACC TTCATTTTCC AAGAAATAGA ACTCTAGCTT AGAATTATGG ATGCTCTAAA 1080
 60

270

	ATGTCAGAAT GGGAACTCTC CTCGAAGTTC TCCCAAATC AGAGACAGCA CTGCCTTCTC	1140
	CTAAATGATT ATTCTTTTCT CCCTGTTTTC TGGTATTTTC TAGGCATCCT TCTCACCACA	1200
5	GCCATAACCC TTTTCTACTT CCATTAGGCC GTATAACTGG NGGGACNGCT GGTCGGTATA	1260
	TAATACTGGT WCCAACAMAG GGGTTCTGGA TGTACACMAG GTTATCTT	1308
10		
	(2) INFORMATION FOR SEQ ID NO: 121:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1411 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:	
	GGCACAGGAG CGACCCGGGA GAAGGAGGGC CAMGAKGCGG AAGCGGAGGA GTCTCCAGGA	60
	GACCCGGGGA CAGCATCGCC CAGGCCCTTG TTTGCAGGCC TTTCAGATAT ATCCATCTCA	120
25	CAAGACATCC CCGTAGAAGG AGAAATCACC ATTCCTATGA GATCTCGCAT CCGGGAGTTT	180
	GACAGCTCCA CATTAAATGA ATCTGTTCGC AATACCATCA TCGTGATCT AAAAGCTGTT	240
30	GGGAAAAAAT TCATGCATGT TTTGTACCCA AGGAAAAGTA ATACTCTTTT GAGAGATTGG	300
	GATTTGTGGG GCCCTTTGAT CCTTGTGTG ACACTCGCAT TAATGCTGCA AAGAGACTCT	360
	GCAGATAGTG AAAAAGATGG AGGGCCCCAA TTTGCAGAGG TGTTTGTGTCAT TGTCTGGTTT	420
35	GGTGCAGTTA CCATCACCTT CAACTCAAAA CTCTCTGGAG GGAACATATC TTTTMTTCAG	480
	AGCCTCTGTG TGCTGGGTTA CTGTATACTT CCCCTGACAG TAGCAATGCT GATTTGCCGG	540
40	CTGGTACTTT TGGCTGATCC AGGACCTGTA AACTTCATGG TTCGGCTTTT TGTGGTGATT	600
	GTGATGTTTG CCTGGTCTAT AGTTCCTCC ACAGCTTTC TTGCTGATAG CCAGCCTCCA	660
	AACCGCAGAG CCCTAGCTGT TTATCCTGTT TTCCTGTTTT ACTTTGTCAT CAGTTGGATG	720
45	ATTCTCACCT TTAATCCTCA GTAAATCAGG AATGGGAAAT TAAAAACCAG TGAATTGAAA	780
	GCACATCTGA AAGATGCAAT TCACCATGGA GCTTTGTCTC TGGCCCTTAT TTGTCTAATT	840
50	TTGGAGGTAT TTGATAACTG AGTAGGTGAG GAGATTAAAA GGGAGCCATA TAGCACTGTC	900
	ACCCCTTATT TGAGGAACTG ATGTTTGAAA GGCTGTTCTT TTCTCTCTTA ATGTCATTTT	960
	TTTAAAAATA CATGTGCATA CTACACACAG TATATAATGC CTCCTTAAGG CATGATGGAG	1020
55	TCACCGTGGT CCATTGGGGT GACAACCACT GACTTGGGAA GCACATAGAT ACATCTTACA	1080
	AGTTGAATAG AGTTGATAAC TATTTTCAGT TTTGAGAATA CCAGTTCAGG TGCAGCTCTT	1140
60	AAACACATTG CCTTATGACT ATTAGAATAT GCCTCTCTTT TCATAAATAA AAATACATGG	1200

271

TCTATATCCA TTTTCTTTTA TTTCTCTCTC TTAAGCTTAA AAAGGCAATG AGAGAGGTTA 1260
 GGAGTGGGTT CATAACCGGA GAATGAGAAA ACATGCATTA ACCAATATTC AGATTTTGAT 1320
 5 CAGGGGAAAT TCTAYACTTG TTGCAAAAAA AAAAAAAAAA AACTCGAGG GGGGCCCCGT 1380
 ACCCAATCGC NGTATATGAT CGNAAACAAT C 1411

10

(2) INFORMATION FOR SEQ ID NO: 122:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

GCTTTGGCTT TTTTGGCGG ACTGGGCGC CCTCCGAAG CGTTTCCAAC TTTCCAGAAG 60
 25 TTTCTCGGGA CGGGCAGGAG GGGGTGGGGA CTGCCATATA TAGATCCCGG GAGCAGGGGA 120
 GCGGGCTAAG AGTAGAATCG TGTGCGGGCT CGAGAGCGAG AGTCACGTCC CGGCGCTAGC 180
 CAGCCCGACC CAGGCCACC GTGGTGCACG CAAACCACTT CCTGGCCATG CGCTCCCTCC 240
 30 TGCTTCTCAG CGCCTTCTGC CTCCTGGAGG CGGCCCTGGC CGCCGAGGTG AAGAAACCTG 300
 CAGCCGCAGC AGCTCCTGGC ACTGCGGAGA AGTTGAGCCC CAAGGCGGCC ACGCTTGCCG 360
 35 AGCGCANGCC GGCCTGGCCT TCAGCTTGTA CCAGGCCATG GCCAAGGACC AGGCAGTGGA 420
 GAACATCCTG TGGTACCCG TGGTGGTGGC CTCGTCGCTG GGGCTCGTGT CGCTGGGCGG 480
 CAAGGCGACC ACGGCGTCGC AGGCCAAGGC AGTGCTGAGC GCCGAGCAGC TGCGCGACGA 540
 40 GGAGGTGCAC GCCGGCCTGG GCGAGCTGCT GCGCTCACTC AGCAACTCGA CGGCGCGCAA 600
 CGTGACCTGG AAGCTGGGCA GCCGACTGTA CGGACCCAGC TCAGTGAGCT TCGCTGATGA 660
 45 CTTCTGTGCGC ACAGCAAGCA GCACTACAAC TGCGAGCACT CCAAGATCAA CTTCGCGAC 720
 AAGCGCAGNG CGCTGCAGTC CATCAACGAG TGGGCCGCGC AGACCACCGA CGGCAAGCTG 780
 CCCGAGGTCA CCAAGGACGT GGAGCGCAG GACGGCGCCC TGCTAGTCAA CGCCATGTTT 840
 50 TTCAAGCCAC ACTGGGATGA GAAATTCAC CACAAGATGG TGGACAACCG TGGCTTCATG 900
 GTGACTCGGT CCTATACYGT GGGTGTGATG ATGATGCACC GGACAGGCCT CTACAACTAC 960
 55 TACGACGACG AGAAGGAAAA GCTGCAATC GTGGAGATGC CCCTGGCCCA CAAGCTCTCC 1020
 AGCCTCATCA TCCTCATGCC CCAATCACGT GAGCCTCTCG AGCGCCTTGA AAAGCTGCTA 1080
 ACCAAAGAGC AGCTGAAGAT CTGGATGGGG AAGATGCAGA AGAAGGCTGT TGCCATCTCC 1140
 60

	TTGCCCAAGG GTGTGGTGA GGTGACCCAT GACCTGCAGA AACACCTGGC TGGGCTGGGC	1200
	CTGACTGAGG CCATTGACAA GAACAAGGCC GACTTTRTCAC GCATGTCAGG CAAGAAGGAC	1260
5	CTGTACCTGG CCAGCGTGT CCACGCCACC GCCTTTGAGT TGGACACAGA TGGCAACCCC	1320
	TTTGACCAGG ACATCTACGG GCGCGAGGAG CTGCGCANCC CAAGCTGTTC TACGCCGACC	1380
10	ACCCCTTCAT CTTCCTAGTG CGGGACACCC AAAGCGGCTC CCTGCTATTC ATTGGGCGCC	1440
	TGGTCCG GCC TAAGGGTGAC AAGATGCGAG ACGAGTTATA GGGCCTCAGG GTGCACACAG	1500
	GATGGCAGGA GGCATCCAAA GGCTCCTGAG ACACATGGGT GCTATTGGGG TTGGGGGGGA	1560
15	GGTGAGGTAC CAGCCTTGA TACTCCATGG GGTGGGGGTG GAAAARCAGA CCGGGGTTC	1620
	CGTGTGCCTG AGCGGACCTT CCCAGCTAGA ATTCACCTCA CTGGACATG GGGCCAGAT	1680
20	ACCATGATGC TGAGCCCGGA AACTCCACAT CCTGTGGGAC CTGGGCCATA GTCATCTGC	1740
	CTGCCCTGAA AGTCCCAGAT CAAGCCTGCC TCAATCAGTA TTCATATTTA TAGCCAGGTA	1800
	CCTTCTCACC TGTGAGACCA AATTGAGCTA GGGGGGTCAG CCAGCCCTCT TCTGACACTA	1860
25	AAACACCTCA GCTGCCTCCC CAGCTCTATC CCAACCTCTC CCAACTATAA AACTAGGTGC	1920
	TGCAGCCCCCT GGGACCAGGC ACCCCCAGAA TGACCTGGCC GCAGTGAGGC GGATTGAGAA	1980
30	GGAGCTCCCA GGAGGGGCTT CTGGGCAGAC TCTGGTCAAG AAGCATCGTG TCTGGCGTTG	2040
	TGGGGATGAA CTTTTTGT TTGTCTCTCC TTTTITAGTT CTCAAAGAT AGGGAGGGAA	2100
	GGGGGAACAT GAGCCTTTGT TGCTATCAAT CCAAGAACTT ATTTGTACAT TTTTITTTTC	2160
35	AATAAACTT TTCCAATGAC AAAAAAAAAA AAAAAAAAAA AAAAAGGGS GGGCCGCTCC	2220
	TAGAGGGATC CCTCCGANGG NGCCCAATCG AAAATN	2256

40

(2) INFORMATION FOR SEQ ID NO: 123:

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 829 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

	ATGCGCTCCC TCCTGCTTCT CAGCGCCTTC TGCCTCCTGG AGGCGGCCCT GGCCGCCGAG	60
55	GTGAAGAAAC CTGCAGCCGC AGCAGCTCCT GGCAGTGCAG AGAAGTTGAG CCCAAGGCG	120
	GCCACGCTTG CCGAGCGCAA GCGGCCCTGGC CTTGAGCTTG TACCAGGCCA TGGCCAAGGA	180
	CCAGGCAGTG GAGAACATCC TGGTGTACCC CGTGGTGGTG GCCTCGTCGC TGGGGCTCGT	240
60	GTCGCTGGGC GGCAAGGCGA CCACGGCGTC GCAGGCCAAG GCAGTGCTGA GCGCCGAGCA	300

GCTGCGCGAC GAGGAGGTGC ACGCCGGCCT GGGCGAGCTG CTGCGCTCAC TCAGCAACTC 360
 CACGGCGCGC AACGTGACCT GGAAGCTGGG CAGCCGACTG TACCGACCCA GCTCAGTGAG 420
 5 CTTCGCTGAT GACTTCGTGC GCAGCAGCAA GCAGCACTAC AACTGCGAGC ACTCCAAGAT 480
 CAACTTCCGC GACAAGCGCA GCGCGCTGCA GTCCATCAAC GAGTGGGCCG CGCAGACCAC 540
 10 CGACGGCAAG CTGCCCCGAGG TCACCAAGGA CGTGGAGCGC ACGGACGGCG CCCTGTTAGT 600
 CAACGCCATG TTCTTCAAGC CACACTGGGA TGAGAAATTC CACCACAAGA TGGTGGACAA 660
 CCGTGGCTTC ATGGTGACTC GGTCTATAC CGTGGGTGTC ATGATGATGC ACCGGACAGG 720
 15 CCTCTACAAC TACTACGACG ACGAGAAGGA AAAGCTGCAA ATCGTGGAGA TGCCCCTGGC 780
 CCACAAGCTC TCCAGCCTCA TCATCCTCAT GCCCCATCAC GTGGAGCCT 829
 20

(2) INFORMATION FOR SEQ ID NO: 124:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

CCTCCGGAAG CGTTTCCAAC TTTCCAGAAG TTTCTCGGA CGGGCAGGAG GGGGTGGGA 60
 35 CTGCCATATA TAGATCCCGG GAGCAGGGGA GCGGGCTAAG AGTAGAATCG TGTCGCGGCT 120
 CGAGAGCGAG AGTCACGTCC CGGCGCTAGC CAGCCCGACC CAGGCCACCC GTGGTGCACG 180
 40 CAAACCACTT CCTGGCCATG CGTCCCTCC TGCTTCTCAG CGCCTTCTGC CTCCTGGAGG 240
 CGGCCCTGGC CGCCGAGGTG AAGAAACCTG CAGCCGCAGC AGCTCCTGGC ACTGCGGAGA 300
 AGTTGAGCCC CAAGGCGGCC ACGCTTGCCG AGCGCAGNCG GCCTGGCCTT CAGCTTGATC 360
 45 CAGGCCATGG CCAAGGACCA GGCAGTGGAG AACATCCTGG TGTACCCCGT GGTGGTGGCC 420
 TCGTCGCTGG GGCTCGTGTC GCTGGGCGGC AAGGCGACCA CGGCGTCGCA GGCCAAGGCA 480
 GTGCTGAGCG CCGAGCAGCT GCGCGACGAG GAGGTGCACG CCGGCCTGGG CGAGCTGCTG 540
 50 CGCTCACTCA GCAACTCSAC GGCGCGCAAC GTGACCTGGA AGCTGGGCAG CCGACTGTAC 600
 GGACCCAGCT CAGTGAGCTT CGCTGATGAC TTCGTGCGCA CAGCAAGCAG CACTACAAC 660
 55 GCGAGCACTC CAAGATCAAC TTCCGCGACA AGCGCACGCG CTGCAGTCCA TCAACGAGTG 720
 GGCCGCGCAG ACCACCGACG GCAAGCTGCC CGAGGTCACC AAGGACGTGG AGCGCACGGA 780
 CGGCGCCCTG YTAGTCAACG CCATGTTCTT CAAGCCACAC TGGGATGAGA AATTCCACCA 840
 60

	CAAGATGGTG GACAACCGTG GCTTCATGGT GACTCGGTCC TATACYGTGG GTGTCATGAT	900
	GATGCACCGG ACAGGCCTCT ACAACTACTA CGACGACGAG AAGGAAAAGC TGCAAATCGT	960
5	GGAGATGCCC CTGGCCCACA AGCTCTCCAG CCTCATCATC CTCATGCCCC ATCACGTGGA	1020
	GCCTCTCGAG CGCCTTGAAA AGCTGCTAAC CAAAGAGCAG CTGAAGATCT GGATGGGGAA	1080
10	GATGCAGAAG AAGGCTGTTG CCATCTCCTT GCCCAAGGGT GTGGTGGAGG TGACCCATGA	1140
	CCTGCAGAAA CACCTGGCTG GGCTGGGCCT GACTGAGGCC ATTGACAAGA ACAAGGCCGA	1200
	CTTRTCACGC ATGTCAGGCA AGAAGGACCT GTACCTGGCC AGCGTGTTC ACGCCACCGC	1260
15	CTTTGAGTTG GACACAGATG GCAACCCCTT TGACCAGGAC ATCTACGGGC GCGAGGAGCT	1320
	GCGCASCCEA AGCTGTTCTA CGCCGACCAC CCCTTCATCT TCCTAGTGCG GGACACCCAA	1380
20	AGCGGCTCCC TGCTATTCAT TGGGCGCCTG GTCCGGCCTA AGGGTGACAA GATGCGAGAC	1440
	GAGTTATAGG GCCTCAGGGT GCACACAGGA TGGCAGGAGG CATCCAAAGG CTCCTGAGAC	1500
	ACATGGGTGC TATTGGGGTT GGGGGGAGG TGAGGTACCA GCCTTGATA CTCCATGGGG	1560
25	TGGGGGTGGA AAARCAGACC GGGGTTCCTG TGTGCCTGAG CGGACCTTCC CAGCTAGAAT	1620
	TCACTCCACT TGGACATGGG CCCAGATAC CATGATGCTG AGCCCGGAAA CTCCACATCC	1680
30	TGTGGGACCT GGGCCATAGT CATTCTGCCT GCCCTGAAAG TCCCAGATCA AGCCTGCCTC	1740
	AATCAGTATT CATATTTATA GCCAGGTACC TTCTCACCTG TGAGACCAA TTGAGCTAGG	1800
	GGGGTCAGCC AGCCCTCTTC TGACACTAAA ACACCTCAGC TGCCTCCCCA GCTCTATCCC	1860
35	AACCTCTCCC AACTATAAAA CTAGGTGCTG CAGCCCCTGG GACCAGGCAC CCCCAGAATG	1920
	ACCTGGCCGC AGTGAGGCGG ATTGAGAAGG AGCTCCCAGG AGGGGCTTCT GGGCAGACTC	1980
40	TGGTCAAGAA GCATCGTGTG TGGCGTTGTG GGGATGAACT TTTTGTTTTG TTTCTTCCTT	2040
	TTTTAGTTCT TCAAAGATAG GGAGGAAGG GGAACATGA GCCTTTGTTG CTATCAATCC	2100
	AAGAACTTAT TTGTACATTT TTTTTTTCAA TAAAACTTTT CCAATGACAA AAAAAAAAAA	2160
45	AAAAAAAAA MWMGGGSGG GCCGCTCCTA GAGGGATCCC TCCGANGNG CCCAATCGAA	2220
	AAT	2223

50

(2) INFORMATION FOR SEQ ID NO: 125:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

60

Met Lys Lys Gln Ser Lys Arg Cys Leu Trp Lys Pro Pro Gly Ser Leu

275

1 5 10 15
 Arg Arg Leu Trp Trp Met Arg Ala Leu Leu Ile Leu Lys Tyr Ile
 20 25 30

5

(2) INFORMATION FOR SEQ ID NO: 126:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

15

Met Lys Lys Ser Leu Glu Asn Leu Asn Arg Leu Gln Val Met Leu Leu
 1 5 10 15

20

His Leu Thr Ala Ala Phe Leu Gln Arg Ala His Xaa Ile Leu Thr Thr
 20 25 30

Arg Met Ser Leu Gly Phe Gln Ser Pro His Leu Thr Met
 35 40 45

25

(2) INFORMATION FOR SEQ ID NO: 127:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

35

Met His Asn Gln Arg Gln Val Phe Leu Phe His Leu Phe Ser Asn Tyr
 1 5 10 15

Leu Leu Ser Ile Asn Ser Val Pro Gly Thr Leu Leu Ala Ala Thr Tyr
 20 25 30

40

Cys Leu Asn Met Thr Tyr Gly
 35

45

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

50

Met Arg Lys Lys Phe Leu Leu Ala Gln Val Phe Leu Ser Leu Ser Val
 1 5 10 15

55

Met Pro Ser Met Pro Val Thr
 20

60

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

5

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

10 Met Val Leu Leu Cys Leu Leu Leu Val Pro Leu Leu Leu Ser Leu Phe
1 5 10 15

Val Leu Gly Leu Phe Leu Trp Phe Leu Lys Arg Glu Arg Gln Glu Glu
20 25 30

15 Tyr Ile Glu Glu Lys Lys Arg Val Asp Ile Cys Arg Glu Thr Pro Asn
35 40 45

20 Ile Cys Pro His Ser Gly Glu Asn Thr Glu Tyr Asp Thr Ile Pro His
50 55 60

Thr Asn Arg Thr Ile Leu Lys Glu Asp Pro Ala Asn Thr Val Tyr Ser
65 70 75 80

25 Thr Val Glu Ile Pro Lys Lys Met Glu Asn Pro His Ser Leu Leu Thr
85 90 95

Met Pro Asp Thr Pro Arg Leu Phe Ala Tyr Glu Asn Val Ile
100 105 110

30

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

40

Met Leu Leu Leu Phe Ile Tyr Phe Tyr Ser His Pro Ala Pro Val Pro
1 5 10 15

Ala Gly Ala Thr Ser Lys Pro Arg Tyr Arg Val Ile Thr Cys Gly Pro
20 25 30

Ala Ser Val Phe Ser Thr Ser Phe Ser His Ser Pro Pro Ala Arg Cys
35 40 45

50 Leu Gly Arg Leu Glu Gln Met Phe His Phe Gly Leu Ala Ser Gly
50 55 60

55 (2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Met Pro Phe Pro Ile Ser Ile Leu Gln Leu Cys Leu Gln Ile Ser Asn
1 5 10 15

Leu Ser Phe Cys Leu Gln Lys Ile Tyr Lys Ile Pro Phe Val
20 25 30

10

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Met Ala Ala Ala Cys Arg Ser Val Lys Gly Leu Val Ala Val Ile Thr
1 5 10 15

Gly Gly Ala Ser Gly Leu Gly Leu Ala Thr Ala Asp Asp Leu Trp Gly
20 25 30

Arg Glu Pro Leu Leu Cys Phe Trp Thr Cys Pro Thr Arg Val Gly Arg
35 40 45

Pro Lys Pro Arg Ser
50

30

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

Met Leu Leu Val Tyr Asp Leu Tyr Leu Xaa Pro Lys Leu Trp Ala Leu
1 5 10 15

Ala Thr Pro Gln Lys Asn Gly Lys Gly Ala Arg Xaa Gly Asp Gly Thr
20 25 30

Pro Ala Gln Ala Phe Trp Asp Phe Trp Ser His Leu Ile Ser Ala Asp
35 40 45

Pro Gln Thr Trp Glu Arg Ala Ala Pro
50 55

55 (2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

5 Met Arg Leu Ser Ala Leu Leu Ala Leu Ala Ser Lys Val Thr Leu Pro
 1 5 10 15
 Pro His Tyr Arg Tyr Gly Met Ser Pro Pro Gly Ser Val Ala Asp Lys
 20 25 30
 10 Arg Lys Asn Pro Pro Trp Ile Arg Arg Arg Pro Val Val Val Glu Pro
 35 40 45
 Ile Ser Asp Glu Asp Trp Tyr Leu Phe Cys Gly Asp Thr Val Glu Ile
 50 55 60
 15 Leu Glu Gly Lys Asp Ala Gly Lys Gln Gly Lys Val Val Gln Val Ile
 65 70 75 80
 Arg Gln Arg Asn Trp Val Val Val Gly Gly Leu Asn Thr His Tyr Arg
 85 90 95
 20 Tyr Ile Gly Lys Thr Met Asp Tyr Arg Gly Thr Met Ile Pro Ser Glu
 100 105 110
 Ala Pro Leu Leu His Arg Gln Val Lys Leu Val Asp Pro Met Asp Arg
 115 120 125
 Lys Pro Thr Glu Ile Glu Trp Arg Phe Thr Glu Ala Gly Glu Arg Val
 130 135 140
 30 Arg Val Ser Thr Arg Ser Gly Arg Ile Ile Pro Lys Pro Glu Phe Pro
 145 150 155 160
 Arg Ala Asp Gly Ile Val Pro Glu Thr Trp Ile Asp Gly Pro Lys Asp
 165 170 175
 35 Thr Ser Val Glu Asp Ala Leu Glu Arg Thr Tyr Val Pro Cys Leu Lys
 180 185 190
 Thr Leu Gln Glu Glu Val Met Glu Ala Met Gly Ile Lys Glu Thr Arg
 195 200 205
 Lys Tyr Lys Lys Val Tyr Trp Tyr
 210 215

45

(2) INFORMATION FOR SEQ ID NO: 135:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

55 Met Ser Leu Arg Gln Lys Ser Ser Phe Arg Leu Met Val Met Ser Leu
 1 5 10 15
 Thr Ile Leu Lys Leu Ser Lys Thr Thr Val Leu Cys Leu Arg Cys Leu
 20 25 30

60

279

His Ser Leu Lys Leu Thr Trp Arg Asp Gly Ala Arg Cys Ile Asn Ala
 35 40 45

Glu

5

(2) INFORMATION FOR SEQ ID NO: 136:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

Met Ser Gly Ser Phe Ile Leu Cys Leu Ala Leu Val Thr Arg Trp Ser
 1 5 10 15

20

Pro Gln Ala Ser Ser Val Pro Leu Ala Val Tyr Glu Ser Lys Thr Arg
 20 25 30

Lys Ser Tyr Arg Ser Gln Arg Asp Arg Asp Gly Lys Asp Arg Ser Gln
 35 40 45

25

Gly Met Gly Leu Ser Leu Leu Val Glu Thr Arg Lys Leu Leu Leu Ser
 50 55 60

Ala Asn Gln Gly
 65

30

(2) INFORMATION FOR SEQ ID NO: 137:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

Met Cys Phe Arg Phe Phe Leu Phe Cys Ser Arg Ile Leu Leu Lys Leu
 1 5 10 15

45

Phe Phe Leu Leu Phe Pro Ala Ser Ala Phe Pro Leu Ser Thr Arg Ser
 20 25 30

Ser Leu Ser Val Asn Glu His Val Val Val Ser Pro Arg Ser Thr Val
 35 40 45

50

Ser Ile Ser Arg
 50

55

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 541 amino acids

60

(B) TYPE: amino acid

280

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

5 Met Val Arg Thr Asp Gly His Thr Leu Ser Glu Lys Arg Asn Tyr Gln
 1 5 10 15
 Val Thr Asn Ser Met Phe Gly Ala Ser Arg Lys Lys Phe Val Glu Gly
 20 25 30
 10 Val Asp Ser Asp Tyr His Asp Glu Asn Met Tyr Tyr Ser Gln Ser Ser
 35 40 45
 Met Phe Pro His Arg Ser Glu Lys Asp Met Leu Ala Ser Pro Ser Thr
 50 55 60
 15 Ser Gly Gln Leu Ser Gln Phe Gly Ala Ser Leu Tyr Gly Gln Gln Ser
 65 70 75 80
 Ala Leu Gly Leu Pro Met Arg Gly Met Ser Asn Asn Thr Pro Gln Leu
 85 90 95
 20 Asn Arg Ser Leu Ser Gln Gly Thr Gln Leu Pro Ser His Val Thr Pro
 100 105 110
 25 Thr Thr Gly Val Pro Thr Met Ser Leu His Thr Pro Pro Ser Pro Ser
 115 120 125
 Arg Gly Ile Leu Pro Met Asn Pro Xaa Asn Met Met Asn His Ser Gln
 130 135 140
 30 Val Gly Gln Gly Ile Gly Ile Pro Ser Arg Thr Asn Ser Met Ser Ser
 145 150 155 160
 Ser Gly Leu Gly Ser Pro Asn Arg Ser Ser Pro Ser Ile Ile Cys Met
 165 170 175
 35 Pro Lys Gln Gln Pro Ser Arg Gln Pro Phe Thr Val Asn Ser Met Ser
 180 185 190
 40 Gly Phe Gly Met Asn Arg Asn Gln Ala Phe Gly Met Asn Asn Ser Leu
 195 200 205
 Ser Ser Asn Ile Phe Asn Gly Thr Asp Gly Ser Glu Asn Val Thr Gly
 210 215 220
 45 Leu Asp Leu Ser Asp Phe Pro Ala Leu Ala Asp Arg Asn Arg Arg Glu
 225 230 235 240
 Gly Ser Gly Asn Pro Thr Pro Leu Ile Asn Pro Leu Ala Gly Arg Ala
 245 250 255
 50 Pro Tyr Val Gly Met Val Thr Lys Pro Ala Asn Glu Gln Ser Gln Asp
 260 265 270
 55 Phe Ser Ile His Asn Glu Asp Phe Pro Ala Leu Pro Gly Ser Ser Tyr
 275 280 285
 Lys Asp Pro Thr Ser Ser Asn Asp Asp Ser Lys Ser Asn Leu Asn Thr
 290 295 300
 60

281

Ser Gly Lys Thr Thr Ser Ser Thr Asp Gly Pro Lys Phe Pro Gly Asp
 305 310 315 320
 5 Lys Ser Ser Thr Thr Gln Asn Asn Asn Gln Gln Lys Lys Gly Ile Gln
 325 330 335
 Val Leu Pro Asp Gly Arg Val Thr Asn Ile Pro Gln Gly Met Val Thr
 340 345 350
 10 Asp Gln Phe Gly Met Ile Gly Leu Leu Thr Phe Ile Arg Ala Ala Glu
 355 360 365
 Thr Asp Pro Gly Met Val His Leu Ala Leu Gly Ser Asp Leu Thr Thr
 370 375 380
 15 Leu Gly Leu Asn Leu Asn Ser Pro Glu Asn Leu Tyr Pro Lys Phe Ala
 385 390 395 400
 Ser Pro Trp Ala Ser Ser Pro Cys Arg Pro Gln Asp Ile Asp Phe His
 405 410 415
 20 Val Pro Ser Glu Tyr Leu Thr Asn Ile His Ile Arg Asp Lys Leu Ala
 420 425 430
 Ala Ile Lys Leu Gly Arg Tyr Gly Glu Asp Leu Leu Phe Tyr Leu Tyr
 435 440 445
 Tyr Met Asn Gly Gly Asp Val Leu Gln Leu Leu Ala Ala Val Glu Leu
 450 455 460
 30 Phe Asn Arg Asp Trp Arg Tyr His Lys Glu Glu Arg Val Trp Ile Thr
 465 470 475 480
 Arg Ala Pro Gly Met Glu Pro Thr Met Lys Thr Asn Thr Tyr Glu Arg
 485 490 495
 Gly Thr Tyr Tyr Phe Phe Asp Cys Leu Asn Trp Arg Lys Val Ala Lys
 500 505 510
 40 Glu Phe His Leu Glu Tyr Asp Lys Leu Glu Glu Arg Pro His Leu Pro
 515 520 525
 Ser Thr Phe Asn Tyr Asn Pro Ala Gln Gln Ala Phe Xaa
 530 535 540
 45

(2) INFORMATION FOR SEQ ID NO: 139:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:
 55 Met Ile Cys Pro Gln Cys Pro Leu Ser Leu Leu Cys Leu Ile Ser Ser
 1 5 10 15
 60 Leu Cys Ser Leu Val Ile Gln Ile Ser Leu Lys Thr Ile Arg Asp Ile
 20 25 30

282

Thr Leu Leu Asn Met Val Gly Ile Lys Phe Ser Ile Ser Leu Ser Asn
 35 40 45

5 Lys Ile Asn Ile Asn Ser Arg Thr Trp Xaa
 50 55

10 (2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

Met Thr Leu Arg Pro Ser Leu Leu Pro Leu His Leu Leu Leu Leu Leu
 1 5 10 15

20 Leu Leu Ser Ala Ala Val Cys Arg Ala Glu Ala Gly Leu Glu Thr Glu
 20 25 30

25 Ser Pro Val Arg Thr Leu Gln Val Glu Thr Leu Val Glu Pro Pro Glu
 35 40 45

Pro Cys Ala Glu Pro Ala Ala Phe Gly Asp Thr Leu His Ile His Tyr
 50 55 60

30 Thr Gly Ser Leu Val Asp Gly Arg Ile Ile Asp Thr Ser Leu Thr Arg
 65 70 75 80

Asp Pro Leu Val Ile Glu Leu Gly Gln Lys Gln Val Ile Pro Gly Leu
 85 90 95

35 Glu Gln Ser Leu Leu Asp Met Cys Val Gly Glu Lys Arg Arg Ala Ile
 100 105 110

Ile Pro Ser His Leu Ala Tyr Gly Lys Arg Gly Phe Pro Pro Ser Val
 115 120 125

40 Pro Ala Asp Ala Val Val Gln Tyr Asp Val Glu Leu Ile Ala Leu Ile
 130 135 140

45 Arg Ala Asn Tyr Trp Leu Lys Leu Val Lys Gly Ile Leu Pro Leu Val
 145 150 155 160

Gly Met Ala Met Val Pro Ala Leu Leu Gly Leu Ile Gly Tyr His Leu
 165 170 175

50 Tyr Arg Lys Ala Asn Arg Pro Lys Val Ser Lys Lys Lys Leu Lys Glu
 180 185 190

Glu Lys Arg Asn Lys Ser Lys Lys Lys Xaa
 195 200

55

60 (2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

Met Phe Leu Arg Leu Tyr Leu Ile Ala Arg Val Met Leu Leu His Ser
 1 5 10 15

10 Lys Leu Phe Thr Asp Ala Ser Ser Arg Ser Ile Gly Ala Leu Asn Lys
 20 25 30

Ile Asn Phe Asn Thr Arg Phe Val Met Lys Thr Leu Met Thr Ile Cys
 35 40 45

15 Pro Gly Thr Val Leu Leu Val Phe Ser Ile Ser Leu Trp Ile Ile Ala
 50 55 60

Ala Trp Thr Val Arg Val Cys Glu Ser Pro Glu Ser Pro Ala Gln Pro
 20 65 70 75 80

Ser Gly Ser Ser Leu Pro Ala Trp Tyr His Asp Gln Gln Asp Val Thr
 85 90 95

25 Ser Asn Phe Leu Gly Ala Met Trp Leu Ile Ser Ile Thr Phe Leu Ser
 100 105 110

Ile Gly Tyr Gly Asp Met Val Pro His Thr Tyr Cys Gly Lys Gly Val
 115 120 125

30 Cys Leu Leu Thr Gly Ile Met Gly Ala Gly Cys Thr Ala Leu Val Val
 130 135 140

Ala Val Val Ala Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His Val
 35 145 150 155 160

His Asn Phe Met Met Asp Thr Gln Leu Thr Lys Arg Ile Lys Asn Ala
 165 170 175

40 Ala Ala Asn Val Leu Arg Glu Thr Trp Leu Ile Tyr Lys His Thr Lys
 180 185 190

Leu Leu Lys Lys Ile Asp His Ala Lys Val Arg Lys His Gln Arg Lys
 195 200 205

45 Phe Leu Pro Ser Tyr Pro Pro Val Xaa
 210 215

50

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

55 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

60 Met Ser Asn Thr Thr Val Pro Asn Ala Pro Gln Ala Asn Ser Asp Ser
 1 5 10 15

284

Met Val Gly Tyr Val Leu Gly Pro Phe Phe Leu Ile Thr Leu Val Gly
 20 25 30

5 Val Val Val Ala Val Val Met Tyr Val Gln Lys Lys Lys Arg Val Asp
 35 40 45

Arg Leu Arg His His Leu Leu Pro Met Tyr Ser Tyr Asp Pro Ala Glu
 50 55 60

10 Glu Leu His Glu Ala Glu Gln Glu Leu Leu Ser Asp Met Gly Asp Pro
 65 70 75 80

15 Lys Val Val His Gly Trp Gln Ser Gly Tyr Gln His Lys Arg Met Pro
 85 90 95

Leu Leu Asp Val Lys Thr
 100

20

(2) INFORMATION FOR SEQ ID NO: 143:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

30 Met Arg Glu Cys Gln Glu Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe
 1 5 10 15

Ser Leu Val Ser Met Leu Val Thr Gln Lys Leu Val Tyr Gln Gly Tyr
 20 25 30

35 Leu Ala Ala Asn Ser Arg Phe Gly Ser Leu Pro Lys Val Ala Leu Ala
 35 40 45

40 Gly Leu Leu Gly Phe Gly Leu Gly Lys Val Ser Tyr Ile Gly Val Cys
 50 55 60

Gln Ser Lys Phe His Phe Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe
 65 70 75 80

45 Gly Pro Gln His Asn Arg His Cys Leu Thr Cys Glu Glu Cys Lys
 85 90 95

Ile Lys His Gly Leu Ser Glu Lys Gly Asp Ser Gln Pro Ser Ala Ser
 100 105 110

50

55

(2) INFORMATION FOR SEQ ID NO: 144:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid

285

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

5 Met Lys Asn Asp Arg Asn Gln Gly Phe Ser Leu Leu Gln Leu Ile Asp
 1 5 10 15
 Trp Asn Lys Pro
 20

10

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

20 Met Gly Thr Gln Pro Pro Val Val Ala Gly Phe Thr Ile Pro Met Leu
 1 5 10 15
 Gly Tyr Thr Val Arg Val Leu Thr Phe His Leu Ser Cys Ser
 20 25 30

25

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

35

Met Lys Ile Pro Val Leu Pro Ala Val Val Leu Leu Ser Leu Leu Val
 1 5 10 15

40

Leu His Ser Ala Gln Gly Ala Thr Leu Gly Gly Pro Glu Glu Glu Ser
 20 25 30

Thr Ile Glu Asn Tyr Ala Ser Arg Pro Glu Ala Phe Asn Thr Pro Phe
 35 40 45

45

Leu Asn Ile Asp Lys Leu Arg Ser Ala Phe Lys Ala Asp Glu Phe Leu
 50 55 60

50

Asn Trp His Ala Leu Phe Glu Ser Ile Lys Arg Lys Leu Pro Phe Leu
 65 70 75 80

Asn Trp Asp Ala Phe Pro Lys Leu Lys Gly Leu Arg Ser Ala Thr Pro
 85 90 95

55

Asp Ala Gln

60

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

Met Val Trp Gly Leu Leu Leu Gly
 1 5

10

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

20 Met Leu Pro Leu Leu Ser Leu Leu Phe Leu Phe Phe Ser Thr Val Ser
 1 5 10 15

Ser Phe Cys Gly Met Pro Leu Arg Ala His Thr Arg Ala Xaa Ala His
 20 25 30

25

Thr Arg Thr Phe Ala Ser Arg
 35

30

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

40 Met Ile Cys Glu Thr Lys Ala Arg Lys Ser Ser Gly Gln Pro Gly Arg
 1 5 10 15

Leu Pro Pro Pro Thr Leu Ala Pro Pro Gln Pro Pro Leu Pro Glu Thr
 20 25 30

45 Ile Glu Arg Pro Val Gly Thr Gly Ala Met Val Ala Arg Ser Ser Asp
 35 40 45

Leu Pro Tyr Leu Ile Val Gly Val Val Leu Gly Ser Ile Val Leu Ile
 50 55 60

50

Ile Val Thr Phe Ile Pro Phe Cys Leu Trp Arg Ala Trp Ser Lys Gln
 65 70 75 80

55

Lys His Thr Thr Asp Leu Gly Phe Pro Arg Ser Ala Leu Pro Pro Ser
 85 90 95

Cys Pro Tyr Thr Met Val Pro Leu Gly Gly Leu Pro Gly His Gln Ala
 100 105 110

60

Val Asp Ser Pro Thr Ser Val Ala Ser Val Asp Gly Pro Val Leu Met

115 120 125

Gly Ser Thr
130

5

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

15

Met Gly Ala Pro Ser Leu Thr Met Leu Leu Leu Lys Val Gln Pro
1 5 10 15

Arg Arg Thr Gln Ala Phe Asp Ala His Trp Val Gly Leu Pro Leu Leu
20 25 30

25

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

35 Met Cys Leu Ile Phe Leu Leu Leu Leu Leu Ser Phe Ser

1 5 10

40 (2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

His Pro His Gln Asp Ser Gln Pro
1 5

(2) INFORMATION FOR SEQ ID NO: 153:

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

288

Met Asn Thr Ser Tyr Ile Leu Arg Leu Thr Val Val Val Ser Val Val
 1 5 10 15

Ile Tyr Leu Ala Ile His Pro Leu Leu Ser Phe Ser Leu Glu Ser Pro
 5 20 25 30

Leu Leu Val Pro Trp Arg Asp Cys Cys Gln Asn Ile Trp Lys Ser Gly
 35 40 45

Ser Val Trp Tyr Lys Arg Trp Thr Leu Pro His Met Glu Val Cys Cys
 10 50 55 60

Gln Asp Leu His
 65

15

(2) INFORMATION FOR SEQ ID NO: 154:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

Met Leu Lys Ile Phe Lys Glu Trp Glu Asn Leu Asn Leu Ile Leu Thr
 1 5 10 15

Ser Ile Arg Ile Leu Glu Arg Gln Asn Met
 30 20 25

35

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

Met Asp Cys Glu Val Asn Asn Gly Ser Ser Leu Arg Asp Glu Cys Ile
 1 5 10 15

Thr Asn Leu Leu Val Phe Gly Phe Leu Gln Ser Cys Ser Asp Asn Ser
 45 20 25 30

Phe Arg Arg Glu Leu Asp Ala Leu Gly His Glu Leu Pro Val Leu Ala
 35 40 45

Pro Gln Trp Glu Gly Tyr Asp Glu Leu Gln Thr Asp Gly Asn Arg Ser
 50 55 60

Ser His Ser Arg Leu Gly Arg Ile Glu Ala Asp Ser Glu Ser Gln Glu
 55 65 70 75 80

Asp Ile Ile Arg Asn Ile Ala Arg His Leu Ala Gln Val Gly Asp Ser
 85 90 95

Met Asp Arg Ser Ile Pro Pro Gly Leu Val Asn Gly Leu Ala Leu Gln
 60

100 105 110

Leu Arg Asn Thr Ser Arg Ser Glu Glu Asp Arg Asn Arg Asp Leu Ala
115 120 125

5 Thr Ala Leu Glu Gln Leu Leu Gln Ala Tyr Pro Arg Asp Met Glu Lys
130 135 140

10 Glu Lys Thr Met Leu Val Leu Ala Leu Leu Leu Ala Lys Lys Val Ala
145 150 155 160

Ser His Thr Pro Ser Leu Leu Arg Asp Val Phe His Thr Thr Val Asn
165 170 175

15 Phe Ile Asn Gln Asn Leu Arg Thr Tyr Val Arg Ser Leu Ala Arg Asn
180 185 190

Gly Met Asp
195

20

(2) INFORMATION FOR SEQ ID NO: 156:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

30

Met Ser Leu Ser Leu Val Ser Val Ser Val Gly Pro Ser Thr Leu Ala
1 5 10 15

35

Cys Ser Phe Leu Arg Pro Lys Ala Arg Pro Ser Lys Arg Ser Pro Arg
20 25 30

Asn Tyr Thr Asp Ser Thr Ser Pro Gly Gly Pro Arg Ala Pro Arg Gly
35 40 45

40

Gly Ala Trp Arg Leu Ser Ser Gln Gln Asn Ser Ser Pro Lys Gly Val
50 55 60

Ala Val Ala Lys Ala Ser Tyr Arg Pro Val Leu Cys Phe Leu Pro Gly
65 70 75 80

45

Pro Trp Ser Ser Xaa Pro Xaa Ala Phe Leu Ile
85 90

50

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

55

Met Gly Thr Leu Ser Ala Glu Cys Ser Gly Pro Ala Thr Leu Gly Leu
1 5 10 15

60

290

Cys Leu Val Val Pro Trp Asn Ser Ser Gly Leu Ser Gln Pro Pro
 20 25 30

5

(2) INFORMATION FOR SEQ ID NO: 158:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

15

Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile Phe Leu
 1 5 10 15

Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr Tyr Pro
 20 25 30

20

Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu Thr Thr Ala
 35 40 45

25

Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr Ala Thr Thr Ala
 50 55 60

Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val Leu Pro Lys Trp Val
 65 70 75 80

30

Gly Asp Leu Pro Asn Gly Arg Val Cys Pro Xaa
 85 90

35

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

45

Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser Asn Thr
 1 5 10 15

Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala
 20 25 30

50

Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe
 35 40 45

Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His Leu Ile
 50 55 60

55

Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Trp Asp Trp Ala
 65 70 75 80

Glu Ala Gly Ala Ser Leu Tyr Ser Pro
 85

60

(2) INFORMATION FOR SEQ ID NO: 160:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

10 Met Ser Ser Ala Ala Ala Asp His Trp Ala Trp Leu Leu Val Leu Ser
 1 5 10 15

15 Phe Val Phe Gly Cys Asn Val Leu Arg Ile Leu Leu Pro Ser Phe Ser
 20 25 30

Ser Phe Met Ser Arg Val Leu Gln Lys Asp Ala Glu Gln Glu Ser Gln
 35 40 45

20 Met Arg Ala Glu Ile Gln Asp Met Lys Gln Glu Leu Ser Thr Val Asn
 50 55 60

Met Met Asp Glu Phe Ala Arg Tyr Ala Arg Leu Glu Arg Lys Ile Asn
 65 70 75 80

25 Lys Met Thr Asp Lys Leu Lys Thr His Val Lys Ala Arg Thr Ala Gln
 85 90 95

Leu Ala Lys Ile Lys Trp Val Ile Ser Val Ala Phe Tyr Val Leu Gln
 100 105 110

Ala Ala Leu Met Ile Ser Leu Ile Trp Lys Tyr Tyr Ser Val Pro Val
 115 120 125

35 Ala Val Val Pro Ser Lys Trp Ile Thr Pro Leu Asp Arg Leu Val Ala
 130 135 140

Phe Pro Thr Arg Val Ala Gly Gly Val Gly Ile Thr Cys Trp Ile Leu
 145 150 155 160

40 Val Cys Asn Lys Val Val Ala Ile Val Leu His Pro Phe Ser
 165 170

(2) INFORMATION FOR SEQ ID NO: 161:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

55 Met Gly Lys Leu Ile Asn Ile Val Ile Arg Lys Pro Leu Leu Leu Leu
 1 5 10 15

Leu Val Gln Cys Glu Asn Cys Cys Arg Lys Asn Met Leu Tyr Asn Ile
 20 25 30

60 Phe Leu Asn Ile His Asn Ile His Lys Phe Ser Asn His

35

40

45

5 (2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Met Val Ala Ser Thr Leu Val Thr Asn Leu Phe Gly Val Ala Phe Ala

15 1 5 10 15

Thr Thr Ala Ala Thr Arg Ala

20

20

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

25 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

Met Leu Met Ala Pro Val Val Cys Leu Ser Phe Ser Pro Cys Pro Ala

30 1 5 10 15

Asp Thr Ser Leu Thr Gly Asp Gly Leu Lys Ala Gly Leu Glu Arg Gly

20 25 30

35 Xaa Ala Leu Val Thr Leu Phe Asp Ser Val Thr His Phe Leu Ala His

35 40 45

Thr Leu Phe Glu Leu Leu Asp Phe Gln Leu Ala Phe Leu Arg Ser Gly

40 50 55 60

Lys Gln Thr Ala Pro His

65 70

45

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 amino acids

50 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Met Leu Leu Leu Leu Leu Leu Gly Ser Gly Gln Gly Pro Gln Gln

55 1 5 10 15

Val Gly Ala Gly Gln Thr Phe Glu Tyr Leu Lys Arg Glu His Ser Leu

20 25 30

60 Ser Lys Pro Tyr Gln Gly Val Gly Thr Gly Ser Ser Ser Leu Trp Asn

35 40 45
 Leu Met Gly Asn Ala Met Val Met Thr Gln Tyr Ile Arg Leu Thr Pro
 50 55 60
 5 Asp Met Gln Ser Lys Gln Gly Ala Leu Trp Asn Arg Val Pro Cys Phe
 65 70 75 80
 10 Leu Arg Asp Trp Glu Leu Gln Val His Phe Lys Ile His Gly Gln Gly
 85 90 95
 Lys Lys Asn Leu His Gly Asp Gly Leu Ala Ile Trp Tyr Thr Arg Asn
 100 105 110
 15 Arg Met Gln Pro Gly Pro Val Phe Gly Asn Met Asp Lys Phe Val Gly
 115 120 125
 Leu Gly Val Phe Val Asp Thr Tyr Pro Asn Glu Glu Lys Gln Gln Glu
 130 135 140
 20 Arg Val Phe Pro Tyr Ile Ser Ala Met Val Asn Asn Gly Ser Leu Ser
 145 150 155 160
 25 Tyr Asp His Glu Arg Asp Gly Arg Pro Thr Glu Leu Gly Gly Cys Thr
 165 170 175
 Ala Ile Val Arg Asn Leu His Tyr Asp Thr Phe Leu Val Ile Arg Tyr
 180 185 190
 30 Val Lys Arg His Leu Thr Ile Met Met Asp Ile Asp Gly Lys His Glu
 195 200 205
 Trp Arg Asp Cys Ile Glu Val Pro Gly Val Arg Leu Pro Arg Gly Tyr
 210 215 220
 35 Tyr Phe Gly Thr Ser Ser Ile Thr Gly Asp Leu Ser Asp Asn His Asp
 225 230 235 240
 Val Ile Ser Leu Lys Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu
 245 250 255
 Glu Glu Lys Leu His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met
 260 265 270
 45 Lys Leu Pro Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala
 275 280 285
 Leu Phe Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile
 290 295 300
 50 Val Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys
 305 310 315 320
 55 Arg Phe Tyr
 60 (2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

Met Pro Ser Glu Tyr Thr Tyr Val Lys Leu Arg Ser Asp Cys Ser Arg
 1 5 10 15
 10 Pro Ser Leu Gln Trp Tyr Thr Arg Ala Gln Ser Lys Met Arg Arg Pro
 20 25 30
 Ser Leu Leu Leu Lys Asp Ile Leu Lys Cys Thr Leu Leu Val Phe Gly
 35 40 45
 15 Val Trp Ile Leu Tyr Ile Leu Lys Leu Asn Tyr Thr Thr Glu Glu Cys
 50 55 60
 20 Asp Met Lys Lys Met His Tyr Val Asp Pro Asp His Val Lys Arg Ala
 65 70 75 80
 Gln Lys Tyr Ala Gln Gln Val Leu Gln Lys Glu Cys Arg Pro Lys Phe
 85 90 95
 25 Ala Lys Thr Ser Met Ala Leu Leu Phe Glu His Arg Tyr Ser Val Asp
 100 105 110
 Leu Leu Pro Phe Val Gln Lys Xaa Pro Lys Asp Ser Glu Ala Glu Ser
 115 120 125
 30 Lys Tyr Asp Pro Pro Phe Gly Phe Arg Lys Phe Ser Ser Lys Val Gln
 130 135 140
 35 Thr Leu Leu Glu Leu Leu Pro Glu His Asp Leu Pro Glu His Leu Lys
 145 150 155 160
 Ala Lys Thr Cys Arg Arg Cys Val Val Ile Gly Ser Gly Gly Ile Leu
 165 170 175
 40 His Gly Leu Glu Leu Gly His Thr Leu Asn Gln Phe Asp Val Val Ile
 180 185 190
 Arg Leu Asn Ser Ala Pro Val Glu Gly Tyr Ser Glu His Val Gly Asn
 195 200 205
 45 Lys Thr Thr Ile Arg Met Thr Tyr Pro Glu Gly Ala Pro Leu Ser Asp
 210 215 220
 50 Leu Glu Tyr Tyr Ser Asn Asp Leu Phe Val Ala Val Leu Phe Lys Ser
 225 230 235 240
 Val Asp Phe Asn Trp Leu Gln Ala Met Val Lys Lys Glu Thr Leu Pro
 245 250 255
 55 Phe Trp Val Arg Leu Phe Phe Trp Lys Gln Val Ala Glu Lys Ile Pro
 260 265 270
 60 Leu Gln Pro Lys His Phe Arg Ile Leu Asn Pro Val Ile Ile Lys Glu
 275 280 285

295

Thr Ala Phe Xaa His Pro Ser Val Leu Arg Ala Ser Val Lys Val Leu
 290 295 300

5 Gly Ala Glu Ile Arg Thr Ser Pro Gln Ser Val Ser Leu Pro Leu Ser
 305 310 315 320

Xaa

10

(2) INFORMATION FOR SEQ ID NO: 166:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

20 Met Thr Leu Asp Val Gln Thr Val Val Val Phe Ala Val Ile Val Val
 1 5 10 15

Leu Leu Leu Val Asn Val Ile Leu Met Phe Phe Leu Gly Thr Arg
 20 25 30

25

(2) INFORMATION FOR SEQ ID NO: 167:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

35 Met Leu Pro Leu Leu Phe Cys Ala Phe Cys Leu His Lys Leu Gly Pro
 1 5 10 15

40 Leu Leu Phe Leu Tyr Asp Val Leu Met Xaa His Glu Ala Val Met Arg
 20 25 30

Thr His Gln Ile Gln Leu Pro Asp Pro Glu Phe Pro Ser Gln Gln Asn
 35 40 45

45 Gln Val Leu Asn Lys Thr Leu Phe Asn Lys Leu Lys Lys Lys Lys
 50 55 60

Lys Lys Lys Xaa Xaa Xaa Lys Lys
 65 70

50

(2) INFORMATION FOR SEQ ID NO: 168:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 282 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

60

296

Met Ala Ser Arg Gly Arg Arg Pro Glu His Gly Gly Pro Pro Glu Leu
 1 5 10 15
 Phe Tyr Asp Glu Thr Glu Ala Arg Lys Tyr Val Arg Asn Ser Arg Met
 5 20 25 30
 Ile Asp Ile Gln Thr Arg Met Ala Gly Arg Ala Leu Glu Leu Leu Tyr
 35 40 45
 Leu Pro Glu Asn Lys Pro Cys Tyr Leu Leu Asp Ile Gly Cys Gly Thr
 10 50 55 60
 Gly Leu Ser Gly Ser Tyr Leu Ser Asp Glu Gly His Tyr Trp Val Gly
 15 65 70 75 80
 Leu Asp Ile Ser Pro Ala Met Leu Asp Glu Ala Val Asp Arg Glu Ile
 85 90 95
 Glu Gly Asp Leu Leu Leu Gly Asp Met Gly Gln Gly Ile Pro Phe Lys
 20 100 105 110
 Pro Gly Thr Phe Asp Gly Cys Ile Ser Ile Ser Ala Val Gln Trp Leu
 115 120 125
 Cys Asn Ala Asn Lys Lys Ser Glu Asn Pro Ala Lys Arg Leu Tyr Cys
 25 130 135 140
 Phe Phe Ala Ser Leu Phe Ser Val Leu Val Arg Gly Ser Arg Ala Val
 145 150 155 160
 Leu Gln Leu Tyr Pro Glu Asn Ser Glu Gln Leu Glu Leu Ile Thr Thr
 165 170 175
 Gln Ala Thr Lys Ala Gly Phe Ser Gly Gly Met Val Val Asp Tyr Pro
 35 180 185 190
 Asn Ser Ala Lys Ala Lys Lys Phe Tyr Leu Cys Leu Phe Ser Gly Pro
 195 200 205
 Ser Thr Phe Ile Pro Glu Gly Leu Ser Glu Asn Gln Asp Glu Val Glu
 40 210 215 220
 Pro Arg Glu Ser Val Phe Thr Asn Glu Arg Phe Pro Leu Arg Met Ser
 225 230 235 240
 Arg Arg Gly Met Val Arg Lys Ser Arg Ala Trp Val Leu Glu Lys Lys
 245 250 255
 Glu Arg His Arg Arg Gln Gly Arg Glu Val Arg Pro Asp Thr Gln Tyr
 50 260 265 270
 Thr Gly Arg Lys Arg Lys Pro Arg Phe Xaa
 275 280

55

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

5 Met Leu Gly Lys Thr Lys Phe Gln Ser Tyr Lys Ser Phe Ser Arg Lys
 1 5 10 15
 Leu Met Val Cys Pro Ser Thr
 20

10

(2) INFORMATION FOR SEQ ID NO: 170:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

20

Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His Gly
 1 5 10 15

25

Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly Arg
 20 25 30

Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala His
 35 40 45

30

Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val Ala
 50 55 60

35

Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu Gly
 65 70 75 80

Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp Val
 85 90 95

40

Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg His
 100 105 110

Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp Arg
 115 120 125

45

Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly His
 130 135 140

Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr Tyr
 145 150 155 160

50

Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp Gln
 165 170 175

55

Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu His
 180 185 190

Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr Leu
 195 200 205

60

Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu Tyr

210 215 220

Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala Trp
 225 230 235 240

5 Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn Lys
 245 250 255

Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro Pro
 10 260 265 270

Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu Ser
 275 280 285

15 Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Xaa Ile Leu Gly Asn
 290 295 300

Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp Leu
 20 305 310 315 320

Thr Arg His His Asp Glu Leu Xaa
 325

25

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

35 Met Cys Trp Leu Arg Ala Trp Xaa Gln Ile Xaa Leu Pro Val Phe Xaa
 1 5 10 15

Ser Xaa Phe Leu Ile Gln Leu Leu Ile Ser Phe Ser Glu Asn Gly Phe
 20 25 30

40 Ile His Ser Pro Arg Asn Asn Gln Lys Pro Arg Asp Gly Asn Xaa Glu
 35 40 45

Glu Cys Ala Val Lys Lys Ser Cys Gln Leu Cys Thr Glu Asp Lys Lys
 45 50 55 60

Tyr Met Met Asn Arg
 65

50

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 160 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

60 Met Trp Leu Phe Ile Leu Leu Ser Leu Ala Leu Ile Ser Asp Ala Met
 1 5 10 15

299

Val Met Asp Glu Lys Val Lys Arg Ser Phe Val Leu Asp Thr Ala Ser
 20 25 30

5 Ala Ile Cys Asn Tyr Asn Ala His Tyr Lys Asn His Pro Lys Tyr Trp
 35 40 45

Cys Arg Gly Tyr Phe Arg Asp Tyr Cys Asn Ile Ile Ala Phe Ser Pro
 50 55 60

10 Asn Ser Thr Asn His Val Ala Leu Lys Asp Thr Gly Asn Gln Leu Ile
 65 70 75 80

15 Val Thr Met Ser Cys Leu Asn Lys Glu Asp Thr Gly Trp Tyr Trp Cys
 85 90 95

Gly Ile Gln Arg Asp Phe Ala Arg Asp Asp Met Asp Phe Thr Glu Leu
 100 105 110

20 Ile Val Thr Asp Asp Lys Gly Thr Trp Pro Met Thr Leu Val Trp Glu
 115 120 125

Arg Leu Ser Gly Thr Lys Pro Glu Ala Ala Arg Leu Pro Lys Leu Ser
 130 135 140

25 Ala Arg Leu Thr Ala Pro Gly Arg Pro Phe Ser Ser Phe Ala Tyr Xaa
 145 150 155 160

30

(2) INFORMATION FOR SEQ ID NO: 173:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

Met Ala Xaa His Phe Leu Leu Val Ala Leu Gln Ser Val Pro His Cys
 1 5 10 15

45 Pro His Leu Leu Glu Glu Glu His Lys Leu Cys Lys Val Ser His Phe
 20 25 30

Ser Gly Val Thr Leu Val Thr Ser Arg Gln Asp Ser Ser Ser Tyr Val
 35 40 45

50 Pro Val Gln Thr Leu Phe Ile His Leu Gly Pro Trp Ala Trp Asp Leu
 50 55 60

55 Xaa Pro Cys Thr Ala Glu Asp Pro Glu Ala Glu Arg Ser Leu Arg Leu
 65 70 75 80

Cys His Ser His Leu Ala Arg Xaa Asn Val Ser Pro Ser Gln Ala Ala
 85 90 95

60 Glu Gly Xaa Xaa Xaa Arg Gly Cys Gln His Arg Gly Ser Arg Glu Leu

300

100 105 110
 Thr Phe Leu Ser Ala Glu Asn Glu Ala Gly Ile
 115 120

5

(2) INFORMATION FOR SEQ ID NO: 174:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

15

Met Lys Val Gly Ala Arg Ile Arg Val Lys Met Ser Val Asn Lys Ala
 1 5 10 15

20

His Pro Val Val Ser Thr His Trp Arg Trp Pro Ala Glu Trp Pro Gln
 20 25 30

Met Phe Leu His Leu Ala Gln Glu Pro Arg Thr Glu Val Lys Ser Arg
 35 40 45

25

Pro Leu Gly Leu Ala Gly Phe Ile Arg Gln Asp Ser Lys Thr Arg Lys
 50 55 60

30

Pro Leu Glu Gln Glu Thr Ile Met Ser Ala Ala Asp Thr Ala Leu Trp
 65 70 75 80

Pro Tyr Gly His Gly Asn Arg Glu His Gln Glu Asn Glu Leu Gln Lys
 85 90 95

35

Tyr Leu Gln Tyr Lys Asp Met His Leu Leu Asp Ser Gly Gln Ser Leu
 100 105 110

Gly His Thr His Thr Leu Gln Gly Ser His Asn Leu Thr Ala Leu Asn
 115 120 125

40

Ile

45

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 amino acids

(B) TYPE: amino acid

50

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

Met Ala Tyr His Ser Phe Leu Val Glu Pro Ile Ser Cys His Ala Trp
 1 5 10 15

55

Asn Lys Asp Arg Thr Gln Ile Ala Ile Cys Pro Asn Asn His Glu Val
 20 25 30

60

His Ile Tyr Glu Lys Ser Gly Ala Lys Trp Thr Lys Val His Glu Leu
 35 40 45

301

Lys Glu His Asn Gly Gln Val Thr Gly Ile Asp Trp Ala Pro Glu Ser
 50 55 60

5 Asn Arg Ile Val Thr Cys Gly Thr Asp Arg Asn Ala Tyr Val Trp Thr
 65 70 75 80

Leu Lys Gly Arg Thr Trp Lys Pro Thr Leu Val Ile Leu Arg Ile Asn
 85 90 95

10 Arg Ala Ala Arg Cys Val Arg Trp Ala Pro Asn Glu Asn Lys Phe Ala
 100 105 110

Val Gly Ser Gly Ser Arg Val Ile Ser Ile Cys Tyr Phe Glu Gln Glu
 115 120 125

15 Asn Asp Trp Trp Val Cys Lys His Ile Lys Lys Pro Ile Arg Ser Thr
 130 135 140

20 Val Leu Ser Leu Asp Trp His Pro Asn Asn Val Leu Leu Ala Ala Gly
 145 150 155 160

Ser Cys Asp Phe Lys Cys Arg Ile Phe Ser Ala Tyr Ile Lys Glu Val
 165 170 175

25 Glu Glu Arg Pro Ala Pro Thr Pro Trp Gly Ser Lys Met Pro Phe Gly
 180 185 190

Glu Leu Met Phe Glu Ser Ser Ser Ser Cys Gly Trp Val His Gly Val
 195 200 205

30 Cys Phe Ser Ala Ser Gly Ser Arg Val Ala Trp Val Ser His Asp Ser
 210 215 220

35 Thr Val Cys Leu Ala Asp Ala Asp Lys Lys Met Ala Val Ala Thr Leu
 225 230 235 240

Ala Ser Glu Thr Leu Pro Leu Leu Ala Leu Thr Phe Ile Thr Asp Asn
 245 250 255

40 Ser Leu Val Ala Ala Gly His Asp Cys Phe Pro Val Leu Phe Thr Tyr
 260 265 270

Asp Ala Ala Ala Gly Met Leu Ser Phe Gly Gly Arg Leu Asp Val Pro
 275 280 285

Lys Gln Ser Ser Gln Arg Gly Leu Thr Ala Arg Glu Arg Phe Gln Asn
 290 295 300

50 Leu Asp Lys Lys Ala Ser Ser Glu Gly Gly Thr Ala Ala Gly Ala Gly
 305 310 315 320

Leu Asp Ser Leu His Lys Asn Ser Val Ser Gln Ile Ser Val Leu Ser
 325 330 335

55 Gly Gly Lys Ala Lys Cys Ser Gln Phe Cys Thr Thr Gly Met Asp Gly
 340 345 350

Gly Met Ser Ile Trp Asp Val Lys Ser Leu Glu Ser Ala Leu Lys Asp
 355 360 365

60

302

Leu Lys Ile Lys
370

5

(2) INFORMATION FOR SEQ ID NO: 176:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

15

Met Trp Ser Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu
1 5 10 15

Leu Leu Ala Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala
20 25 30

20

Leu Glu Tyr Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro
35 40 45

25

Arg Thr Phe Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile
50 55 60

Met Ala Val Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala
65 70 75 80

30

Asp Leu Ser Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu
85 90 95

Tyr Ala Val Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln
100 105 110

35

Pro Tyr Phe Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr
115 120 125

40

Gly Pro Gln Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly
130 135 140

Val Trp Tyr Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn
145 150 155 160

45

Leu Glu Gly Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser
165 170 175

Gly Lys Gln Gly Ile Leu Leu Glu His Arg Glu Lys Glu Phe Gly Asp
180 185 190

50

Lys Val Asn Leu Leu Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro
195 200 205

55

Gln Thr Leu Ala Ser Glu Lys Lys
210 215

60

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

Met Lys Pro Val Ser Arg Arg Thr Leu Asp Trp Ile Tyr Ser Val Leu
 1 5 10 15

10 Leu Leu Ala Ile Val Leu Ile Ser Trp Gly Cys Ile Ile Tyr Ala Ser
 20 25 30

Met Val Ser Ala Arg Arg Gln Leu Arg Lys Lys Tyr Pro Asp Lys Ile
 35 40 45

15 Phe Gly Thr Asn Glu Asn Leu
 50 55

20

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

25 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

30 Met Ala Ala Asn Thr Phe Val Leu Ile Met Gly Ile Pro Thr Ser Ala
 1 5 10 15

Asn Ala Xaa Arg Asp Leu Phe
 20

35

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

45 Met Ser Ile Cys His Arg Gly Thr Gly Ile Ala Leu Ser Ala Gly Val
 1 5 10 15

Ser Leu Phe Gly Met Ser Ala Leu Leu Leu Pro Gly Asn Phe Glu Ser
 20 25 30

50 Tyr Leu Glu Leu Val Lys Ser Leu Cys Leu Gly Pro Ala Leu Ile His
 35 40 45

Thr Ala Lys Phe Ala Leu Val Phe Pro Leu Met Tyr His Thr Trp Asn
 55 50 55 60

Gly Ile Arg His Leu Met Trp Asp Leu Gly Lys Gly Leu Lys Ile Pro
 65 70 75 80

60 Gln Leu Tyr Gln Ser Gly Val Val Val Leu Val Leu Thr Val Leu Ser

304

85 90 95

Ser Met Gly Leu Ala Ala Met
100

5

(2) INFORMATION FOR SEQ ID NO: 180:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

15

Met Thr Lys Ala Ser Ser Leu Trp Pro Leu Lys Thr Thr Cys Gln Ile
1 5 10 15

20

Ser Gly Thr Val Phe Phe Phe Leu Phe Leu Phe Ser Cys Phe Leu Met
20 25 30

Gln Ala Gln Cys Asp Lys Phe Val Gly Trp Asp Phe Phe Phe Phe Leu
35 40 45

25

30

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

35

Met Arg Arg Ala Leu Ile Pro Pro Cys Arg Gly Gly Pro Ser Ala Ser
1 5 10 15

40

Asp Xaa Cys Cys Ser Cys Ser Pro Ser Gly Phe Ser Ala Gly Arg Gly
20 25 30

45

Arg Cys Pro Val Gln Gly Cys Leu Arg Pro His Arg Val Gln Leu Leu
35 40 45

Arg Arg Trp Gly Pro Gly Ser Pro Ala Gly Gln Arg Leu Ser Lys Gly
50 55 60

50

Phe Gln Leu Leu Arg Trp Trp Gly Pro Gly Ser Pro Ala Pro Glu Pro
65 70 75 80

Arg Lys Gly Pro Phe Pro Pro Pro Asp Pro Pro Trp Pro Val Thr Leu
85 90 95

55

60

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

5 Met Leu Glu Thr Thr Lys His Val Gln Ile Ala Cys Met Leu Leu Leu
 10 1 5 10 15
 Thr Cys Gln Ile Phe Leu Pro Ser Ser Leu Ser Pro Ser Phe Ile His
 20 25 30
 15 Ser Leu Thr Asp Ser Phe Ile Pro Leu Lys Lys Leu Tyr Val Cys Phe
 35 40 45
 Val Gln Ser Thr Leu Leu Lys Ala Ala Gly Tyr Lys Ser Ile Ser Glu
 50 55 60
 20 Ala Leu Gly Phe Asp Xaa Leu Leu Cys Ser Ser Ala Arg Phe Val Trp
 65 70 75 80
 25 Ile Cys His Thr Tyr Ser Arg Pro Leu Val Thr Cys Ala Leu His
 85 90 95

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

30 Met Ser Val Ile Gly Gly Leu Leu Leu Val Val Ala Leu Gly Pro Gly
 1 5 10 15
 40 Gly Val Ser Met Asp Glu Lys Lys Lys Glu Trp
 20 25

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

50 Met Ser Gly Gly Leu Ser Phe Leu Leu Leu Val
 1 5 10
 55

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

306

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

5 Met Phe Ala Asp Phe Ile Val Val Thr Ala Thr Val Gln Arg Cys Pro
 1 5 10 15
 10 Gly Ser Pro Pro Leu Ser Glu Ile Leu Trp Lys Asp Glu Pro Phe Ala
 20 25 30
 Ile Ser Ser His Ala Gly Leu Pro Trp Leu Ser Ser Trp Pro Ala Pro
 35 40 45
 15 Pro Trp Thr Trp Ser Trp Ile Ser Arg Arg Arg Glu His Gly Arg Gly
 50 55 60
 Ser
 65
 20

(2) INFORMATION FOR SEQ ID NO: 186:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

30 Met Val Glu Ser Val Met Pro Val Val Val Cys Thr Leu Ser Pro Gly
 1 5 10 15
 35 Ile Asp Ser Ser Pro Ser
 20

(2) INFORMATION FOR SEQ ID NO: 187:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

Met Asp Val Leu Phe Val Ala Ile Phe Ala Val Pro Leu Ile Leu Gly
 1 5 10 15
 50 Gln Glu Tyr Glu Asp Glu Glu Arg Leu Gly Glu Asp Glu Tyr Tyr Gln
 20 25 30
 Val Val Tyr Tyr Tyr Thr Val Thr Pro Ser Tyr Asp Asp Phe Ser Ala
 35 40 45
 55 Asp Phe Thr Ile Asp Tyr Ser Ile Phe Glu Ser Glu Asp Arg Leu Asn
 50 55 60
 60 Arg Leu Asp Lys Asp Ile Thr Glu Ala Ile Glu Thr Thr Ile Ser Leu
 65 70 75 80

307

Glu Thr Ala Arg Ala Asp His Pro Lys Pro Val Thr Val Lys Pro Val
 85 90 95
 5 Thr Thr Glu Pro Gln Ser Pro Asp Leu Asn Asp Ala Val Ser Ser Leu
 100 105 110
 Arg Ser Pro Ile Pro Leu Leu Leu Ser Cys Ala Phe Val Gln Val Gly
 115 120 125
 10 Met Tyr Phe Met
 130

15

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 amino acids
 20 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

25 Met Pro Cys Gln Pro Gly Gln Val Pro Ser Cys Gln Cys Thr Phe Gly
 1 5 10 15
 Leu Leu Leu Met Leu Pro Ser Leu Pro Ser Pro Ala Ser Gln Pro Arg
 20 25 30
 30 Pro Phe Cys Ser Ser Met Glu Tyr Phe His Gly Cys Ala Ser Pro Ser
 35 40 45
 Gln Ala Ile Ile Gly Gly Phe Pro Phe Ala Ser Val Ala Leu Ala Asp
 50 55 60
 35 Ile Leu Cys Leu Gln
 65

40

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 45 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

50 Met Ser Leu Leu Ser Pro Ala Ile Pro Ala Leu Thr Leu Ile Phe Ile
 1 5 10 15
 Leu Met Phe Phe Ser Phe Pro Phe Arg Ala His Thr Val Val Thr Ile
 20 25 30
 55 Val Ala Ser Gly Phe Leu Gly Leu Ser Pro Leu Cys Gly
 35 40 45

60

(2) INFORMATION FOR SEQ ID NO: 190:

308

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Met Ala Phe Gly Leu Gln Met Phe Ile Gln Arg Lys Phe Pro Tyr Pro
 1 5 10 15
 Leu Gln Trp Ser Leu Leu Val Ala Val Val Ala Gly Ser Val Val Ser
 20 25 30
 Tyr Gly Val Thr Arg Val Glu Ser Glu Lys Cys Asn Asn Leu Trp Leu
 35 40 45
 Phe Leu Glu Thr Gly Gln Leu Pro Lys Asp Arg Ser Thr Asp Gln Arg
 50 55 60
 Ser
 65

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

Met Asn Leu Leu Gly Met Ile Phe Ser Met Cys Gly Leu Met Leu Lys
 1 5 10 15
 Leu Lys Trp Cys Ala Trp Val Ala Val Tyr Cys Ser Phe Ile Ser Phe
 20 25 30
 Ala Asn Ser Arg Ser Ser Glu Asp Thr Lys Gln Met Met Ser Ser Phe
 35 40 45
 Met Xaa
 50

45

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Met Leu Leu Asn Val Ala Leu Val Ala Leu Val Leu Leu Gly Ala Tyr
 1 5 10 15
 Arg Leu Trp Val Arg Trp Gly Arg Arg Gly Leu Gly Ala Gly Ala Gly
 20 25 30

60

309

Ala Gly Glu Glu Ser Pro Ala Thr Ser Leu Pro Arg Met Lys Lys Arg
 35 40 45

5 Asp Phe Ser Leu Glu Gln Leu Arg Gln Tyr Asp Gly Ser Arg Asn Pro
 50 55 60

Arg Ile Leu Leu Ala Val Asn Gly Lys Val Phe Asp Val Thr Lys Gly
 65 70 75 80

10 Ser Lys Phe Tyr Gly Pro Ala Gly Pro Tyr Gly Ile Phe Ala Gly Arg
 85 90 95

Asp Ala Ser Arg Gly Leu Ala Thr Phe Cys Leu Asp Lys Asp Ala Leu
 100 105 110

15 Arg Asp Glu Tyr Asp Asp Leu Ser Asp Leu Asn Ala Val Gln Met Glu
 115 120 125

Ser Val Arg Glu Trp Glu Met Gln Phe Lys Glu Lys Tyr Asp Tyr Val
 20 130 135 140

Gly Arg Leu Leu Lys Pro Gly Glu Glu Pro Ser Glu Tyr Thr Asp Glu
 145 150 155 160

25 Glu Asp Thr Lys Asp His Asn Lys Gln Asp
 165 170

30 (2) INFORMATION FOR SEQ ID NO: 193:

 (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 66 amino acids

 (B) TYPE: amino acid

 (D) TOPOLOGY: linear

35

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

Met Thr Tyr Phe Ser Gly Leu Leu Val Ile Leu Ala Phe Ala Ala Trp
 1 5 10 15

40 Val Ala Leu Ala Glu Gly Leu Gly Val Ala Val Tyr Ala Ala Ala Val
 20 25 30

Leu Leu Gly Ala Gly Cys Ala Thr Ile Leu Val Thr Ser Leu Ala Met
 45 35 40 45

Thr Ala Asp Leu Ile Gly Pro His Thr Asn Ser Gly Leu Ser Cys Thr
 50 55 60

50 Ala Pro
 65

55 (2) INFORMATION FOR SEQ ID NO: 194:

 (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 92 amino acids

 (B) TYPE: amino acid

 (D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

5 Met Ala Ala Gly Pro Ser Gly Cys Leu Val Pro Ala Phe Gly Leu Arg
 1 5 10 15
 Leu Leu Leu Ala Thr Val Leu Gln Ala Val Ser Ala Phe Gly Ala Glu
 20 25 30
 10 Phe Ser Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser Asn Leu Leu
 35 40 45
 Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu Gln Leu Asp
 50 55 60
 15 Pro Asp Cys Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe Glu Thr Lys
 65 70 75 80
 Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val Cys Gly
 85 90
 20

(2) INFORMATION FOR SEQ ID NO: 195:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 176 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

30 Met Arg Gly Ser His Leu Arg Leu Leu Pro Tyr Leu Val Ala Ala Asn
 1 5 10 15
 35 Pro Val Asn Tyr Gly Arg Pro Tyr Arg Leu Ser Cys Val Glu Ala Phe
 20 25 30
 Ala Ala Thr Phe Cys Ile Val Gly Phe Pro Asp Leu Ala Val Ile Leu
 35 40 45
 40 Leu Arg Lys Phe Lys Trp Gly Lys Gly Phe Leu Asp Leu Asn Arg Gln
 50 55 60
 Leu Leu Asp Lys Tyr Ala Ala Cys Gly Ser Pro Glu Glu Val Leu Gln
 65 70 75 80
 45 Ala Glu Gln Glu Phe Leu Ala Asn Ala Lys Glu Ser Pro Gln Glu Glu
 85 90 95
 50 Glu Ile Asp Pro Phe Asp Val Asp Ser Gly Arg Glu Phe Gly Asn Pro
 100 105 110
 Asn Arg Pro Val Ala Ser Thr Arg Leu Pro Ser Asp Thr Asp Asp Ser
 115 120 125
 55 Asp Ala Ser Glu Asp Pro Gly Pro Xaa Ala Glu Arg Gly Gly Ala Ser
 130 135 140
 Ser Ser Cys Cys Glu Glu Glu Gln Thr Gln Gly Arg Gly Ala Glu Ala
 145 150 155 160
 60

311

Arg Ala Pro Ala Glu Val Trp Lys Gly Ile Lys Lys Arg Gln Arg Asp
 165 170 175

5

10 (2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Met Ser Asn Ala Cys Lys Glu Leu Ala Ile Phe Leu Thr Thr Gly Ile
 1 5 10 15
 20 Val Val Ser Ala Phe Gly Leu Pro Ile Val Phe Ala Arg Ala His Leu
 20 25 30
 Ile Glu Trp Gly Ala Cys Ala Leu Val Leu Thr Gly Asn Thr Val Ile
 35 40 45
 25 Phe Ala Thr Ile Leu Gly Phe Phe Leu Val Phe Gly Ser Asn Asp Asp
 50 55 60
 Phe Ser Trp Gln Gln Trp
 30 65 70

35 (2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

Met Thr Leu Leu Ile Ile Phe Leu Pro Phe Xaa Phe Thr Thr Xaa Thr
 1 5 10 15
 45 Asn Ser Gly Gly Ser Phe Pro Val Arg
 20 25

50 (2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Met Lys Gly Glu Leu Leu Pro Phe Leu Phe Leu Thr Val Trp Leu Trp
 1 5 10 15
 60

312

Leu Tyr Lys Leu Xaa Phe Gly Glu Ser Pro Arg Tyr Pro Asn Val Ile
 20 25 30

5 Gly Lys Thr Tyr Phe Phe Phe Trp Thr Asp Gln Ile Ser Arg Glu Ser
 35 40 45

Arg Phe Leu Glu Arg Leu Ala Phe Ile Val Ser Glu Asn Cys Leu Ile
 50 55 60

10 Phe Leu Ile His Ala Ile Thr Gly Gln
 65 70

15 (2) INFORMATION FOR SEQ ID NO: 199:

 (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 289 amino acids

 (B) TYPE: amino acid

20 (D) TOPOLOGY: linear

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

Met Ser Gly Phe Ser Thr Glu Glu Arg Ala Ala Pro Phe Ser Leu Glu
 1 5 10 15

25 Tyr Arg Val Phe Leu Lys Asn Glu Lys Gly Gln Tyr Ile Ser Pro Phe
 20 25 30

30 His Asp Ile Pro Ile Tyr Ala Asp Lys Asp Val Phe His Met Val Val
 35 40 45

Glu Val Pro Arg Trp Ser Asn Ala Lys Met Glu Ile Ala Thr Lys Asp
 50 55 60

35 Pro Leu Asn Pro Ile Lys Gln Asp Val Lys Lys Gly Lys Leu Arg Tyr
 65 70 75 80

Val Ala Asn Leu Phe Pro Tyr Lys Gly Tyr Ile Trp Asn Tyr Gly Ala
 85 90 95

40 Ile Pro Gln Thr Trp Glu Asp Pro Gly His Asn Asp Lys His Thr Gly
 100 105 110

45 Cys Cys Gly Asp Asn Asp Pro Ile Asp Val Cys Glu Ile Gly Ser Lys
 115 120 125

Val Cys Ala Arg Gly Glu Ile Ile Gly Val Lys Val Leu Gly Ile Leu
 130 135 140

50 Ala Met Ile Asp Glu Gly Glu Thr Asp Trp Lys Val Ile Ala Ile Asn
 145 150 155 160

Val Asp Asp Pro Asp Ala Ala Asn Tyr Asn Asp Ile Asn Asp Val Lys
 165 170 175

55 Arg Leu Lys Pro Gly Tyr Leu Glu Ala Thr Val Asp Trp Phe Arg Arg
 180 185 190

60 Tyr Lys Val Pro Asp Gly Lys Pro Glu Asn Glu Phe Ala Phe Asn Ala
 195 200 205

Glu Phe Lys Asp Lys Asp Phe Ala Ile Asp Ile Ile Lys Ser Thr His
 210 215 220
 5 Asp His Trp Lys Ala Leu Val Thr Lys Lys Thr Asn Gly Lys Gly Ile
 225 230 235 240
 Ser Cys Met Asn Thr Thr Leu Ser Glu Ser Pro Phe Lys Cys Asp Pro
 245 250 255
 10 Asp Ala Ala Arg Ala Ile Val Asp Ala Leu Pro Pro Pro Cys Glu Ser
 260 265 270
 Ala Cys Thr Val Pro Thr Asp Val Asp Lys Trp Phe His His Gln Lys
 15 275 280 285
 Asn
 20
 (2) INFORMATION FOR SEQ ID NO: 200:
 (i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 625 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:
 30 Met Glu Ile Pro Gly Ser Leu Cys Lys Lys Val Lys Leu Ser Asn Asn
 1 5 10 15
 Ala Gln Asn Trp Gly Met Gln Arg Ala Thr Asn Val Thr Tyr Gln Ala
 20 25 30
 35 His His Val Ser Arg Asn Lys Arg Gly Gln Val Val Gly Thr Arg Gly
 35 40 45
 Gly Phe Arg Gly Cys Thr Val Trp Leu Thr Gly Leu Ser Gly Ala Gly
 40 50 55 60
 Lys Thr Thr Val Ser Met Ala Leu Glu Glu Tyr Leu Val Cys His Gly
 65 70 75 80
 45 Ile Pro Cys Tyr Thr Leu Asp Gly Asp Asn Ile Arg Gln Gly Leu Asn
 85 90 95
 Lys Asn Leu Gly Phe Ser Pro Glu Asp Arg Glu Glu Asn Val Arg Arg
 100 105 110
 50 Ile Ala Glu Val Ala Lys Leu Phe Ala Asp Ala Gly Leu Val Cys Ile
 115 120 125
 Thr Ser Phe Ile Ser Pro Tyr Thr Gln Asp Arg Asn Asn Ala Arg Gln
 130 135 140
 55 Ile His Glu Gly Ala Ser Leu Pro Phe Phe Glu Val Phe Val Asp Ala
 145 150 155 160
 60 Pro Leu His Val Cys Glu Gln Arg Asp Val Lys Gly Leu Tyr Lys Lys

	165	170	175
	Ala Arg Ala Gly Glu Ile Lys Gly Phe Thr Gly Ile Asp Ser Glu Tyr		
	180	185	190
5	Glu Lys Pro Glu Ala Pro Glu Leu Val Leu Lys Thr Asp Ser Cys Asp		
	195	200	205
10	Val Asn Asp Cys Val Gln Gln Val Val Glu Leu Leu Gln Glu Arg Asp		
	210	215	220
	Ile Val Pro Val Asp Ala Ser Tyr Glu Val Lys Glu Leu Tyr Val Pro		
	225	230	235
15	Glu Asn Lys Leu His Leu Ala Lys Thr Asp Ala Glu Thr Leu Pro Ala		
	245	250	255
	Leu Lys Ile Asn Lys Val Asp Met Gln Trp Val Gln Val Leu Ala Glu		
	260	265	270
20	Gly Trp Ala Thr Pro Leu Asn Gly Phe Met Arg Glu Arg Glu Tyr Leu		
	275	280	285
25	Gln Cys Leu His Phe Asp Cys Leu Leu Asp Gly Gly Val Ile Asn Leu		
	290	295	300
	Ser Val Pro Ile Val Leu Thr Ala Thr His Glu Asp Lys Glu Arg Leu		
	305	310	315
30	Asp Gly Cys Thr Ala Phe Ala Leu Met Tyr Glu Gly Arg Arg Val Ala		
	325	330	335
	Ile Leu Arg Asn Pro Glu Phe Phe Glu His Arg Lys Glu Glu Arg Cys		
	340	345	350
35	Ala Arg Gln Trp Gly Thr Thr Cys Lys Asn His Pro Tyr Ile Lys Met		
	355	360	365
40	Val Met Glu Gln Gly Asp Trp Leu Ile Gly Gly Asp Leu Gln Val Leu		
	370	375	380
	Asp Arg Val Tyr Trp Asn Asp Gly Leu Asp Gln Tyr Arg Leu Thr Pro		
	385	390	395
45	Thr Glu Leu Lys Gln Lys Phe Lys Asp Met Asn Ala Asp Ala Val Phe		
	405	410	415
	Ala Phe Gln Leu Arg Asn Pro Val His Asn Gly His Ala Leu Leu Met		
	420	425	430
50	Gln Asp Thr His Lys Gln Leu Leu Glu Arg Gly Tyr Arg Arg Pro Val		
	435	440	445
55	Leu Leu Leu His Pro Leu Gly Gly Trp Thr Lys Asp Asp Asp Val Pro		
	450	455	460
	Leu Met Trp Arg Met Lys Gln His Ala Ala Val Leu Glu Glu Gly Val		
	465	470	475
60	Leu Asn Pro Glu Thr Thr Val Val Ala Ile Phe Pro Ser Pro Met Met		

315

485 490 495
 Tyr Ala Gly Pro Thr Glu Val Gln Trp His Cys Arg Ala Arg Met Val
 500 505 510
 5 Ala Gly Ala Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met Pro
 515 520 525
 10 His Pro Glu Thr Gly Lys Asp Leu Tyr Glu Pro Ser His Gly Ala Lys
 530 535 540
 Val Leu Thr Met Ala Pro Gly Leu Ile Thr Leu Glu Ile Val Pro Phe
 545 550 555 560
 15 Arg Val Ala Ala Tyr Asn Lys Lys Lys Lys Arg Met Asp Tyr Tyr Asp
 565 570 575
 Ser Glu His His Glu Asp Phe Glu Phe Ile Ser Gly Thr Arg Met Arg
 580 585 590
 20 Lys Leu Ala Arg Glu Gly Gln Lys Pro Pro Glu Gly Phe Met Ala Pro
 595 600 605
 25 Lys Ala Trp Thr Val Leu Thr Glu Tyr Tyr Lys Ser Leu Glu Lys Ala
 610 615 620
 Xaa
 625

30

(2) INFORMATION FOR SEQ ID NO: 201:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 649 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

40 Met Ser Ala Ser Gln Asp Leu Glu Pro Lys Pro Leu Phe Pro Lys Pro
 1 5 10 15
 Ala Phe Gly Gln Lys Pro Pro Leu Ser Thr Glu Asn Ser His Glu Asp
 20 25 30
 45 Glu Ser Pro Met Lys Asn Val Ser Ser Ser Lys Gly Ser Pro Ala Pro
 35 40 45
 50 Leu Gly Val Arg Ser Lys Ser Gly Pro Leu Lys Pro Ala Arg Glu Asp
 50 55 60
 Ser Glu Asn Lys Asp His Ala Gly Glu Ile Ser Ser Leu Pro Phe Pro
 65 70 75 80
 55 Gly Val Val Leu Lys Pro Ala Ala Ser Arg Gly Gly Pro Gly Leu Ser
 85 90 95
 Lys Asn Gly Glu Glu Lys Lys Glu Asp Arg Lys Ile Asp Ala Ala Lys
 100 105 110

60

316

Asn Thr Phe Gln Ser Lys Ile Asn Gln Glu Glu Leu Ala Ser Gly Thr
 115 120 125
 5 Pro Pro Ala Arg Phe Pro Lys Ala Pro Ser Lys Leu Thr Val Gly Gly
 130 135 140
 Pro Trp Gly Gln Ser Gln Glu Lys Glu Lys Gly Asp Lys Asn Ser Ala
 145 150 155 160
 10 Thr Pro Lys Gln Lys Pro Leu Pro Pro Leu Phe Thr Leu Gly Pro Pro
 165 170 175
 Pro Pro Lys Pro Asn Arg Pro Pro Asn Val Asp Leu Thr Lys Phe His
 180 185 190
 15 Lys Thr Ser Ser Gly Asn Ser Thr Ser Lys Gly Gln Thr Ser Tyr Ser
 195 200 205
 20 Thr Thr Ser Leu Pro Pro Pro Pro Pro Ser His Pro Ala Ser Gln Pro
 210 215 220
 Pro Leu Pro Ala Ser His Pro Ser Gln Pro Pro Val Pro Ser Leu Pro
 225 230 235 240
 25 Pro Arg Asn Ile Lys Pro Pro Phe Asp Leu Lys Ser Pro Val Asn Glu
 245 250 255
 Asp Asn Gln Asp Gly Val Thr His Ser Asp Gly Ala Gly Asn Leu Asp
 260 265 270
 30 Glu Glu Gln Asp Ser Glu Gly Glu Thr Tyr Glu Asp Ile Glu Ala Ser
 275 280 285
 35 Lys Glu Arg Glu Lys Lys Arg Glu Lys Glu Glu Lys Lys Arg Leu Glu
 290 295 300
 Leu Glu Lys Lys* Glu Gln Lys Glu Lys Glu Lys Lys Glu Gln Glu Ile
 305 310 315 320
 40 Lys Lys Lys Phe Lys Leu Thr Gly Pro Ile Gln Val Ile His Leu Ala
 325 330 335
 Lys Ala Cys Cys Asp Val Lys Gly Gly Lys Asn Glu Leu Ser Phe Lys
 340 345 350
 45 Gln Gly Glu Gln Ile Glu Ile Ile Arg Ile Thr Asp Asn Pro Glu Gly
 355 360 365
 50 Lys Trp Leu Gly Arg Thr Ala Arg Gly Ser Tyr Gly Tyr Ile Lys Thr
 370 375 380
 Thr Ala Val Glu Ile Asp Tyr Asp Ser Leu Lys Leu Lys Lys Asp Ser
 385 390 395 400
 55 Leu Gly Ala Pro Ser Arg Pro Ile Glu Asp Asp Gln Glu Val Tyr Asp
 405 410 415
 Asp Val Ala Glu Gln Asp Asp Ile Ser Ser His Ser Gln Ser Gly Ser
 420 425 430
 60

317

Gly Gly Ile Phe Pro Pro Pro Pro Asp Asp Asp Ile Tyr Asp Gly Ile
 435 440 445
 5 Glu Glu Glu Asp Ala Asp Asp Gly Ser Thr Leu Gln Val Gln Glu Lys
 450 455 460
 Ser Asn Thr Trp Ser Trp Gly Ile Leu Lys Met Leu Lys Gly Lys Asp
 465 470 475 480
 10 Asp Arg Lys Lys Ser Ile Arg Glu Lys Pro Lys Val Ser Asp Ser Asp
 485 490 495
 Asn Asn Glu Gly Ser Ser Phe Pro Ala Pro Pro Lys Gln Leu Asp Met
 500 505 510
 15 Gly Asp Glu Val Tyr Asp Asp Val Asp Thr Ser Asp Phe Pro Val Ser
 515 520 525
 Ser Ala Glu Met Ser Gln Gly Thr Asn Val Gly Lys Ala Lys Thr Glu
 20 530 535 540
 Glu Lys Asp Leu Lys Lys Leu Lys Lys Gln Xaa Lys Xaa Xaa Lys Asp
 545 550 555 560
 25 Phe Arg Lys Lys Phe Lys Tyr Asp Gly Glu Ile Arg Val Leu Tyr Ser
 565 570 575
 Thr Lys Val Thr Thr Ser Ile Thr Ser Lys Lys Trp Gly Thr Arg Asp
 580 585 590
 30 Leu Gln Val Lys Pro Gly Glu Ser Leu Glu Val Ile Gln Thr Thr Asp
 595 600 605
 Asp Thr Lys Val Leu Cys Arg Asn Glu Glu Gly Lys Tyr Gly Tyr Val
 35 610 615 620
 Leu Arg Ser Tyr Leu Ala Asp Asn Asp Gly Glu Ile Tyr Asp Asp Ile
 625 630 635 640
 40 Ala Asp Gly Cys Ile Tyr Asp Asn Asp
 645

45 (2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Met Ala Trp Pro Ser Arg Ser Lys Met Phe Thr Leu Leu Pro Val Leu
 1 5 10 15
 55 Cys Tyr Leu Trp Ser Leu Trp Leu Pro Gln Phe Ser Trp Ile Gln Glu
 20 25 30
 Leu Lys Ala Val Leu Arg Asp Asp Gly Leu Ile Ser Ala Val Ala Trp
 60 35 40 45

Asn Ala Glu Phe Gln Thr Cys
50 55

5

(2) INFORMATION FOR SEQ ID NO: 203:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

15

Met Val Lys Val Thr Phe Asn Ser Ala Leu Ala Gln Lys Glu Ala Lys
1 5 10 15

Lys Asp Glu Pro Lys Ser Gly Glu Glu Ala Leu Ile Ile Pro Pro Asp
20 25 30

20

Ala Val Ala Val Asp Cys Lys Asp Pro Asp Asp Val Val Pro Val Gly
35 40 45

25

Gln Arg Arg Ala Trp Cys Trp Cys Met Cys Phe Gly Leu Ala Phe Met
50 55 60

Leu Ala Gly Val Ile Leu Gly Gly Ala Tyr Leu Tyr Lys Tyr Phe Ala
65 70 75 80

30

Leu Gln Pro Asp Asp Val Tyr Tyr Cys Gly Ile Lys Tyr Ile Lys Asp
85 90 95

Asp Val Ile Leu Asn Glu Pro Ser Ala Asp Ala Pro Ala Ala Leu Tyr
100 105 110

35

Gln Thr Ile Glu Glu Asn Ile Lys Ile Phe Glu Glu Glu Glu Val Glu
115 120 125

40

Phe Ile Ser Val Pro Val Pro Glu Phe Ala Asp Ser Asp Pro Ala Asn
130 135 140

Ile Val His Asp Phe Asn Lys Lys Leu Thr Ala Tyr Leu Asp Leu Asn
145 150 155 160

45

Leu Asp Lys Cys Tyr Val Ile Pro Leu Asn Thr Ser Ile Val Met Pro
165 170 175

Pro Arg Asn Leu Leu Glu Leu Leu Ile Asn Ile Lys Ala Gly Thr Tyr
180 185 190

50

Leu Pro Gln Ser Tyr Leu Ile His Glu His Met Val Ile Thr Asp Arg
195 200 205

55

Ile Glu Asn Ile Asp His Leu Gly Phe Phe Ile Tyr Arg Leu Cys His
210 215 220

Asp Lys Glu Thr Tyr Lys Leu Gln Arg Arg Glu Thr Ile Lys Gly Ile
225 230 235 240

60

Gln Lys Arg Glu Ala Ser Asn Cys Phe Ala Ile Arg His Phe Glu Asn

245 250 255

Lys Phe Ala Val Glu Thr Leu Ile Cys Ser Xaa
260 265

5

(2) INFORMATION FOR SEQ ID NO: 204:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe
1 5 10 15
Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro
20 25 30
Gln Leu Ser Asp Lys Val His Asn Asp Ala Gln Ser Phe Asp Tyr Asp
35 40 45
His Asp Ala Phe Leu Gly Ala Glu Glu Ala Lys Thr Phe Asp Gln Leu
50 55 60
Thr Pro Glu Glu Ser Lys Glu Arg Leu Gly Lys Ile Val Ser Lys Ile
65 70 75 80
Asp Gly Asp Lys Asp Gly Phe Val Thr Val Asp Glu Leu Lys Asp Trp
85 90 95
Ile Lys Phe Ala Gln Lys Arg Trp Ile Tyr Glu Asp Val Glu Arg Gln
100 105 110
Trp Lys Gly His Asp Leu Asn Glu Asp Gly Leu Val Ser Trp Glu Glu
115 120 125
Tyr Lys Asn Ala Thr Tyr Gly Tyr Val Leu Asp Asp Pro Asp Pro Asp
130 135 140
Asp Gly Phe Asn Tyr Lys Gln Met Met Val Arg Asp Glu Arg Arg Phe
145 150 155 160
Lys Met Ala Asp Lys Asp Gly Asp Leu Ile Ala Thr Lys Glu Glu Phe
165 170 175
Thr Ala Phe Leu His Pro Glu Glu Tyr Asp Tyr Met Lys Asp Ile Val
180 185 190
Val Gln Glu Thr Met Glu Asp Ile Asp Lys Asn Ala Asp Gly Phe Ile
195 200 205
Asp Leu Glu Glu Tyr Ile Gly Asp Met Tyr Ser His Asp Gly Asn Thr
210 215 220
Asp Glu Pro Glu Trp Val Lys Thr Glu Arg Glu Gln Phe Val Glu Phe
225 230 235 240

60

320

	Arg	Asp	Lys	Asn	Arg	Asp	Gly	Lys	Met	Asp	Lys	Glu	Glu	Thr	Lys	Asp
				245						250					255	
5	Trp	Ile	Leu	Pro	Ser	Asp	Tyr	Asp	His	Ala	Glu	Ala	Glu	Ala	Arg	His
				260					265						270	
	Leu	Val	Tyr	Glu	Ser	Asp	Gln	Asn	Lys	Asp	Gly	Lys	Leu	Thr	Lys	Glu
			275					280					285			
10	Glu	Ile	Val	Asp	Lys	Tyr	Asp	Leu	Phe	Val	Gly	Ser	Gln	Ala	Thr	Asp
		290					295					300				
	Phe	Gly	Glu	Ala	Leu	Val	Arg	His	Asp	Glu	Phe					
15	305					310					315					

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

Met Phe Asp Ala Val Leu Ile Leu Leu Leu Ile Pro Leu Lys Asp Lys
1 5 10 15
Leu Val Asp Pro Ile Leu Arg Arg His Gly Leu Leu Pro Ser Ser Leu
20 25 30
Lys Arg Ile Ala Val Gly Met Phe Phe Val Met Cys Ser Ala Phe Ala
35 40 45
Ala Gly Ile Leu Glu Ser Lys Arg Leu Asn Leu Val Lys Glu Lys Thr
50 55 60
Ile Asn Gln Thr Ile Gly Asn Val Val Tyr His Ala Ala Asp Leu Ser
65 70 75 80
Leu Trp Trp Gln Val Pro Gln Tyr Leu Leu Ile Gly Ile Ser Glu Ile
85 90 95
Phe Ala Ser Ile Ala Gly Leu Glu Phe Ala Tyr Ser Ala Ala Pro Lys
100 105 110
Ser Met Gln Ser Ala Ile Met Gly Leu Phe Phe Phe Phe Ser Gly Val
115 120 125
Gly Ser Phe Val Gly Ser Gly Leu Leu Ala Leu Val Ser Ile Lys Ala
130 135 140
Ile Gly Trp Met Ser Ser His Thr Asp Phe Gly Asn Ile Asn Gly Cys
145 150 155 160
Tyr Leu Asn Tyr Tyr Phe Phe Leu Leu Ala Ala Ile Gln Gly Ala Thr
165 170 175
Leu Leu Leu Phe Leu Ile Ile Ser Val Lys Tyr Asp His His Arg Asp
180 185 190

321

His Gln Arg Ser Arg Ala Asn Gly Val Pro Thr Ser Arg Arg Ala
 195 200 205

5

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

15 Met Arg Ser Arg Ile Arg Glu Phe Asp Ser Ser Thr Leu Asn Glu Ser
 1 5 10 15
 Val Arg Asn Thr Ile Met Arg Asp Leu Lys Ala Val Gly Lys Lys Phe
 20 20 25 30
 Met His Val Leu Tyr Pro Arg Lys Ser Asn Thr Leu Leu Arg Asp Trp
 35 40 45
 Asp Leu Trp Gly Pro Leu Ile Leu Cys Val Thr Leu Ala Leu Met Leu
 25 50 55 60
 Gln Arg Asp Ser Ala Asp Ser Glu Lys Asp Gly Gly Pro Gln Phe Ala
 65 70 75 80
 30 Glu Val Phe Val Ile Val Trp Phe Gly Ala Val Thr Ile Thr Leu Asn
 85 90 95
 Ser Lys Leu Leu Gly Gly Asn Ile Ser Phe Phe Gln Ser Leu Cys Val
 100 105 110
 35 Leu Gly Tyr Cys Ile Leu Pro Leu Thr Val Ala Met Leu Ile Cys Arg
 115 120 125
 Leu Val Leu Leu Ala Asp Pro Gly Pro Val Asn Phe Met Val Arg Leu
 40 130 135 140
 Phe Val Val Ile Val Met Phe Ala Trp Ser Ile Val Ala Ser Thr Ala
 145 150 155 160
 45 Phe Leu Ala Asp Ser Gln Pro Pro Asn Arg Arg Ala Leu Ala Val Tyr
 165 170 175
 Pro Val Phe Leu Phe Tyr Phe Val Ile Ser Trp Met Ile Leu Thr Phe
 180 185 190
 50 Thr Pro Gln Xaa
 195

55

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 amino acids
 (B) TYPE: amino acid

60

322

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

5 Met Ala Lys Asp Gln Ala Val Glu Asn Ile Leu Val Ser Pro Val Val
 1 5 10 15
 Val Ala Ser Ser Leu Gly Leu Val Ser Leu Gly Gly Lys Ala Thr Thr
 20 25 30
 10 Ala Ser Gln Ala Lys Ala Val Leu Ser Ala Glu Gln Leu Arg Asp Glu
 35 40 45
 Glu Val His Ala Gly Leu Gly Glu Leu Leu Arg Ser Leu Ser Asn Ser
 50 55 60
 15 Thr Ala Arg Asn Val Thr Trp Lys Leu Gly Ser Arg Leu Tyr Gly Pro
 65 70 75 80
 Ser Ser Val Ser Phe Ala Asp Asp Phe Val Arg Ser Ser Lys Gln His
 85 90 95
 Tyr Asn Cys Glu His Ser Lys Ile Asn Phe Arg Asp Lys Arg Ser Ala
 100 105 110
 25 Leu Gln Ser Ile Asn Glu Trp Ala Ala Gln Thr Thr Asp Gly Lys Leu
 115 120 125
 Pro Glu Val Thr Lys Asp Val Glu Arg Thr Asp Gly Ala Leu Leu Val
 130 135 140
 30 Asn Ala Met Phe Phe Lys Pro His Trp Asp Glu Lys Phe His His Lys
 145 150 155 160
 Met Val Asp Asn Arg Gly Phe Met Val Thr Arg Ser Tyr Thr Val Gly
 165 170 175
 Val Met Met Met His Arg Thr Gly Leu Tyr Asn Tyr Tyr Asp Asp Glu
 180 185 190
 40 Lys Glu Lys Leu Gln Ile Val Glu Met Pro Leu Ala His Lys Leu Ser
 195 200 205
 Ser Leu Ile Ile Leu Met Pro His His Val Glu Pro Leu Glu Arg Leu
 210 215 220
 45 Glu Lys Leu Leu Thr Lys Glu Gln Leu Lys Ile Trp Met Gly Lys Met
 225 230 235 240
 Gln Lys Lys Ala Val Ala Ile Ser Leu Pro Lys Gly Val Val Glu Val
 245 250 255
 50 Thr His Asp Leu Gln Lys His Leu Ala Gly Leu Gly Leu Thr Glu Ala
 260 265 270
 55 Ile Asp Lys Asn Lys Ala Asp Leu Ser Arg Met Ser Gly Lys Lys Asp
 275 280 285
 Leu Tyr Leu Ala Ser Val Phe His Ala Thr Ala Phe Glu Leu Asp Thr
 290 295 300
 60

323

Asp Gly Asn Pro Leu Thr Arg Ile Thr Gly Gly Gly Val Arg Thr Gln
 305 310 315 320

5 Val Phe Tyr Ala Asp His Pro Phe Ile Ser Xaa
 325 330

10 (2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

Met Cys Met Gln Leu Phe Gly Phe Leu Ala Phe Met Ile Phe Met Cys
 1 5 10 15

20 Trp Val Gly Asp Val Tyr Pro Val Tyr Gln Pro Val Gly Pro Lys Gln
 20 25 30

Tyr Pro Tyr Asn Asn Leu Tyr Leu Glu Arg Gly Gly Asp Pro Ser Lys
 35 40 45

25 Glu Pro Glu Arg Val Val His Tyr Glu Ile
 50 55

30 (2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 392 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

40 Met Asp Ala Leu Val Glu Asp Asp Ile Cys Ile Leu Asn His Glu Lys
 1 5 10 15

Ala His Lys Arg Asp Thr Val Thr Pro Val Ser Ile Tyr Ser Gly Asp
 20 25 30

45 Glu Ser Val Ala Ser His Phe Ala Leu Val Thr Ala Tyr Glu Asp Ile
 35 40 45

Lys Lys Arg Leu Lys Asp Ser Glu Lys Glu Asn Ser Leu Leu Lys Lys
 50 55 60

50 Arg Ile Arg Phe Leu Glu Glu Lys Leu Ile Ala Arg Phe Glu Glu Glu
 65 70 75 80

55 Thr Ser Ser Val Gly Arg Glu Gln Val Asn Lys Ala Tyr His Ala Tyr
 85 90 95

Arg Glu Val Cys Ile Asp Arg Asp Asn Leu Lys Ser Lys Leu Asp Lys
 100 105 110

60 Met Asn Lys Asp Asn Ser Glu Ser Leu Lys Val Leu Asn Glu Gln Leu

324

	115	120	125
	Gln Ser Lys Glu Val Glu Leu Leu Gln Leu Arg Thr Glu Val Glu Thr		
	130	135	140
5	Gln Gln Val Met Arg Asn Leu Asn Pro Pro Ser Ser Asn Trp Glu Val		
	145	150	155 160
10	Glu Lys Leu Ser Cys Asp Leu Lys Ile His Gly Leu Glu Gln Glu Leu		
	165	170	175
	Glu Leu Met Arg Lys Glu Cys Ser Asp Leu Lys Ile Glu Leu Gln Lys		
	180	185	190
15	Ala Lys Gln Thr Asp Pro Tyr Gln Glu Asp Asn Leu Lys Ser Arg Asp		
	195	200	205
	Leu Gln Lys Leu Ser Ile Ser Ser Asp Asn Met Gln His Ala Tyr Trp		
	210	215	220
20	Glu Leu Lys Arg Glu Met Ser Asn Leu His Leu Val Thr Gln Val Gln		
	225	230	235 240
25	Ala Glu Leu Leu Arg Lys Leu Lys Thr Ser Thr Ala Ile Lys Lys Ala		
	245	250	255
	Cys Ala Pro Val Gly Cys Ser Glu Asp Leu Gly Arg Asp Ser Thr Lys		
	260	265	270
30	Leu His Leu Met Asn Phe Thr Ala Thr Tyr Thr Arg His Pro Pro Leu		
	275	280	285
	Leu Pro Asn Gly Lys Ala Leu Cys His Thr Thr Ser Ser Pro Leu Pro		
	290	295	300
35	Gly Asp Val Lys Val Leu Ser Glu Lys Ala Ile Leu Gln Ser Trp Thr		
	305	310	315 320
40	Asp Asn Glu Arg Ser Ile Pro Asn Asp Gly Thr Cys Phe Gln Glu His		
	325	330	335
	Ser Ser Tyr Gly Arg Asn Ser Leu Glu Asp Asn Ser Trp Val Phe Pro		
	340	345	350
45	Ser Pro Pro Lys Ser Ser Glu Thr Ala Phe Gly Glu Thr Lys Thr Lys		
	355	360	365
	Thr Leu Pro Leu Pro Asn Leu Pro Pro Leu His Tyr Leu Asp Gln His		
	370	375	380
50	Asn Gln Asn Cys Leu Tyr Lys Asn		
	385	390	

55

(2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

60

325

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

5 Met His His His Thr Gln Leu Met Phe Ile Tyr Leu Phe Ile Tyr Leu
 1 5 10 15
 Phe Ile Leu Gly Val Phe Phe Phe Phe Phe Xaa
 20 25

10

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

20 Met Asn Cys Ile Leu Leu Leu Tyr Leu Leu Ile Pro Thr Ile Ser Ile
 1 5 10 15
 Ser Val Val Pro Tyr Val Ala Leu Asn Ile Lys Tyr Ile Lys Glu Cys
 20 25 30
 25 Thr Glu Asn Ser Phe Tyr Xaa
 35

30

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

40 Met Leu Leu His Leu Thr Ala Ala Phe Leu Gln Arg Ala Gln Phe Ser
 1 5 10 15
 Thr Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val
 20 25 30
 45 Phe Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr
 35 40 45
 Ala Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr
 50 55 60
 50 Arg Val Leu Phe Ile Tyr Xaa
 65 70

55

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

326

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

5 Met Leu Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe
 1 5 10 15
 Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile
 20 25 30
 10 Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe
 35 40 45
 Ser Thr Tyr Phe Pro Ala Phe Met Asn Ser Leu Ser Arg Ser Lys Arg
 50 55 60
 15 Thr Pro Ala Gly Ser Glu Ser Arg Cys Arg Thr Gln Arg Asn Asn His
 65 70 75 80
 Leu Leu Xaa
 20

(2) INFORMATION FOR SEQ ID NO: 214:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

Met Ser Lys Arg Ser Ala Ser Phe Ile Leu Leu Pro Leu Leu Phe Leu
 1 5 10 15
 35 Lys Gly Ser Phe Ala Lys Leu Asn Ala Arg Ile Ser Asp Cys Leu Glu
 20 25 30
 Glu Arg Tyr Cys His Asn Leu Trp Met Val Phe Gln Gly Cys Val Ile
 35 40 45
 40 Thr Glu Leu His Leu Ser Arg Met Ser Lys Thr Leu Ser Ser Leu Cys
 50 55 60
 Tyr Asp Phe Val Ile Asn Val Tyr Ile Phe Phe Lys Phe Leu Asp Ile
 45 65 70 75 80
 Thr

50

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

60 Met Cys Ser Leu Phe Glu Ser Arg Phe Phe Cys Phe Val Leu Phe Ser

327

1 5 10 15

Glu Lys Ile Ile Gln Leu Cys Ala Ser Ile Ala Phe Leu Cys Phe Val
20 25 30

5

Lys His Val Pro Trp Pro Lys Trp Lys Arg Lys Cys Leu Ile Asn Ala
35 40 45

10

Phe

15 (2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

	Met	Thr	Leu	Arg	Pro	Ser	Leu	Leu	Pro	Leu	His	Leu	Leu	Leu	Leu	Leu
	1				5					10					15	
25	Leu	Leu	Ser	Ala	Ala	Val	Cys	Arg	Ala	Glu	Ala	Gly	Leu	Glu	Thr	Glu
				20					25					30		
	Ser	Pro	Val	Arg	Thr	Leu	Gln	Val	Glu	Thr	Leu	Val	Glu	Pro	Pro	Glu
			35					40					45			
30	Pro	Cys	Ala	Glu	Pro	Ala	Ala	Phe	Gly	Asp	Thr	Leu	His	Ile	His	Tyr
		50					55					60				
	Thr	Gly	Ser	Leu	Val	Asp	Gly	Arg	Ile	Ile	Asp	Thr	Ser	Leu	Thr	Arg
	65					70					75					80
	Asp	Pro	Leu	Val	Ile	Glu	Leu	Gly	Gln	Lys	Gln	Val	Ile	Pro	Gly	Leu
					85					90					95	
40	Glu	Gln	Ser	Leu	Leu	Asp	Met	Cys	Val	Gly	Glu	Lys	Arg	Arg	Ala	Ile
				100					105					110		
	Ile	Pro	Ser	His	Leu	Ala	Tyr	Gly	Lys	Arg	Gly	Phe	Pro	Pro	Ser	Val
			115					120					125			
45	Pro	Ala	Asp	Ala	Val	Val	Gln	Tyr	Asp	Val	Glu	Leu	Ile	Ala	Leu	Ile
		130					135					140				
	Arg	Ala	Asn	Tyr	Trp	Leu	Lys	Leu	Val	Lys	Gly	Ile	Leu	Pro	Leu	Val
	145					150					155					160
	Gly	Met	Ala	Met	Val	Pro	Pro	Ser	Trp	Ala	Ser	Leu	Gly	Ile	Thr	Tyr
				165						170					175	
55	Thr	Glu	Arg	Pro	Ile	Asp	Pro	Lys	Ser	Pro	Lys	Arg	Ser	Ser	Arg	Lys
				180					185					190		
	Arg	Asn	Glu	Thr	Arg	Ala	Lys	Arg	Asn	Asn	Lys					
			195					200								

(2) INFORMATION FOR SEQ ID NO: 217:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

10

Met Lys Thr Leu Met Thr Ile Cys Pro Gly Thr Val Leu Leu Val Phe
 1 5 10 15

15

Ser Ile Ser Leu Trp Ile Ile Ala Ala Trp Thr Val Arg Val Cys Glu
 20 25 30

Ser Pro Glu Ser Pro Ala Gln Pro Ser Gly Ser Ser Leu Pro Ala Trp
 35 40 45

20

Tyr His Asp Gln Gln Asp Val Thr Ser Asn Phe Leu Gly Ala Met Trp
 50 55 60

25

Leu Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr Gly Asp Met Val Pro
 65 70 75 80

His Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu Thr Gly Ile Met Gly
 85 90 95

30

Ala Gly Cys Thr Ala Leu Val Val Ala Val Val Ala Arg Lys Leu Glu
 100 105 110

Leu Thr Lys Ala Glu Lys His Val His Xaa Phe Met Met Asp Thr Gln
 115 120 125

35

Leu Thr Lys Arg Ile Lys Asn Xaa Ala Ala Asn Val Leu Xaa Glu Thr
 130 135 140

40

Trp Leu Ile Tyr Lys His Thr Lys Leu Leu Lys Lys Ile Asp His Ala
 145 150 155 160

Lys Val Arg Asn Thr Arg Gly Ser Ser Ser Lys Tyr Pro Pro Val Glu
 165 170 175

45

Glu Arg Gln Asp Gly Thr Glu Glu Ala Glu
 180 185

(2) INFORMATION FOR SEQ ID NO: 218:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile Phe Leu
 1 5 10 15

60

Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr Tyr Pro

329

20 25 30

Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu Thr Thr Ala
35 40 45

5 Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr Ala Thr Thr Ala
50 55 60

10 Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val Leu Pro Lys Trp Val
65 70 75 80

Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
85 90

15

(2) INFORMATION FOR SEQ ID NO: 219:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

25 Met Ser Ser Ala Ala Ala Asp His Trp Ala Trp Leu Leu Val Leu Ser
1 5 10 15

Phe Val Phe Gly Cys Asn Val Leu Arg Ile Leu Leu Pro Ser Phe Ser
20 25 30

30 Ser Phe Met Ser Arg Val Leu Gln Lys Asp Ala Glu Gln Glu Ser Gln
35 40 45

35 Met Arg Ala Glu Ile Gln Asp Met Lys Gln Glu Leu Ser Thr Val Asn
50 55 60

Met Met Asp Glu Phe Ala Arg Tyr Ala Arg Leu Glu Arg Lys Ile Asn
65 70 75 80

40 Lys Met Thr Asp Lys Leu Lys Thr His Val Lys Ala Arg Thr Ala Gln
85 90 95

Leu Ala Lys Ile Lys Trp Val Ile Ser Val Ala Phe Tyr Val Leu Gln
100 105 110

45 Ala Ala Leu Met Ile Ser Leu Ile Trp Lys Tyr Tyr Ser Val Pro Val
115 120 125

Ala Val Val Pro Ser Lys Trp Ile Thr Leu Xaa
130 135

50

(2) INFORMATION FOR SEQ ID NO: 220:

55

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

330

Met Ser Ser Ala Ala Ala Asp His Trp Ala Trp Leu Leu Val Leu Ser
 1 5 10 15
 5 Phe Val Phe Gly Cys Asn Val Leu Arg Ile Leu Leu Pro Ser Phe Ser
 20 25 30
 Ser Phe Met Ser Arg Val Leu Gln Lys Asp Ala Asp Arg Ser His Arg
 35 40 45

10

15

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

20

25

Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe Leu Ile
 1 5 10 15

Val Phe Phe Ser Leu Gly Val Phe Cys Ile Cys His Ser His Trp Tyr
 20 25 30

30

His Thr Leu Gln Gln Met Ala Gly Thr Glu Pro Lys Ala Leu Leu Leu
 35 40 45

Ser Pro Pro Ala Ala Thr Thr Phe Val Thr Val Thr His Glu Val Trp
 50 55 60

35

Lys Glu Gln Ala Leu Ala
 65 70

40

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

45

50

Met Thr Cys Ser Val Ala Leu Leu Leu Ile Leu Gly Leu Arg Cys Ser
 1 5 10 15

Gly Val Arg Pro Gly Leu Val Gly Glu Gly His Asn Pro Ser Leu Leu
 20 25 30

55

Val Cys Leu Leu Leu Lys Asp Ser Arg Thr Asn Gln Gly Ser Cys Pro
 35 40 45

Gly Gly Pro Trp Ser Glu Arg Asp Ile Glu Ser Val Thr Ser Asp Asn
 50 55 60

60

Cys Glu Ala Thr Leu Gly Tyr Arg Asn His Ser Leu Pro Ser Asn Tyr
 65 70 75 80

Tyr Asn Ser

5

(2) INFORMATION FOR SEQ ID NO: 223:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

Met Leu Thr Arg Ser Leu Lys Thr Leu Pro Ser Ala Cys Thr Ala Phe
 1 5 10 15

20

Leu Leu Leu Phe Phe Leu Phe Ser Ser Gly Asp Pro Glu Leu Ser Cys
 20 25 30

Ser Cys Thr Leu Arg Thr Gln Ser Ser Trp Ser
 35 40

25

(2) INFORMATION FOR SEQ ID NO: 224:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

35

Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His Gly
 1 5 10 15

40

Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly Arg
 20 25 30

Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala His
 35 40 45

45

Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val Ala
 50 55 60

50

Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu Gly
 65 70 75 80

Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp Val
 85 90 95

55

Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg His
 100 105 110

Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp Arg
 115 120 125

60

Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Xaa Thr Tyr Gly His

332

130 135 140

Xaa Xaa Pro Xaa Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr Tyr
 145 150 155 160

5 Lys Lys Met Leu Xaa Arg Asp Glu Arg Arg Phe Arg Val Ala Asp Gln
 165 170 175

Asp Gly Asp Ser Met Ala Thr Arg
 10 180

(2) INFORMATION FOR SEQ ID NO: 225:

15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

Met Trp Leu Phe Ile Leu Leu Ser Leu Ala Leu Ile Ser Asp Ala Met
 1 5 10 15

25 Val Met Asp Glu Lys Val Lys Arg Ser Leu Cys Trp Thr Arg Leu Leu
 20 25 30

Pro Ser Ala Thr Thr Met Pro Xaa Thr Arg Ile Thr Pro Asn Thr Gly
 35 40 45

30 Ala Glu Xaa Ile Ser Val Xaa Thr Ala Thr Ser Ser Pro Ser Pro Leu
 50 55 60

Thr Ala Pro Ile Met Trp Pro
 35 65 70

(2) INFORMATION FOR SEQ ID NO: 226:

40

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

Met His Val Phe Val Leu Glu Ile Phe Leu
 1 5 10

50

(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 138 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

60 Met Ala Val Ala Thr Leu Ala Ser Glu Thr Leu Pro Leu Leu Ala Leu

333

[illegible]

(2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

Leu Gly Ser Leu Ser Thr Ala Pro Ser Ser Ala Leu Pro Thr Leu Gly
1 5 10 15

40 Ala Arg Arg Thr Arg Ser Lys
20

45 (2) INFORMATION FOR SEQ ID NO: 229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

55 Met Thr Tyr Phe Ser Gly Leu Leu Val Ile Leu Ala Phe Ala Ala Trp
1 5 10 15

Val Ala Leu Ala Glu Gly Leu Gly Val Ala Val Tyr Ala Ala Ala Val
20 25 30

60 Leu Leu Gly Ala Gly Cys Ala Thr Ile Leu Val Thr Ser Leu Ala Met
35 40 45

334

Thr Ala Asp Leu Ile Gly Pro His Thr Asn Ser Gly Ala Phe Val Tyr
 50 55 60
 5 Gly Ser Met Ser Phe Leu Asp Lys Val Ala Asn Gly Leu Ala Val Met
 65 70 75 80
 Ala Ile Gln Ser Leu His Pro Cys Pro Ser Glu Leu Cys Cys Arg Ala
 85 90 95
 10 Cys Val Ser Phe Tyr His Trp Ala Met Val Ala Val Thr Gly Gly Val
 100 105 110
 15 Gly Val Ala Ala Ala Leu Cys Leu Cys Ser Leu Leu Leu Trp Pro Thr
 115 120 125
 Arg Leu Arg Arg Xaa
 130

20

(2) INFORMATION FOR SEQ ID NO: 230:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

30 Gly Lys Pro Thr Gly Lys Ser Leu Pro Leu Met Trp Met Ile Leu Met
 1 5 10 15
 Gln Pro Ile Ile Met Ile Ser Met Met Ser Asn Gly
 20 25
 35

(2) INFORMATION FOR SEQ ID NO: 231:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

45 Met Gln Gly Lys Phe Met Lys Val Gln Val Tyr Arg Phe Leu Lys Tyr
 1 5 10 15
 50 Leu Leu Met Leu Leu Cys Met Phe Val Asn Arg Gly Met Ser Lys Asp
 20 25 30
 Ser Thr Lys Lys Pro Gly Gln Glu Lys Leu Lys Val Ser Leu Gly Ser
 35 40 45
 55 Ile Leu Asn Met Lys Ser Gln Arg Pro Leu Ser Trp Cys
 50 55 60

60 (2) INFORMATION FOR SEQ ID NO: 232:

335

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

Met Met Glu Arg Ser Met Met Ile Leu Leu Met Ala Ala Ser Met Thr
1 5 10 15
Met Thr Ser Thr Gln Leu Trp Ser Phe Cys Cys Val His
20 25

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

Met Trp Tyr Gln Leu Ala Lys Glu Glu Pro Gly Val Gly Ala Cys Ala
1 5 10 15
Leu Asp

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

Leu Xaa
1

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

Met Leu Ile Cys Arg Leu Val Leu Leu Ala Asp Pro Gly Pro Val Asn
1 5 10 15
Phe Met Val Arg Leu Phe Val Val Ile Val Met Phe Ala Trp Ser Ile
20 25 30
Val Ala Ser Thr Ala Phe Leu Ala Asp Ser Gln Pro Pro Asn Arg Arg
35 40 45

336

Ala Leu Ala Val Tyr Pro Val Phe Leu Phe Tyr Phe Val Ile Ser Trp
 50 55 60

5 Met Ile Leu Thr Phe Thr Pro Gln
 65 70

10 (2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

Met Arg Ser Leu Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala
 1 5 10 15

20 Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Pro Gly Thr
 20 25 30

25 Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Xaa Pro
 35 40 45

Ala Trp Pro Ser Ala Cys Thr Arg Pro Trp Pro Arg Thr Arg Gln Trp
 50 55 60

30 Arg Thr Ser Trp Cys His Pro Trp Trp Trp Pro Arg Arg Trp Gly Ser
 65 70 75 80

Cys Arg Trp Ala Ala Arg Arg Pro Arg Arg Arg Pro Arg Gln Cys
 85 90 95

35

40

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

45 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

Met Arg Ser Leu Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala
 1 5 10 15

Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Pro Gly Thr
 20 25 30

55 Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Lys Arg
 35 40 45

Pro Gly Leu Gln Leu Val Pro Gly His Gly Gln Gly Pro Gly Ser Gly
 50 55 60

60

337

Glu His Pro Gly Val Thr Arg Gly Gly Gly Leu Val Ala Gly Ala Arg
 65 70 75 80
 Val Ala Gly Arg Gln Gly Asp His Gly Val Ala Gly Gln Gly Ser Ala
 5 85 90 95
 Glu Arg Arg Ala Ala Ala Arg Arg Gly Gly Ala Arg Arg Pro Gly Arg
 100 105 110
 Ala Ala Ala Leu Thr Gln Gln Leu His Gly Ala Gln Arg Asp Leu Glu
 10 115 120 125
 Ala Gly Gln Pro Thr Val Arg Thr Gln Leu Ser Glu Leu Arg Xaa
 130 135 140
 15

(2) INFORMATION FOR SEQ ID NO: 238:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 142 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:
 25

Met Arg Ser Leu Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala
 1 5 10 15
 Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Pro Gly Thr
 30 20 25 30
 Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Xaa Arg
 35 35 40 45
 Pro Gly Leu Gln Leu Val Pro Gly His Gly Gln Gly Pro Gly Ser Gly
 50 55 60
 Glu His Pro Gly Val Thr Arg Gly Gly Gly Leu Val Ala Gly Ala Arg
 65 70 75 80
 Val Ala Gly Arg Gln Gly Asp His Gly Val Ala Gly Gln Gly Ser Ala
 85 90 95
 Glu Arg Arg Ala Ala Ala Arg Arg Gly Gly Ala Arg Arg Pro Gly Arg
 45 100 105 110
 Ala Ala Ala Leu Thr Gln Gln Leu Xaa Gly Ala Gln Arg Asp Leu Glu
 115 120 125
 Ala Gly Gln Pro Thr Val Arg Thr Gln Leu Ser Glu Leu Arg
 50 130 135 140

55 (2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

5 Asp Pro Glu Ala Ala Asp Ser Gly Glu Pro Gln Asn Lys Arg Thr Pro
 1 5 10 15
 Asp Leu Pro Glu Glu Glu Tyr Val Lys Glu Glu Ile Gln Glu Asn Glu
 20 25 30
 10 Glu Ala Val Lys Lys Met Leu Val Glu Ala Thr Arg Glu Phe Glu Glu
 35 40 45
 Val Val Val Asp Glu Ser
 50

15

(2) INFORMATION FOR SEQ ID NO: 240:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

25 Gln Lys Leu Lys Arg Lys Ala Glu Glu Asp Pro Glu Ala Ala Asp Ser
 1 5 10 15
 Gly Glu Pro Gln Asn Lys Arg Thr Pro Asp Leu Pro Glu Glu Glu Tyr
 20 25 30
 30 Val Lys Glu Glu Ile Gln Glu Asn Glu Glu Ala Val Lys Lys Met Leu
 35 40 45
 Val Glu Ala Thr Arg Glu Phe Glu Glu Val Val Val Asp Glu Ser
 35 50 55 60

40 (2) INFORMATION FOR SEQ ID NO: 241:
 (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

 Lys Ala Met Glu Lys Ser Ser Leu Thr Gln His Ser Trp Gln Ser Leu
 1 5 10 15
 50 Lys Asp Arg Tyr Leu Lys His Leu Arg Gly Gln Glu His Lys Tyr Leu
 20 25 30
 Leu Gly Asp Ala Pro Val Ser Pro Ser Ser Gln Lys Leu Lys Arg Lys
 35 40 45
 55 Ala Glu Glu Asp Pro Glu Ala Ala Asp Ser Gly Glu Pro Gln Asn Lys
 50 55 60
 Arg Thr Pro Asp Leu Pro Glu Glu Glu Tyr Val Lys Glu Glu Ile Gln
 60 65 70 75 80

339

Glu Asn Glu Glu Ala Val Lys Lys Met Leu Val Glu Ala Thr Arg Glu
 85 90 95

5 Phe Glu Glu Val Val Val Asp Glu Ser Pro Pro Asp Phe Glu Ile His
 100 105 110

Ile

10

(2) INFORMATION FOR SEQ ID NO: 242:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

20

Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr Ile
 1 5 10 15

25

Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp Phe
 20 25 30

Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met Leu
 35 40 45

30

Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu Ser
 50 55 60

Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser Gly
 65 70 75 80

35

Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Thr
 85 90 95

40

Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val Phe
 100 105 110

Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr Ala
 115 120 125

45

Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr Arg
 130 135 140

Val Leu Phe Ile
 145

50

(2) INFORMATION FOR SEQ ID NO: 243:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

60

340

Ala Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys
 1 5 10 15

5 Trp Ile Leu Ile Val Arg Phe Ser
 20

10 (2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

Met Lys His Leu Ser Ala Trp Asn Phe Thr Lys Leu Thr Phe Leu Gln
 1 5 10 15

20 Leu Trp Glu Ile Phe Glu Gly Ser Val Glu Asn Cys Gln Thr Leu Thr
 20 25 30

Ser Tyr Ser Lys Leu Gln Ile Lys Tyr Thr Phe Ser Arg Gly Ser Thr
 35 40 45

25 Phe Tyr Ile
 50

30 (2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

40 Phe Ser Ser Asp Phe Arg Thr Ser Pro Trp Glu Ser Arg Arg Val Glu
 1 5 10 15

Ser Lys Ala Thr Ser Ala Arg Cys Gly Leu Trp Gly Ser Gly Pro Arg
 20 25 30

45 Arg Arg Pro Ala Ser Gly Met Phe Arg Gly Leu Ser Ser Trp Leu Gly
 35 40 45

Leu Gln Gln Pro Val Ala Gly Gly Gly Gln Pro Asn Gly Asp Ala Pro
 50 55 60

50 Pro Glu Gln Pro Ser Glu Thr Val Ala Glu Ser Ala Glu Glu Glu Leu
 65 70 75 80

55 Gln Gln Ala Gly Asp Gln Glu Leu Leu His Gln Ala Lys Asp Phe Gly
 85 90 95

Asn Tyr Leu Phe Asn Phe Ala Ser Ala Ala Thr Lys Lys Ile Thr Glu
 100 105 110

60 Ser Val Ala Glu Thr Ala Gln Thr Ile Lys Lys Ser Val Glu Glu Gly

341

115 120 125
 Lys Ile Asp Gly Ile Ile Asp Lys Thr Ile Ile Gly Asp Phe Gln Lys
 130 135 140
 5 Glu Gln Lys Lys Phe Val Glu Glu Gln His Thr Lys Lys Ser Glu Ala
 145 150 155 160
 10 Ala Val Pro Pro Trp Val Asp Thr Asn Asp Glu Glu Thr Ile Gln Gln
 165 170 175
 Gln Ile Leu Ala Leu Ser Ala Asp Lys Arg Asn Phe Leu Arg Asp Pro
 180 185 190
 15 Pro Ala Gly Val Gln Phe Asn Phe Asp Phe Asp Gln Met Tyr Pro Val
 195 200 205
 Ala Leu Val Met Leu
 210
 20

(2) INFORMATION FOR SEQ ID NO: 246:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

30 Met Arg Phe Ala Leu Val Pro Lys Leu Val Lys Glu Glu Val Phe Trp
 1 5 10 15
 35 Arg Asn Tyr Phe Tyr Arg Val Ser Leu Ile Lys Gln Ser Ala Gln Leu
 20 25 30
 Thr Ala Leu Ala Ala Gln Gln Gln Ala Ala Gly Lys Gly Gly Glu Glu
 35 40 45
 40 Gln

(2) INFORMATION FOR SEQ ID NO: 247:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 50 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

55 Ser Thr Ser Pro Gly Val Ser Glu Phe Val Ser Asp Ala Phe Asp Ala
 1 5 10 15
 Cys Asn Leu Asn Gln Glu Asp Leu Arg Lys Glu Met Glu Gln Leu Val
 20 25 30
 60 Leu Asp Lys Lys Gln Glu Glu Thr Ala Val Leu Glu Glu Asp Ser Ala
 35 40 45

342

Asp Trp Glu Lys Glu Leu Gln Gln Glu Leu Gln Glu Tyr Glu Val Val
 50 55 60

5 Thr Glu Ser Glu Lys Arg Asp Glu Asn Trp Asp Lys
 65 70 75

10 (2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

Ser Pro Trp Glu Ser Arg Arg Val Glu Ser Lys Ala Thr Ser Ala Arg
 1 5 10 15

20 Cys Gly Leu Trp Gly Ser Gly Pro Arg Arg Arg Pro Ala Ser Gly Met
 20 25 30

25 Phe Arg Gly Leu Ser Ser Trp Leu Gly Leu Gln Gln Pro Val Ala Gly
 35 40 45

Gly Gly Gln Pro Asn Gly Asp Ala Pro Pro Glu Gln Pro Ser
 50 55 60

30

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

40 Pro Val Ala Gly Gly Gly Gln Pro Asn Gly Asp Ala Pro Pro Glu Gln
 1 5 10 15

Pro Ser Glu Thr Val Ala Glu Ser Ala Glu Glu Glu Leu Gln Gln Ala
 20 25 30

45 Gly Asp Gln Glu Leu Leu His Gln Ala Lys Asp Phe Gly Asn Tyr Leu
 35 40 45

50 Phe Asn Phe Ala Ser Ala Ala Thr Lys Lys Ile Thr Glu Ser Val Ala
 50 55 60

Glu
 65

55

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 72 amino acids

343

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

5 Phe Gln Lys Glu Gln Lys Lys Phe Val Glu Glu Gln His Thr Lys Lys
 1 5 10 15
 Ser Glu Ala Ala Val Pro Pro Trp Val Asp Thr Asn Asp Glu Glu Thr
 20 25 30
 10 Ile Gln Gln Gln Ile Leu Ala Leu Ser Ala Asp Lys Arg Asn Phe Leu
 35 40 45
 Arg Asp Pro Pro Ala Gly Val Gln Phe Asn Phe Asp Phe Asp Gln Met
 15 50 55 60
 Tyr Pro Val Ala Leu Val Met Leu
 65 70

20

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

30 Pro Phe Ile Cys Val Ala Arg Asn Pro Val Ser Arg Asn Phe Ser Ser
 1 5 10 15
 Pro Ile Leu Ala Arg Lys Leu Cys Glu Gly Ala Ala
 20 25

35

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

45 Lys Glu Asp Pro Ala Asn Thr Val Tyr Ser Thr Val Glu Ile Pro Lys
 1 5 10 15
 Lys Met Glu Asn Pro His Ser Leu Leu Thr Met Pro Asp Thr Pro Arg
 50 20 25 30
 Leu

55

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 amino acids

60

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

[illegible]

50

(2) INFORMATION FOR SEO ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

55 (17) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

60 Ser Val Ala Ala Phe Glu Gly Gln Val Gly Gln Ala Ala Tyr Ser Ala

345

1 5 10 15
 Ser Lys Gly Gly Ile Val Gly Met Thr Leu Pro Ile Ala
 20 25

5

(2) INFORMATION FOR SEQ ID NO: 255:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

15

Ala Arg Arg Ser Gly Ala Glu Leu Ala Trp Asp Tyr Leu Cys Arg Trp
 1 5 10 15

20

Ala Gln Lys His Lys Asn Trp Arg Phe Gln Lys Thr Arg Gln Thr Trp
 20 25 30

Leu Leu Leu His Met Tyr Asp Ser Asp Lys Val Pro Asp Glu His Phe
 35 40 45

25

Ser Thr Leu Leu Ala Tyr Leu Glu Gly Leu Gln Gly Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO: 256:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

His Pro Ile Glu Trp Ala Ile Asn Ala Ala Thr Leu Ser Gln Phe Tyr
 1 5 10 15

40

Ile Asn Lys Leu Cys Phe
 20

45

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

Cys Trp Ile Lys Tyr Cys Leu Thr Leu Met Gln Asn Ala Gln Leu Ser
 1 5 10 15

55

Met Gln Asp Asn Ile Gly
 20

60

346

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

Lys Val Ser Tyr Leu Arg Pro Leu Asp Phe Glu Glu Ala Arg Glu Leu
1 5 10 15

Phe Leu Leu Gly Gln His Tyr Val Phe
20 25

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

Met Glu Arg Arg Cys Lys Met His Lys Arg Xaa Ile Ala Met Leu Glu
1 5 10 15

Pro Leu Thr Val Asp Leu Asn Pro Gln
20 25

(2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

Ser His Ile Val Lys Lys Ile Asn Asn Leu Asn Lys Ser Ala Leu Lys
1 5 10 15

Tyr Tyr Gln Leu Phe Leu Asp
20

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

Phe Thr His Leu Ser Thr Cys Leu Leu Ser Leu Leu Leu Val Arg Met
1 5 10 15

Ser Gly Phe Leu Leu Leu Ala Arg Ala Ser Pro Ser Ile Cys Ala Leu

347

20 25 30

Asp Ser Ser Cys Phe Val Gln Glu Tyr Cys Ser Ser Tyr Ser Ser Ser
35 40 45

5 Cys Phe Leu His Gln His Phe Pro Ser Leu Leu Asp His Leu Cys Gln
50 55 60

10

(2) INFORMATION FOR SEQ ID NO: 262:

15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

Phe Leu Leu Leu Ala Arg Ala Ser Pro Ser Ile Cys Ala Leu Asp Ser
1 5 10 15

25

Ser Cys Phe Val Gln Glu Tyr
20

30

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

Pro Asp Gly Arg Val Thr Asn Ile Pro Gln Gly Met Val Thr Asp Gln
1 5 10 15

40

Phe Gly Met Ile Gly Leu Leu Thr Phe Ile Arg Ala Ala Glu Thr Asp
20 25 30

45

Pro Gly Met Val His Leu Ala Leu Gly Ser Asp Leu Thr Thr Leu Gly
35 40 45

Leu Asn Leu Asn Ser
50

50

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

60

Glu Asp Leu Leu Phe Tyr Leu Tyr Tyr Met Asn Gly Gly Asp Val Leu

348

1 5 10 15
 Gln Leu Leu Ala Ala Val Glu Leu Phe Asn Arg Asp Trp Arg Tyr His
 20 25 30
 5 Lys Glu Glu Arg Val Trp Ile Thr Arg
 35 40

10

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

20 Val His Leu Ala Leu Gly Ser Asp Leu Thr Thr Leu Gly Leu Asn Leu
 1 5 10 15
 Asn Ser Pro Glu Asn Leu Tyr Pro
 20

25

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

35 His Asn Glu Asp Phe Pro Ala Leu Pro Gly Ser
 1 5 10

40

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

50 Gly Arg Ile Ile Asp Thr Ser Leu Thr Arg Asp Pro Leu Val Ile Glu
 1 5 10 15
 Leu Gly Gln Lys Gln Val Ile P: Gly Leu Glu Gln Ser Leu Leu Asp
 20 25 30
 55 Met Cys Val Gly Glu Lys Arg Arg Ala Ile Ile Pro Ser His Leu Ala
 35 40 45
 Tyr Gly Lys Arg Gly Phe Pro Pro Ser Val Pro Ala Asp Ala Val Val
 50 55 60

60 Gln Tyr Asp Val Glu Leu Ile Ala Leu Ile Arg

349

65

70

75

5 (2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

Ile His Tyr Thr Gly Ser Leu Val Asp Gly Arg Ile Ile Asp Thr Ser
1 5 10 15

15

20

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

Cys Glu Ser Pro Glu Ser Pro Ala Gln Pro Ser Gly Ser Ser Leu Pro
1 5 10 15

30

Ala Trp Tyr His
20

35

(2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

45 Glu Glu Ala Gly Ala Gly Arg Arg Cys Ser His Gly Gly Ala Arg Pro
1 5 10 15

Ala Gly Leu Gly Asn Glu Gly Leu Gly Leu Gly Gly Asp Pro Asp His
20 25 30

50

Thr Asp Thr Gly Ser Arg Ser Lys Gln Arg Ile Asn Asn Trp Lys Glu
35 40 45

55

Ser Lys His Lys Val Ile Met Ala Ser Ala Ser Ala Arg Gly Asn Gln
50 55 60

Asp Lys Asp Ala His Phe Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe
65 70 75 80

60

Cys Pro Lys Ser Lys Leu His Ile His Arg Ala Glu Ile Ser Lys

350

85

90

95

5 (2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

Ser Lys Gln Arg Ile Asn Asn Trp Lys Glu Ser Lys His Lys Val Ile
 1 5 10 15
 Met Ala Ser Ala Ser Ala Arg
 20

20

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

25 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

30 Leu Phe His Trp Ala Cys Leu Asn Glu Arg Ala Ala Gln Leu Pro Arg
 1 5 10 15
 Asn Thr Ala Xaa Ala Gly Tyr Gln Cys Pro Ser Cys Asn Gly Pro Ser
 20 25 30

35

40 (2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

45 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

50 Phe Tyr Ile Tyr Tyr Arg Pro Thr Asp Ser Asp Asn Asp Ser Asp Tyr
 1 5 10 15
 Lys Lys Asp Met Val Glu Gly Asp Lys Tyr Trp His Ser Ile Ser His
 20 25 30

55 Leu Gln Pro Glu Thr Ser Tyr Asp Ile Lys Met Gln Cys Phe Asn Glu
 35 40 45

Gly Gly Glu Ser Glu Phe Ser Asn Val Met Ile Cys Glu Thr Lys Ala
 50 55 60

60 Arg Lys Ser Ser Gly Gln Pro Gly Arg Leu Pro Pro Pro Thr Leu Ala

65					70					75					80
Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg	Pro	Val	Gly	Thr
				85					90					95	
Gly	Ala	Met	Val	Ala	Arg	Ser	Ser	Asp	Leu	Pro	Tyr	Leu	Ile	Val	Gly
			100					105					110		
Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile	Val	Thr	Phe	Ile	Pro	Phe
		115					120					125			
Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln	Lys	His	Thr	Thr	Asp	Leu	Gly
	130					135					140				
Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro	Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro
145					150					155					160
Leu	Gly	Gly	Leu	Pro	Gly	His	Gln	Ala	Val	Asp	Ser	Pro	Thr	Ser	Val
				165					170					175	
Ala	Ser	Val	Asp	Gly	Pro	Val	Leu	Met							
			180					185							

```

Tyr Ile Tyr Tyr Arg Pro Thr Asp Ser Asp Asn Asp Ser Asp Tyr Lys
  1                               5                               10                               15
Lys Asp Met Val Glu Gly Asp Lys Tyr Trp His Ser Ile Ser His Leu
                20                                25                                30
Gln Pro Glu Thr Ser Tyr Asp Ile Lys Met Gln Cys Phe Asn Glu Gly
            35                                40                                45
Gly Glu Ser Glu Phe Ser Asn Val Met Ile Cys Glu Thr Lys Ala Arg
    50                                55                                60
Lys Ser
  65

```

Asn Val Arg Ala Leu Leu His Arg Met Pro Glu Pro Pro Lys Ile Asn
1 5 10 15

352

Thr Ala Lys Phe Asn Asn Asn Lys Arg Lys Asn Leu Ser Leu
 20 25 30

5

(2) INFORMATION FOR SEQ ID NO: 276:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

15

Asn Thr Asn Gln Arg Glu Ala Leu Gln Tyr Ala Lys Asn Phe Gln Pro
 1 5 10 15

20

Phe Ala Leu Asn His Gln Lys Asp Ile Gln Val Leu Met Gly Ser Leu
 20 25 30

Val Tyr Leu Arg Gln Gly Ile Glu Asn Ser Pro Tyr Val His Leu Leu
 35 40 45

25

Asp Ala Asn Gln Trp Ala Asp Ile Cys Asp Ile Phe Thr Arg Asp Ala
 50 55 60

Cys Ala Leu Leu Gly Leu Ser Val Glu Ser Pro Leu Ser Val Ser Phe
 65 70 75 80

30

Ser Ala Gly Cys Val Ala Leu Pro Ala Leu Ile Asn Ile Lys Ala Val
 85 90 95

35

Ile Glu Gln Arg Gln Cys Thr Gly Val Trp Asn Gln Lys Asp Glu Leu
 100 105 110

Pro Ile Glu Val Asp Leu Gly Lys Lys Cys Trp Tyr His Ser Ile Phe
 115 120 125

40

Ala Cys Pro Ile Leu Arg Gln Gln Thr Thr Asp Asn Asn Pro Pro Met
 130 135 140

Lys Leu Val Cys Gly His Ile Ile Ser Arg Asp Ala Leu Asn Lys Met
 145 150 155 160

45

Phe Asn Gly Ser Lys Leu Lys Cys Pro Tyr Cys Pro Met Glu Gln Ser
 165 170 175

Pro Gly Asp Ala Lys Gln Ile Phe Phe
 180 185

50

(2) INFORMATION FOR SEQ ID NO: 277:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

60

353

Ser Tyr Leu Ser Ala Cys Phe Ala Gly Cys Asn Ser Thr Asn Leu Thr
 1 5 10 15
 Gly Cys Ala Cys Leu Thr Thr Val Pro Ala Glu Asn Ala Thr Val Val
 5 20 25 30
 Pro Gly Lys Cys Pro Ser Pro Gly Cys Gln Glu Ala Phe Leu Thr Phe
 35 40 45
 10 Leu Cys Val Met Cys Ile Cys Ser Leu Ile Gly Ala Met Ala Arg His
 50 55 60
 Pro
 15 65

(2) INFORMATION FOR SEQ ID NO: 278:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

25 Pro Ser Val Ile Ile Leu Ile Arg Thr Val Ser Pro Glu Leu Lys Ser
 1 5 10 15
 Tyr Ala Leu Gly Val Leu Phe Leu Leu Leu Arg Leu Leu Gly Phe Ile
 30 20 25 30
 Pro Pro Pro Leu Ile Phe Gly Ala Gly Ile Asp Ser Thr Cys Leu Phe
 35 35 40 45
 35 Trp Ser Thr Phe Cys Gly Glu Gln Gly Ala Cys Val Leu Tyr Asp Asn
 50 55 60
 Val Val Tyr Arg Tyr Leu Tyr Val Ser Ile Ala Ile Ala Leu Lys Ser
 40 65 70 75 80
 Phe Ala Phe Ile

45

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 182 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

50 Gln Ser Leu Phe Thr Arg Phe Val Arg Val Gly Val Pro Thr Val Asp
 55 1 5 10 15
 Leu Asp Ala Gln Gly Arg Ala Arg Ala Ser Leu Cys Xaa Xaa Tyr Asn
 20 25 30
 60 Trp Arg Tyr Lys Asn Leu Gly Asn Leu Pro His Val Gln Leu Leu Pro

354

35 40 45
 Glu Phe Ser Thr Ala Asn Ala Gly Leu Leu Tyr Asp Phe Gln Leu Ile
 50 55 60
 5 Asn Val Glu Asp Phe Gln Gly Val Gly Glu Ser Glu Pro Asn Pro Tyr
 65 70 75 80
 10 Phe Tyr Gln Asn Leu Gly Glu Ala Glu Tyr Val Val Ala Leu Phe Met
 85 90 95
 Tyr Met Cys Leu Leu Gly Tyr Pro Ala Asp Lys Ile Ser Ile Leu Thr
 100 105 110
 15 Thr Tyr Asn Gly Gln Lys His Leu Ile Arg Asp Ile Ile Asn Arg Arg
 115 120 125
 Cys Gly Asn Asn Pro Leu Ile Gly Arg Pro Asn Lys Val Thr Thr Val
 130 135 140
 20 Asp Arg Phe Gln Gly Gln Gln Asn Asp Tyr Ile Leu Leu Ser Leu Val
 145 150 155 160
 25 Arg Thr Arg Ala Val Gly His Leu Arg Asp Val Arg Arg Leu Val Val
 165 170 175
 Ala Met Ser Arg Ala Arg
 180

30

(2) INFORMATION FOR SEQ ID NO: 280:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

40 Leu Val Lys Glu Ala Lys Ile Ile Ala Met Thr Cys Thr His Ala Ala
 1 5 10 15
 Leu Lys Arg His Asp Leu Val Lys Leu Gly Phe Lys Tyr Asp Asn Ile
 20 25 30
 45 Leu Met Glu Glu Ala Ala Gln Ile Leu Glu Ile Glu Thr Phe Ile Pro
 35 40 45
 50 Leu Leu Leu Gln Asn Pro Gln Asp Gly Phe Ser Arg Leu Lys Arg Trp
 50 55 60
 Ile Met Ile Gly Asp His His Gln Leu Pro Pro Val Ile
 65 70 75

55

(2) INFORMATION FOR SEQ ID NO: 281:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids

355

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

5 Asp Thr Tyr Pro Asn Glu Glu Lys Gln Gln Glu Arg Val Phe Pro Xaa
 1 5 10 15
 Xaa Ser Ala Met Val Asn Asn Gly Ser Leu Ser Tyr Asp His Glu Arg
 20 25 30
 10 Asp Gly Arg Pro Thr Glu Leu Gly Gly Cys Xaa Ala Ile Val Arg Asn
 35 40 45
 Leu His Tyr Asp Thr Phe Leu Val Ile Arg Tyr Val Lys Arg His Leu
 15 50 55 60
 Thr Ile Met Met Asp Ile Asp Gly Lys His Glu Trp Arg Asp Cys Ile
 65 70 75 80
 20 Glu Val Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr Phe Gly Thr Ser
 85 90 95
 Ser Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys
 100 105 110
 25 Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu
 115 120 125

30

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

40 Leu Lys Arg Glu His Ser Leu Ser Lys Pro Tyr Gln Gly Val Gly Thr
 1 5 10 15
 Gly Ser Ser Ser Leu Trp Asn Leu Met Gly Asn Ala Met Val Met Thr
 20 25 30
 45 Gln Tyr Ile Arg Leu Thr Pro Asp Met Gln Ser Lys Gln Gly Ala Leu
 35 40 45
 Trp Asn Arg Val Pro Cys Phe Leu Arg Asp Trp Glu Leu Gln Val His
 50 55 60
 50 Phe Lys Ile His Gly Gln Gly Lys Lys Asn Leu His Gly Asp Gly Leu
 65 70 75 80
 Ala Ile Trp Tyr Thr
 85

55

(2) INFORMATION FOR SEQ ID NO: 283:

60

356

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

Pro Gly Thr Leu Gln Cys Ser Ala Leu His His Asp Pro Gly Cys Ala
 1 5 10 15

10 Asn Cys Ser Arg Phe Cys Arg Asp Cys Ser Pro Pro Ala Cys Gln Cys
 20 25 30

15

(2) INFORMATION FOR SEQ ID NO: 284:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

Phe Leu Tyr Asp Val Leu Met Xaa His Glu Ala Val Met Arg Thr His
 1 5 10 15

30 Gln Ile Gln Leu Pro Asp Pro Glu Phe Pro Ser
 20 25

35 (2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

Gly Trp Tyr Trp Cys Gly
 1 5

45

(2) INFORMATION FOR SEQ ID NO: 286:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

55 Met Lys Val Gly Ala Arg Ile Arg Val Lys Met Ser Val Asn Lys Ala
 1 5 10 15

His Pro Val Val Ser Thr His Trp Arg Trp Pro Ala Glu Trp Pro Gln
 20 25 30

60

357

Met Phe Leu His Leu Ala Gln Glu Pro Arg Thr Glu Val Lys Ser Arg
 35 40 45

5 Pro Leu Gly Leu Ala Gly Phe Ile Arg Gln Asp Ser Lys Thr Arg Lys
 50 55 60

Pro Leu Glu Gln Glu Thr Ile Met Ser Ala Ala Asp Thr Ala Leu Trp
 65 70 75 80

10 Pro Tyr Gly His Gly Asn Arg Glu His Gln Glu Asn Glu Leu Gln Lys
 85 90 95

Tyr Leu Gln Tyr Lys Asp Met His Leu Leu Asp Ser Gly Gln Ser Leu
 100 105 110

15 Gly His Thr His Thr Leu Gln Gly Ser His Asn Leu Thr Ala Leu Asn
 115 120 125

Ile

20

(2) INFORMATION FOR SEQ ID NO: 287:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

Ser Leu His Lys Asn Ser Val Ser Gln Ile Ser Val Leu Ser Gly Gly
 1 5 10 15

35 Lys Ala Lys Cys Ser Gln Phe Cys Thr Thr Gly Met Asp Gly Gly Met
 20 25 30

Ser Ile Trp Asp Val Lys Ser Leu Glu Ser Ala Leu Lys Asp Leu Lys
 35 40 45

40 Ile

45

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

Glu Ala Ser Lys Ser Ser His Ala Gly Leu Asp Leu Phe Ser Val Ala
 1 5 10 15

Ala Cys His Arg Phe
 20

60

(2) INFORMATION FOR SEQ ID NO: 289:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

10 Tyr Met Gly Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe
1 5 10 15
Glu Arg Ser Phe Thr
15 20

(2) INFORMATION FOR SEQ ID NO: 290:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

Val Thr Gly Ile Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg
1 5 10 15
30 Val Gly Leu Leu Gln Tyr Ser Thr Gln Val His
20 25

(2) INFORMATION FOR SEQ ID NO: 291:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

Thr Glu Phe Thr Leu Arg Asn Phe Asn Ser Ala Lys Asp Met Lys Lys
1 5 10 15
45 Ala Val Ala His Met Lys Tyr Met
20

50 (2) INFORMATION FOR SEQ ID NO: 292:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
55 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

Gly Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg
1 5 10 15
60

359

Ser Phe Thr Gln Gly Glu Gly Ala Arg Pro Phe
20 25

5

(2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

15 Ser Thr Arg Val Pro Arg Ala Ala Ile Val Phe Thr Asp Gly Arg Ala
1 5 10 15
Gln Asp Asp Val Ser Glu Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile
20 25 30
20 Thr Met Tyr Ala Val Gly Val Gly Lys Ala Ile Glu
35 40

25

(2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

35 Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro Thr Asn Lys His Leu Phe
1 5 10 15
Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu Ile Ser Glu Lys Leu Lys
20 25 30
40 Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser
35 40

45

(2) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

50

Thr Gln Arg Leu Glu Glu Met Thr Gln Arg Met
1 5 10

55

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

60

360

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

5 Pro Gln Gly Cys Pro Glu Gln Pro Leu His
 1 5 10

10 (2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

Arg Cys Lys Lys Cys Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile
 1 5 10 15
 20 Asp Gly Ser Lys Ser Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln
 25 Phe

30 (2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

Met Ala Ala Leu Leu Leu Arg His Val Gly Arg His Cys Leu Arg Ala
 1 5 10 15
 40 His Phe Ser Pro Gln Leu Cys Ile Arg Asn Ala Val Pro Leu Gly Thr
 20 25 30
 Thr Ala Lys Glu Glu Met Glu Arg Phe Trp Asn Lys Asn Ile Gly Ser
 35 40 45
 45 Asn Arg Pro Leu Ser Pro His Ile Thr Ile Tyr Ser
 50 55 60

50 (2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

60 Val Phe Pro Leu Met Tyr His Thr Trp Asn Gly Ile Arg His Leu Met
 1 5 10 15

Trp Asp Leu Gly Lys Gly Leu Lys Ile Pro Gln Leu Tyr Gln Ser Gly
 20 25 30

5

10 (2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

Met Ala Ala Leu Leu Leu Arg His Val Gly Arg His Cys Leu Arg Ala
 1 5 10 15

20

His

25

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

30

Val Lys Ser Leu Cys Leu Gly Pro Ala Leu Ile His Thr Ala Lys Phe
 1 5 10 15

35

Ala Leu

40

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

45

Val Phe Pro Leu Met Tyr His Thr Trp Asn Gly Ile Arg His Leu Met
 1 5 10 15

50

Trp Asp Leu Gly Lys Gly Leu
 20

55

(2) INFORMATION FOR SEQ ID NO: 303:

60 (i) SEQUENCE CHARACTERISTICS:

362

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

5

Arg Val Trp Asp Val Arg Pro Phe Ala Pro Lys Glu Arg Cys Val Lys
 1 5 10 15

10

Ile Phe Gln Gly Asn Val
 20

(2) INFORMATION FOR SEQ ID NO: 304:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

His Asn Phe Glu Lys Asn Leu Leu Arg Cys Ser Trp Ser Pro Asp Gly
 1 5 10 15

25

Ser Lys Ile Ala Gly Ser Ala Asp Arg Phe Val Tyr Val
 20 25 30

30

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

Trp Asp Thr Thr Ser Arg Arg Ile Leu Tyr Lys Leu Pro Gly His Ala
 1 5 10 15

40

Gly Ser Ile Asn Glu Val Ala Phe His Pro Asp Glu Pro Ile
 20 25 30

45

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

Val Arg Gly Arg Thr Val Leu Arg Pro Gly Leu Asp Ala Glu Pro Glu
 1 5 10 15

55

Leu Ser Pro Glu
 20

60

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

10 Glu Gln Arg Val Leu Glu Arg Lys Leu Lys Lys Glu Arg Lys Lys Glu
 1 5 10 15

Glu Arg Gln

15

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

25 Arg Leu Arg Glu Ala Gly Leu Val Ala Gln His Pro Pro
 1 5 10

30

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

40 Gly Arg Ile Pro Ala Pro Ala Pro Ser Val Pro Ala Gly Pro Asp Ser
 1 5 10 15

Arg

45

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

55 Thr Gly Cys Val Leu Val Leu Ser Arg Asn Phe Val Gln Tyr Ala Cys
 1 5 10 15

Phe Gly Leu Phe Gly Ile Ile Ala Leu Gln Thr Ile Ala Tyr Ser Ile
 20 25 30

60

364

Leu Trp Asp Leu Lys Phe Leu Met Arg Asn
 35 40

5

(2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

10

15

Ser Arg Ser Glu Gly Lys Ser Met Phe Ala Gly Val Pro Thr Met Arg
 1 5 10 15

Glu Ser Ser Pro Lys Gln Tyr Met Gln Leu Gly Gly Arg Val Leu Leu
 20 25 30

20

Val Leu Met Phe Met Thr Leu Leu His Phe Asp Ala Ser Phe Phe Ser
 35 40 45

25

Ile Val Gln Asn Ile Val Gly
 50 55

(2) INFORMATION FOR SEQ ID NO: 312:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

35

Gly Thr Ala Glu Asp Phe Ala Asp Gln Phe Leu Arg Val Thr Lys Gln
 1 5 10 15

40

Tyr Leu Pro His Val Ala Arg Leu Cys Leu Ile Ser Thr Phe Leu Glu
 20 25 30

Asp Gly Ile Arg Met Trp Phe Gln Trp Ser Glu Gln Arg Asp Tyr Ile
 35 40 45

45

Asp Thr Thr Trp Asn Cys Gly Tyr Leu Leu Ala Ser
 50 55 60

50

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

55

Ala Ser Phe Leu Leu Ser Arg Thr Ser Trp Gly Thr Ala Leu Met Ile
 1 5 10 15

60

Leu

5

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

Leu Met Arg Asn Glu Ser Arg Ser

15

1

5

(2) INFORMATION FOR SEQ ID NO: 315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

Ala Ser Phe Leu Leu Ser Arg Thr Ser Trp Gly Thr Ala

1

5

10

30

(2) INFORMATION FOR SEQ ID NO: 316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

40 Phe Ile Ser Phe Ala Asn Ser Arg Ser Ser Glu Asp Thr Lys Gln Met

1

5

10

15

Met Ser Ser Phe

20

45

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

55

Asp Pro Arg Arg Pro Asn Lys Val Leu Arg Tyr Lys Pro Pro Pro Ser

1

5

10

15

Glu Cys Asn Pro Ala Leu Asp Asp Pro Thr Pro

20

25

60

(2) INFORMATION FOR SEQ ID NO: 318:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Asp Tyr Met Asn Leu Leu Gly Met Ile Phe Ser Met Cys Gly Leu Met
1 5 10 15
Leu Lys Leu Lys Trp Cys Ala Trp Val Ala Val Tyr Cys Ser
20 25 30

(2) INFORMATION FOR SEQ ID NO: 319:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

Met Leu Ser Ile Ser Ala Val Val Met Ser Tyr Leu Gln Asn Pro Gln
1 5 10 15
Pro Met Thr Pro Pro Trp
20

(2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

Ala Ala Gly Asp Gly Asp Val Lys Leu Gly Thr Leu Gly Ser Gly Ser
1 5 10 15
Glu Ser Ser Asn Asp Gly Gly Ser Glu Ser Pro Gly Asp Ala Gly Ala
20 25 30
Ala Ala Xaa Gly Gly Gly Trp Ala Ala Ala Ala Leu Ala Leu Leu Thr
35 40 45
Gly Gly Gly Glu
50

(2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:

367

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

5
 Ala Ala Asp Asn Tyr Gly Ile Pro Arg Ala Cys Arg Asn Ser Ala Arg
 1 5 10 15

10
 Ser Tyr Gly Ala Ala Trp Leu Leu Leu Xaa Pro Ala Gly Ser Ser Arg
 20 25 30

Val Glu Pro Thr Gln Asp Ile Ser Ile Ser Asp Gln Leu Gly Gly Gln
 35 40 45

15
 Asp Val Pro Val Phe Arg Asn Leu Ser Leu Leu Val Val Gly Val Gly
 50 55 60

Ala Val Phe Ser Leu Leu Phe His Leu Gly Thr Arg Glu Arg Arg Arg
 65 70 75 80

20
 Pro His Ala Xaa Glu Pro Gly Glu His Thr Pro Leu Leu Ala Pro Ala
 85 90 95

Thr Ala Gln Pro Leu Leu Leu Trp Lys His Trp Leu Arg Glu Xaa Ala
 100 105 110

25
 Phe Tyr Gln Val Gly Ile Leu Tyr Met Thr Thr Arg Leu Ile Val Asn
 115 120 125

30
 Leu Ser Gln Thr Tyr Met Ala Met Tyr Leu Thr Tyr Ser Leu His Leu
 130 135 140

Pro Lys Lys Phe Ile Ala Thr Ile Pro Leu Val Met Tyr Leu Ser Gly
 145 150 155 160

35
 Phe Leu Ser Ser Phe Leu Met Lys Pro Ile Asn Lys Cys Ile Gly Arg
 165 170 175

40
 Asn

(2) INFORMATION FOR SEQ ID NO: 322:

45
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 243 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

50
 Arg Ile Thr Asp Asn Pro Glu Gly Lys Trp Leu Gly Arg Thr Ala Arg
 1 5 10 15

Gly Ser Tyr Gly Tyr Ile Lys Thr Thr Ala Val Glu Ile Xaa Tyr Asp
 20 25 30

55
 Ser Leu Lys Leu Lys Lys Asp Ser Leu Gly Ala Pro Ser Arg Pro Ile
 35 40 45

60
 Glu Asp Asp Gln Glu Val Tyr Asp Asp Val Ala Glu Gln Asp Asp Ile

368

50 55 60
 Ser Ser His Ser Gln Ser Gly Ser Gly Gly Ile Phe Pro Pro Pro Pro
 65 70 75 80
 5 Asp Asp Asp Ile Tyr Asp Gly Ile Glu Glu Glu Asp Ala Asp Asp Gly
 85 90 95
 10 Phe Pro Ala Pro Pro Lys Gln Leu Asp Met Gly Asp Glu Val Tyr Asp
 100 105 110
 Asp Val Asp Thr Ser Asp Phe Pro Val Ser Ser Ala Glu Met Ser Gln
 115 120 125
 15 Gly Thr Asn Val Gly Lys Ala Lys Thr Glu Glu Lys Asp Leu Lys Lys
 130 135 140
 Leu Lys Lys Gln Xaa Lys Glu Xaa Lys Asp Phe Arg Lys Lys Phe Lys
 20 145 150 155 160
 Tyr Asp Gly Glu Ile Arg Val Leu Tyr Ser Thr Lys Val Thr Thr Ser
 165 170 175
 25 Ile Thr Ser Lys Lys Trp Gly Thr Arg Asp Leu Gln Val Lys Pro Gly
 180 185 190
 Glu Ser Leu Glu Val Ile Gln Thr Thr Asp Asp Thr Lys Val Leu Cys
 195 200 205
 30 Arg Asn Glu Glu Gly Lys Tyr Gly Tyr Val Leu Arg Ser Tyr Leu Ala
 210 215 220
 Asp Asn Asp Gly Glu Ile Tyr Asp Asp Ile Ala Asp Gly Cys Ile Tyr
 35 225 230 235 240
 Asp Asn Asp
 40 (2) INFORMATION FOR SEQ ID NO: 323:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:
 Ser Met Ser Ala Leu Thr Arg Leu Ala Ser Phe Ala Arg Val Gly Gly
 1 5 10 15
 50 Arg Leu Phe Arg Ser Gly Cys Ala Arg Thr Ala Gly Asp Gly Gly Val
 20 25 30
 Arg His Ala Gly Gly Gly Val His Ile Glu Pro Arg Tyr Arg Gln Phe
 55 35 40 45
 Pro Gln Leu Thr Arg Ser Gln Val Phe Gln Ser Glu Phe Phe Ser Gly
 50 55 60
 60 Leu Met Trp Phe Trp Ile Leu Trp Arg Phe Trp His Asp Ser Glu Glu

369

65 70 75 80

Val Leu Gly His Phe Pro Tyr Pro Asp Pro Ser Gln Trp Thr Asp Glu

 85 90 95

5

Glu Leu Gly Ile Pro Pro Asp Asp Glu Asp

 100 105

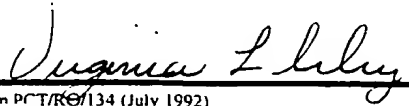
370

Applicant's or agent's file reference number	004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 73 . line N/A	
B. IDENTIFICATION OF DEPOSIT	
Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit March 7, 1997	Accession Number 97923
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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<input checked="checked" type="checkbox"/> This sheet was received with the international application	<input type="checkbox"/> This sheet was received by the International Bureau on:
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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>73</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit May 22, 1997	Accession Number 209071
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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Authorized officer

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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 73 . line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit February 25, 1998	Accession Number 209641
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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Authorized officer <i>Guillermo L. Lelien</i>	Authorized officer

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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 75, line N/A	
B. IDENTIFICATION OF DEPOSIT	
Further deposits are identified on an additional sheet : 1	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit July 24, 1997	Accession Number 209179
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet 1	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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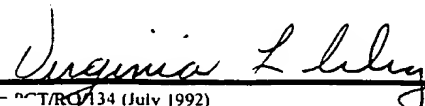
374

Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 77, line N/A	
B. IDENTIFICATION OF DEPOSIT	
Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit	March 7, 1997
Accession Number	97924
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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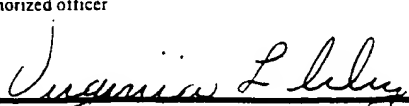
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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 80 . line N/A	
B. IDENTIFICATION OF DEPOSIT	
Further deposits are identified on an additional sheet	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit	March 13, 1997
Accession Number	97958
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>80</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <u>1</u>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>May 22, 1997</u>	Accession Number <u>209072</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <u>1</u>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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Authorized officer <u>Virginia L. Liley</u>	Authorized officer

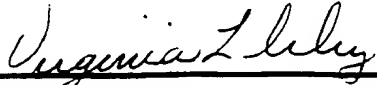
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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>80</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>September 4, 1997</u>	Accession Number <u>209235</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit") 	

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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 84 . line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit August 28, 1997	Accession Number 209226
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 84, line N/A	
B. IDENTIFICATION OF DEPOSIT	
Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit March 13, 1997	Accession Number 97957
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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Authorized officer <i>Virginia L. Lely</i>	Authorized officer

380

Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 84, line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit May 22, 1997	Accession Number 209073
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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Authorized officer <i>Virginia L. Lely</i>	Authorized officer

What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:

5 (a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

10 (c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

15 (e) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X, having biological activity;

20 (f) a polynucleotide which is a variant of SEQ ID NO:X;

(g) a polynucleotide which is an allelic variant of SEQ ID NO:X;

(h) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;

(i) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(h), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.

2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein.

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3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

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4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

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5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

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6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

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7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.

8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.

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9. A recombinant host cell produced by the method of claim 8.

10. The recombinant host cell of claim 9 comprising vector sequences.

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11. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(b) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z, having biological activity;

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(c) a polypeptide domain of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(d) a polypeptide epitope of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

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(e) a secreted form of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(f) a full length protein of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

- (g) a variant of SEQ ID NO:Y;
- (h) an allelic variant of SEQ ID NO:Y; or
- (i) a species homologue of the SEQ ID NO:Y.

5 12. The isolated polypeptide of claim 11, wherein the secreted form or the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.

10 13. An isolated antibody that binds specifically to the isolated polypeptide of claim 11.

14. A recombinant host cell that expresses the isolated polypeptide of claim 11.

15 15. A method of making an isolated polypeptide comprising:
 (a) culturing the recombinant host cell of claim 14 under conditions such that said polypeptide is expressed; and
 (b) recovering said polypeptide.

20 16. The polypeptide produced by claim 15.

17. A method for preventing, treating, or ameliorating a medical condition, comprising administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 11 or the polynucleotide of claim 1.

25 18. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

- (a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and
 - (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or absence of said mutation.
- 30

19. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

- (a) determining the presence or amount of expression of the polypeptide of claim 11 in a biological sample; and
 - (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.
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20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:

- 5 (a) contacting the polypeptide of claim 11 with a binding partner; and
(b) determining whether the binding partner effects an activity of the polypeptide.

21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.

10 22. A method of identifying an activity in a biological assay, wherein the method comprises:

- (a) expressing SEQ ID NO:X in a cell;
(b) isolating the supernatant;
(c) detecting an activity in a biological assay; and
15 (d) identifying the protein in the supernatant having the activity.

23. The product produced by the method of claim 22.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/05311

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C12N5/10 C12N1/21 C07K14/47 C07K16/18
 C12Q1/68 G01N33/50 G01N33/53 G01N33/68 A61K38/17

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K C12Q G01N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	L. HILLIER ET AL.: "The WashU-Merck EST project" EMBL SEQUENCE DATABASE, 2 July 1995, HEIDELBERG, FRG, XP002068365 y187a06.r1 Homo sapiens cDNA clone 44938 5'; Accession no. H08241; ---	1-3, 7-11,21
X	L. HILLIER ET AL.: "The "WashU-Merck EST project" EMBL SEQUENCE DATABASE, 26 August 1995, HEIDELBERG, FRG, XP002068366 ym94e01.r1 Homo sapiens cDNA clone 166584 5', Accession no. R88485; ---	1-3, 7-11,21
A	WO 97 07198 A (GENETICS INSTITUT) 27 February 1997 see the whole document ---	1-23
	-/--	



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *Z* document member of the same patent family

Date of the actual completion of the international search

17 June 1998

Date of mailing of the international search report

16. 09. 1998

Name and mailing address of the ISA

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Authorized officer

HORNIG H.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/05311

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 97 04097 A (GENETICS INST) 6 February 1997 see the whole document ---	1-23
A	US 5 536 637 A (JACOBS KENNETH) 16 July 1996 see the whole document ---	1-23
A	JACOBS K ET AL: "A novel method for isolating eukaryotic cDNA clones encoding secreted proteins." KEYSTONE SYMPOSIUM ON DENDRITIC CELLS: ANTIGEN PRESENTING CELLS OF T AND B LYMPHOCYTES, TAOS, NEW MEXICO, USA, MARCH 10-16, 1995. JOURNAL OF CELLULAR BIOCHEMISTRY SUPPLEMENT 0 (21A). 1995. 19. ISSN: 0733-1959, XP002027246 abstract no. C1-207 see abstract ---	1-23
A	WO 90 14432 A (GENETICS INST) 29 November 1990 see the whole document ---	1-23
A	WO 96 17925 A (IMMUNEX CORP) 13 June 1996 see the whole document -----	1-23

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 98/05311

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claim 17 is directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see further information sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

see further information sheet

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1. Claims: (1-23) partially

-An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from SEQ ID no. 11; wherein said polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein encoding the sequence SEQ ID no.125 or the polypeptide encoded by the cDNA sequence included in ATCC Deposit nos: 97923/209071, which is hybridizable to SEQ ID no.11; a recombinant vector comprising said isolated nucleic acid molecule; a method of making a recombinant host cell comprising said isolated nucleic acid molecule; a recombinant host cell comprising said vector; an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence SEQ ID no. 125; an isolated antibody that binds specifically to said isolated polypeptide; a recombinant host cell that expresses said isolated polypeptide; a method of making said polypeptide; a method for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of said polypeptide; a method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject using said polynucleotide and/or polypeptide sequence; a method for identifying a binding partner to said polypeptide; a gene corresponding to the cDNA sequence of SEQ ID no.11; a method for identifying an activity in a biological assay, by using the expression of SEQ ID no. 125;

Inventions 2 to 87. Claims: (12-23) partially

-Idem as subject 1 but limited to gene nos. 2 to 87 respectively cDNA clone sequences HAGFY16/HBMCF37/HFLQB16 to HCED021. (Invention 2 is limited to SEQ ID nos. 12,98,99,126,212 and 213; Invention 3 is limited to SEQ ID nos.13 and 127;; Invention 87 is limited to SEQ ID nos.97 and 211;)

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 98/05311

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9707198 A	27-02-97	US 5707829 A AU 6712396 A AU 6768596 A EP 0839196 A EP 0851875 A WO 9704097 A	13-01-98 18-02-97 12-03-97 06-05-98 08-07-98 06-02-97
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WO 9014432 A	29-11-90	US 5580753 A AT 147436 T AU 637620 B AU 5928990 A CA 2056997 A DE 69029657 D DK 473724 T EP 0473724 A ES 2099096 T JP 4506006 T US 5734037 A US 5414071 A	03-12-96 15-01-97 03-06-93 18-12-90 24-11-90 20-02-97 14-04-97 11-03-92 16-05-97 22-10-92 31-03-98 09-05-95
WO 9617925 A	13-06-96	AU 4639396 A CA 2206488 A FI 972390 A NO 972455 A	26-06-96 13-06-96 05-06-97 06-08-97

